



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 124765

To: Elizabeth McElwain
Location: REM-2A11/2C18
Art Unit: 1638
Thursday, June 24, 2004

Case Serial Number: 10/069772

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

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Search Notes

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GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: June 18, 2004, 17:33:47 ; Search time 46 Seconds
(without alignments)
2585.877 Million cell updates/sec

Title: US-10-069-772-2
Perfect score: 2047
Sequence: 1 MGAGRMSDPSGKILERV.....IYIEPDESEHKGVFWYHKM 377

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacterioph:*
17: sp_archaeop:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2047	100.0	377	10	Q9SCG2	Q9SCG2 calendula o
2	1922	93.9	377	10	Q7XA13	Q7XA13 helianthus
3	1644	80.3	326	10	Q7XA10	Q7XA10 rudbeckia h
4	1607	78.5	326	10	Q7XA08	Q7XA08 helichrysum
5	1596	78.0	326	10	Q7XA09	Q7XA09 dimorphothe
6	1589.5	77.7	374	10	Q65771	Q65771 crepis pala
7	1396.5	68.2	383	10	Q82729	Q82729 borago offi
8	1387.5	67.8	383	10	Q8G2C3	Q8G2C3 vernicia fo
9	1374.5	67.1	383	10	Q9LL17	Q9LL17 sesamum ind
10	1366.5	66.8	383	10	Q8W2F0	Q8W2F0 helianthus
11	1360	66.4	382	10	Q8H2C3	Q8H2C3 persea amer
12	1359.5	66.4	383	10	Q9SP28	Q9SP28 veronia ga
13	1357	66.3	382	10	Q8W2E9	Q8W2E9 helianthus
14	1350.5	66.0	383	10	Q9SP29	Q9SP29 veronia ga
15	1348.5	65.9	383	10	Q41305	Q41305 solanum com
16	1347.5	65.8	387	10	Q84UB7	Q84UB7 punica gran

17	1337.5	65.3	387	10	Q84VT2	Q84VT2 punica gran
18	1336	65.3	382	10	Q24471	Q24471 petroselinu
19	1336	65.3	382	10	Q8H943	Q8H943 spinacia ol
20	1336	65.3	384	10	Q8W2B9	Q8W2B9 gosypium h
21	1335	65.2	379	10	Q65772	Q65772 crepis pala
22	1332.5	65.1	383	10	Q23956	Q23956 gosypium h
23	1323.5	64.7	383	10	Q9AT72	Q9AT72 calendula o
24	1321.5	64.6	383	10	Q8GVC9	Q8GVC9 olea europa
25	1317	64.3	384	10	Q8LPE8	Q8LPE8 brassica ca
26	1312	64.1	384	10	Q9L138	Q9L138 brassica na
27	1296.5	63.3	384	10	Q9ZP12	Q9ZP12 brassica ca
28	1296.5	63.3	385	10	Q23955	Q23955 gosypium h
29	1293.5	63.2	383	10	Q8LPE8	Q8LPE8 arabidopsis
30	1287.5	62.9	379	10	Q9LKK6	Q9LKK6 arachis hyp
31	1286.5	62.8	379	10	Q9LKK5	Q9LKK5 arachis dur
32	1282	62.6	369	10	Q84UB9	Q84UB9 trichosanthe
33	1281.5	62.6	379	10	Q22628	Q22628 arachis hyp
34	1279.5	62.5	379	10	Q94G88	Q94G88 arachis hyp
35	1277.5	62.4	379	10	Q9LKK4	Q9LKK4 arachis ipa
36	1273.5	62.2	387	10	Q41131	Q41131 ricinus com
37	1270.5	62.1	346	10	Q81364	Q81364 prunus arne
38	1260	61.6	382	10	Q7XA14	Q7XA14 hedera heli
39	1245	60.8	384	10	Q81094	Q81094 lequeretella
40	1241.5	60.6	383	10	Q24472	Q24472 petroselinu
41	1235	60.3	382	10	Q9FW85	Q9FW85 petroselinu
42	1232.5	60.2	383	10	Q9FW91	Q9FW91 petroselinu
43	1232	60.2	384	10	Q9FW88	Q9FW88 petroselinu
44	1230.5	60.1	383	10	Q9FW90	Q9FW90 petroselinu
45	1230	60.1	384	10	Q9FW86	Q9FW86 petroselinu

ALIGNMENTS

RESULT 1

ID	Q9SCG2	PRELIMINARY;	PRT;	377 AA.
AC	Q9SCG2;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)			
DE	(8,11)-linoleoyl desaturase (fragment).			
GN	DES8.11.			
OS	Calendula officinalis.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;			
OC	Campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae;			
OC	Calendula.			
OX	NCBI_TaxID=41496;			
RN	[1]			
RP	SEQUENCE FROM N. A.			
RC	TISSUE=Immature seed;			
RX	MEDLINE=200864117; PubMed=10622705;			
RA	Fritzsche K., Horning E., Peitzsch N., Renz A., Feussner I.;			
RT	"Isolation and characterization of a calendic acid producing (8,11)-			
RT	linoleoyl desaturase."			
RL	FEBS Lett. 462:249-253(1999).			
DR	EMBL, AJ245938; CAB64256.1; -			
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.			
DR	InterPro; IPR005804; FA desat. fam.			
DR	Pfam; PF00487; FA desaturase; 1.			
DR	Prodom; PD001081; FA desat. fam; 2.			
FT	NON TER			
FT	SEQUENCE 377 AA; 43615 MW; 1CBP7650955F26BF CRC64;			

Qy	1	MGAGRMSDPSGKILERVVDPPTLSLKKAIPTHCFSRSTYRSYYVHHLLIVAVY	60
Db	1	MGAGRMSDPSGKILERVVDPPTLSLKKAIPTHCFSRSTYRSYYVHHLLIVAVY	60

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QY 61 FYLLANTYIPLIPPLAYLAMPVTFWFCQASILITGLMTVIGHCCHHAFSDYQIDIDIVGFV 120
DB 61 FYLLANTYIPLIPPLAYLAMPVTFWFCQASILITGLMTVIGHCCHHAFSDYQIDIDIVGFV 120
QY 121 LHSALITPFWSKYSRHHNANTNSLDNDVYIPRKSRYKYSGLNNPGRVFTLVER 180
DB 121 LHSALITPFWSKYSRHHNANTNSLDNDVYIPRKSRYKYSGLNNPGRVFTLVER 180
QY 181 LTLGFPPLVLTNISKKYGFRANHPDPMSPIFNDRERVOVLSDGGLAVFAIKLVA 240
DB 181 LTLGFPPLVLTNISKKYGFRANHPDPMSPIFNDRERVOVLSDGGLAVFAIKLVA 240
QY 241 KGAAMVIMMYAIPVLGVSVFPLITLTHHTLSLPHYSTENMWIKGALSTIDRDPGLN 300
DB 241 KGAAMVIMMYAIPVLGVSVFPLITLTHHTLSLPHYSTENMWIKGALSTIDRDPGLN 300
QY 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFKAMTREAECIYI 360
DB 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFKAMTREAECIYI 360
QY 361 EPDEDESEHKGVFWYHKM 377
DB 361 EPDEDESEHKGVFWYHKM 377

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RESULT 2

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QY 07XA13 PRELIMINARY; PRT; 377 AA.
AC 07XA13;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE Delta12-fatty acid acetylase.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteroideae; Heliantheae;
OC Helianthus.
OX NCBI_TaxID=4232;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22674157; PubMed=12787248;
RA Cahoon E.B., Schmitt J.A., Hultman E.A., Minto R.E.;
RT "Fungal responsive fatty acid acetylases occur widely in
  evolutionarily distant plant families.";
RL Plant J. 34:671-683(2003).
DR EMBL; AY166773; AAC38032.1; -.
SQ SEQUENCE 377 AA; 43750 MW; 832C8A129C6C2A55 CRC64;

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Query Match 93.9%; Score 1922; DB 10; Length 377;

Best Local Similarity 91.8%; Pred. No. 3.5e-158;

Matches 346; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

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QY 1 MGAGRMSDPSGKILRVPVDPPTLSDLKKAIPHCERSVRSYVVHDLIVAV 60
DB 1 MGAGRMSDPSGKILRVPVDPPTLSDLKKAIPHCERSVRSYVVHDLIVAV 60
QY 61 FYLLANTYIPLIPPLAYLAMPVTFWFCQASILITGLMTVIGHCCHHAFSDYQIDIDIVGFV 120
DB 61 FYLLANTYIPLIPPLAYLAMPVTFWFCQASILITGLMTVIGHCCHHAFSDYQIDIDIVGFV 120
QY 121 LHSALITPFWSKYSRHHNANTNSLDNDVYIPRKSRYKYSGLNNPGRVFTLVER 180
DB 121 LHSALITPFWSKYSRHHNANTNSLDNDVYIPRKSRYKYSGLNNPGRVFTLVER 180
QY 181 LTLGFPPLVLTNISKKYGFRANHPDPMSPIFNDRERVOVLSDGGLAVFAIKLVA 240
DB 181 LTLGFPPLVLTNISKKYGFRANHPDPMSPIFNDRERVOVLSDGGLAVFAIKLVA 240
QY 241 KGAAMVIMMYAIPVLGVSVFPLITLTHHTLSLPHYSTENMWIKGALSTIDRDPGLN 300
DB 241 KGAAMVIMMYAIPVLGVSVFPLITLTHHTLSLPHYSTENMWIKGALSTIDRDPGLN 300

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QY 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFKAMTREAECIYI 360
DB 301 RVFHDVTHHTVHLHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFKAMTREAECIYI 360
QY 361 EPDEDESEHKGVFWYHKM 377
DB 361 EPDEDESEHKGVFWYHKM 377

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RESULT 3

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QY 07XA10 PRELIMINARY; PRT; 326 AA.
AC 07XA10;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE Delta12-fatty acid acetylase (Fragment).
OS Rubus hirta.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Campanulids; Asterales; Asteroideae; Heliantheae;
OC Rubus hirta.
OX NCBI_TaxID=52299;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=22674157; PubMed=12787248;
RA Cahoon E.B., Schmitt J.A., Hultman E.A., Minto R.E.;
RT "Fungal responsive fatty acid acetylases occur widely in
  evolutionarily distant plant families.";
RL Plant J. 34:671-683(2003).
DR EMBL; AY166776; AAC38035.1; -.
FT NON-TER 1
FT NON-TER 1
SQ SEQUENCE 326 AA; 37861 MW; D3C65BAD9E25783 CRC64;

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Query Match 80.3%; Score 1644; DB 10; Length 326;

Best Local Similarity 92.0%; Pred. No. 3.6e-134;

Matches 300; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

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QY 33 KAIPHCERSVRSYVVHDLIVAVFYLLANTYIPLIPPLAYLAMPVTFWFCQASIL 92
DB 1 KAIPHCERSVRSYVVHDLIVAVFYLLANTYIPLIPPLAYLAMPVTFWFCQASIL 92
QY 93 TGLMTVIGHCCHHAFSDYQIDIDIVGFVLSALITPFWSKYSRHHNANTNSLDNDVY 152
DB 93 TGLMTVIGHCCHHAFSDYQIDIDIVGFVLSALITPFWSKYSRHHNANTNSLDNDVY 152
QY 61 TGLMTVIGHCCHHAFSDYQIDIDIVGFVLSALITPFWSKYSRHHNANTNSLDNDVY 120
DB 61 TGLMTVIGHCCHHAFSDYQIDIDIVGFVLSALITPFWSKYSRHHNANTNSLDNDVY 120
QY 153 IPKRSRYKYSGLNNPGRVFTLVERLTGFPPLVLTNISKKYGFRANHPDPMSPIF 212
DB 153 IPKRSRYKYSGLNNPGRVFTLVERLTGFPPLVLTNISKKYGFRANHPDPMSPIF 212
QY 213 NDRERVOVLSDGGLAVFAIKLVAAGAMVIMMYAIPVLGVSVFPLITLTHHTL 272
DB 213 NDRERVOVLSDGGLAVFAIKLVAAGAMVIMMYAIPVLGVSVFPLITLTHHTL 272
QY 273 SLPHYSTENMWIKGALSTIDRDPGLN RVHDVTHHTVHLHLISYIPHYHAKARDAIK 332
DB 273 SLPHYSTENMWIKGALSTIDRDPGLN RVHDVTHHTVHLHLISYIPHYHAKARDAIK 332
QY 333 PVLGEYKIDRTPIFKAMTREAECI 358
DB 333 PVLGEYKIDRTPIFKAMTREAECI 358
QY 301 PVLGEYKIDRTPIFKAMTREAECI 326
DB 301 PVLGEYKIDRTPIFKAMTREAECI 326

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RESULT 4

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QY 07XA08 PRELIMINARY; PRT; 326 AA.
AC 07XA08;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE Delta12-fatty acid acetylase (Fragment).
OS Helichrysum bracteatum.

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteroideae; Asteroideae; Gnaphalaceae;
 OC Helicrysum.
 NC NCB1_TaxID=220345;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22674157; PubMed=12787248;
 RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;
 RT "Fungal responsive fatty acid acetylases occur widely in
 RT evolutionarily distant plant families."
 RL Plant J. 34:671-683(2003).
 DR EMBL, AY167778; AAC38037.1; -.
 FT NON_TER 1
 FT NON_TER 326
 SQ SEQUENCE 326 AA; 38024 MW; D355816CF4AA2829 CRC64;

Query Match 78.5%; Score 1607; DB 10; Length 326;
 Best Local Similarity 88.0%; Pred. No. 5.7e-131;
 Matches 287; Conservative 18; Mismatches 21; Indels 0; Gaps 0;

QY 32 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPTPLAYLAMPVYFCQASI 91
 DB 1 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPTPLAYLAMPVYFCQASI 60
 QY 92 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 151
 DB 61 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 120
 QY 152 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNSGKRYGRANHPDPSPI 211
 DB 121 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNSGKRYGRANHPDPSPI 180
 QY 212 FNDREYOVLLSDGILAVFAIKLVAAKGAAMVIMYALPVGVSVFVLTITLHHTH 271
 DB 181 FTERERIOVLLSDGILAVFAIKLVAAKGAAMVIMYALPVGVSVFVLTITLHHTH 240
 QY 272 LSLPHYSTENWIKGALSTIDRDFGLNRFHDTVTHVHLHLSYIPHYAKARDAI 331
 DB 241 LSLPHYSTENWIKGALSTIDRDFGLNRFHDTVTHVHLHLSYIPHYAKARDAI 300
 QY 332 KPVIGERYKIDRPIPFAMTREAKEC 357
 DB 301 NPVLGEYKIDRPIPFAMTREAKEC 326

RESULT 5

QY 07XA09 PRELIMINARY; PRT; 326 AA.
 ID 07XA09
 AC 07XA09;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Delta12-fatty acid acetylase (Fragment).
 OS Dimorphochea sinuata (African daisy).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteroideae; Asteroideae; Calenduleae;
 OC Dimorphochea.
 NC NCB1_TaxID=112408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22674157; PubMed=12787248;
 RA Cahoon E.B., Schnurr J.A., Huffman E.A., Minto R.E.;
 RT "Fungal responsive fatty acid acetylases occur widely in
 RT evolutionarily distant plant families."
 RL Plant J. 34:671-683(2003).
 DR EMBL, AY167777; AAC38036.1; -.
 FT NON_TER 1
 FT NON_TER 326
 SQ SEQUENCE 326 AA; 37813 MW; 978706D1444EA3D0 CRC64;
 Query Match 78.0%; Score 1596; DB 10; Length 326;

Best Local Similarity 87.7%; Pred. No. 5.2e-130;
 Matches 286; Conservative 22; Mismatches 18; Indels 0; Gaps 0;

QY 32 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPTPLAYLAMPVYFCQASI 91
 DB 1 KKAIPTECFERSVRSYVVVDLIVAVFYLLANTYPLIPTPLAYLAMPVYFCQASI 60
 QY 92 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 151
 DB 61 LTGLMVGHECGHAFSDYQIDIDVGFVLSALLTPYFSWKYSHRNHANTNSLDNDEV 120
 QY 152 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNSGKRYGRANHPDPSPI 211
 DB 121 YIPRKSQVNTSKYSLNNPGRVFTLVRLTLGFPYLITNSGKRYGRANHPDPSPI 180
 QY 212 FNDREYOVLLSDGILAVFAIKLVAAKGAAMVIMYALPVGVSVFVLTITLHHTH 271
 DB 181 FTERERIOVLLSDGILAVFAIKLVAAKGAAMVIMYALPVGVSVFVLTITLHHTH 240
 QY 272 LSLPHYSTENWIKGALSTIDRDFGLNRFHDTVTHVHLHLSYIPHYAKARDAI 331
 DB 241 LSLPHYSTENWIKGALSTIDRDFGLNRFHDTVTHVHLHLSYIPHYAKARDAI 300
 QY 332 KPVIGERYKIDRPIPFAMTREAKEC 357
 DB 301 NPVLGEYKIDRPIPFAMTREAKEC 326

RESULT 6

QY 065771 PRELIMINARY; PRT; 374 AA.
 ID 065771
 AC 065771;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Delta 12 fatty acid epoxigenase.
 OS Crepis palustrina.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteroideae; Cichorioideae; Cichorioideae; Crepis.
 NC NCB1_TaxID=72611;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98239771; PubMed=9572738;
 RA Lee M., Lemman M., Banas A., Bator M., Singh S., Schweizer M.,
 RA Nilsson R., Liljeborg C., Dahlqvist A., Gummesson P., Sjoedahl S.,
 RA Green A., Skymne S.;
 RT "Identification of Non-Heme Diron Proteins That Catalyze Triple Bond
 RT and Epoxy Group Formation."
 RL Science 280:915-918(1998).
 DR EMBL, Y16283; CAA76156.1; -.
 DR GO:GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro:IPR005804; FA_desat_fam.
 DR Pfam:PF00487; FA_desaturase; 1.
 DR ProDom:PD001081; FA_desat_fam; 2.
 SQ SEQUENCE 374 AA; 43323 MW; 7764DB17BC7F426 CRC64;

Query Match 77.7%; Score 1589.5; DB 10; Length 374;
 Best Local Similarity 75.4%; Pred. No. 2.2e-129;
 Matches 285; Conservative 40; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGAGGRSDSEGNILERVVDP-PETLSDKKAIPTCFERSVRSYVVVDLIVAV 59
 DB 1 MGAGGR--GRTSEKSVVERSVDPVTSLSLEKAIPTCFERSVRSYVVVDLIVAV 58
 QY 60 VFYLLANTYPLIPTPLAYLAMPVYFCQASITGLMVGHECGHAFSDYQIDIDVGF 119
 DB 59 IFYLLANTYPLIPTPLAYLAMPVYFCQASVLTGLMVGHECGHAFSNVTWFDITVGF 118
 QY 120 VHSALLTPYFSWKYSHRNHANTNSLDNDEVYIPRKSQVNTSKYSLNNPGRVFTLVF 179
 DB 119 IHSFLLTPYFSWKYSHRNHANTNSLDNDEVYIPRKSQVNTSKYSLNNPGRVFTLVF 178

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Qy 180 RLTLGFLYLLTNTSGKKYGFANHFDMSPINFDRERVOYLLSDPGLLAVFYAKLIVA 239
Db 179 MFTLGFLYLLTNTSGKKYGFANHFDMSPINFDRERVOYLLSDPGLLAVFYAKLIVA 238
Qy 240 AKGAAMVYNTMAIPVLGVSVFVLITLYLHHTLSLPHYDSEEMWIKALSTDRDFEL 299
Db 239 NKGAAMVACMGVPLGVFTFDTLHHTHQSPPHDSSTEMWIKALSAIDDFEFL 298
Qy 300 NRVFHDVTHHTVHLHLISYIPHYNAKEARDAIKPVLGSYKIDPTPIFKAMYREKECIY 359
Db 299 NSVFDVTHHTVHLHLISYIPHYNAKEARDAIKPVLGSYKIDPTPIFKAMYREKECM 358
Qy 360 IEPDESEHKGVFWYTHK 377
Db 359 IEP--DSLKGWYVYHKL 374

RESULT 7
ID 082729 PRELIMINARY; PRT; 383 AA.
AC 082729;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Delta-12 fatty acid desaturase.
OS Borago officinalis (Bourrache) (Borage).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Boraginaceae; Borago.
CX NCBI_TaxID=13363;
RN [1]
RP SEQUENCE FROM N.A.
RA Sayanova O., Shewry P.R., Napier J.A.;
RT "Fatty acid desaturases from borage.";
RL Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF074324; AAC31696.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR ProDom; PD001081; FA desat. fam; 2.
SQ SEQUENCE 383 AA; 44048 MW; 13DF2BD076E7B5EF CRC64;

Query Match 68.2%; Score 1396.5; DB 10; Length 383;
Best Local Similarity 63.9%; Pred. No. 1.2e-112;
Matches 242; Conservative 62; Mismatches 70; Indels 5; Gaps 2;

Qy 1 MGAGGRMSDSEBKG---NILERPVDP-PPTLSDLKKAIPHCERBVRVSSYYVNDL 55
Db 1 MGAGGRMSVPPPKKESBVKRVPHSKRPPTLQKKAIIPHCFORSVLRSFSYVVDL 60
Qy 56 IVAVFFYIANTYPLIPPTPLAYLAMPYWFQASILGLWVIGHGCHHAFSYQYLLD 115
Db 61 VIALLFFYASRYTLQHPPLSYVAMPYWCQSVLIGVWVIAHEGCHHAFSYQYLLD 120
Qy 116 IVGFVLSALLTPYFSWKYSHRNHNANTSLDNDESVYIPKRSKVYKISKLINPGRVF 175
Db 121 TVGLLHLSALLVPYFSWKYSHRRHSNTGSLERDEVFVPKKSIGISMSSEYLNPPGRVL 180
Qy 176 TLVPRLTGFPFLYLNTISGKKYGFANHFDMSPINFDRERVOYLLSDPGLLAVFYAK 235
Db 181 VLLVOLTGLWPLVLMFNVSGRPYDRFACHYDPGPIYDRERTEIYISDAGVAVMYGLY 240
Qy 236 LLVAKGAAMVYNTMAIPVLGVSVFVLITLYLHHTLSLPHYDSEEMWIKALSTDRD 295
Db 241 RLVAAGVAVMYCYGVPLLVNGLVLITLYLQHPPLSYVAMPYWCQSVLIGVWVIAHEGCHHAFSYQYLLD 300
Qy 359 FGLNRFVHDVTHHTVHLHLISYIPHYNAKEARDAIKPVLGSYKIDPTPIFKAMYREAK 355
Db 301 YGFLNKFVHLNITDTHVAHLFTSTMPHYAMKATKAIKPILGDYQCDRTPIVFKAMYREVK 360
Qy 356 ECIYIEPDESEHKGVFWY 374
Db 361 ECIYVEADGDKNGVFWY 379
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RESULT 8
ID 08GZC3 PRELIMINARY; PRT; 383 AA.
AC 08GZC3;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Delta 12 oleic acid desaturase FAD2.
OS Vernicia fordii (Tung) (Aleurites fordii).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Crotonoideae; Aleuritiaceae;
OC Vernicia.
CX NCBI_TaxID=73154;
RN [1]
RP SEQUENCE FROM N.A.
RA PubMed=12481086;
RX Dyer J.M., Chapital D.C., Kuan J.-C.W., Mullen R.T., Turner C.,
RA McKeon T.A., Pepperman A.B.;
RT "Molecular Analysis of a Bifunctional Fatty Acid Conjugase/Desaturase
RT from Tung. Implications for the Evolution of Plant Fatty Acid
RT Diversity.";
RL Plant Physiol. 130:2027-2038(2002).
DR EMBL; AF525534; AAN87573.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA desat. fam.
DR Pfam; PF00487; FA desaturase; 1.
DR ProDom; PD001081; FA desat. fam; 2.
SQ SEQUENCE 383 AA; 44152 MW; F5D06112C31B3BC CRC64;

Query Match 67.8%; Score 1387.5; DB 10; Length 383;
Best Local Similarity 63.3%; Pred. No. 7.2e-112;
Matches 241; Conservative 61; Mismatches 74; Indels 5; Gaps 2;

Qy 1 MGAGGRMSDSEBKG---NILERPVDP-PPTLSDLKKAIPHCERBVRVSSYYVNDL 55
Db 1 MGAGGRMSVPPPKKESBVKRVPHSKRPPTLQKKAIIPHCFORSVLRSFSYVVDL 60
Qy 56 IVAVFFYIANTYPLIPPTPLAYLAMPYWFQASILGLWVIGHGCHHAFSYQYLLD 115
Db 61 TVALFTYIANTYHLPLPPLSYVAMPYWMALQCVLTGVWVIAHEGCHHAFSYQYLLD 120
Qy 116 IVGFVLSALLTPYFSWKYSHRNHNANTSLDNDESVYIPKRSKVYKISKLINPGRVF 175
Db 121 IVGLVHSCLLVPPYFSWKYSHRRHSNTASLERDEVFVPKKSISRWFSKYLINPPGRVF 180
Qy 176 TLVPRLTGFPFLYLNTISGKKYGFANHFDMSPINFDRERVOYLLSDPGLLAVFYAK 235
Db 181 TLTTTLTGWPLVLYLAFNVSGRPYDRFACHYDPGPIYDRERTEIYISDAGVAVMYGLY 240
Qy 236 LLVAKGAAMVYNTMAIPVLGVSVFVLITLYLHHTLSLPHYDSEEMWIKALSTDRD 295
Db 241 RLAAKGLAWICYGVPLLVNGLVITLYLQHPPLSYVAMPYWCQSVLIGVWVIAHEGCHHAFSYQYLLD 300
Qy 296 FGLNRFVHDVTHHTVHLHLISYIPHYNAKEARDAIKPVLGSYKIDPTPIFKAMYREAK 355
Db 301 YGILNKFVHLNITDTHVAHLFTSTMPHYAMKATKAIKPILGEYIQFDSCTPIVFKAMYREAK 360
Qy 356 ECIYIEPDESEHKGVFWYTHK 376
Db 361 ECIYVEADGDESGKVWYWNK 381

RESULT 9
ID 09LL17 PRELIMINARY; PRT; 383 AA.
AC 09LL17;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Omega-6 fatty acid desaturase.
```

GN FAD2.
 OS Sesamum indicum (Oriental sesame) (gingelly).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Pedaliaceae; Sesamum.
 NCBI_TaxID=4182;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jin U.H., Chung C.H.;
 RT "Molecular characterization of a omega-6 fatty acid desaturase cDNA of
 sesame (Sesamum indicum L.) seeds.";
 RL Submitted (OCT-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF124466; AAF80560.1; -;
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 SQ SEQUENCE 383 AA; 44265 MW; F324272C3D57BBF5 CRC64;

Query Match 67.1%; Score 1374.5; DB 10; Length 383;
 Best Local Similarity 62.8%; Pred. No. 9.6e-11;
 Matches 238; Conservative 60; Mismatches 76; Indels 5; Gaps 2;

QY 1 MGAGGRMSDPS-----EGKILIERVP-VDPPTLSLTKKALPTHCERSVIRSSYYVHD 55
 DB 1 MGAGGRMSDPTTKDEQKNPLQRPVYAKPPTGLDICKALIPHCERSVIRSSYYVYDL 60
 QY 56 IVAVVFFYLYANTYIPLIPTLAYLAMPVYVFCQASILTGLMWIGHEGCHHAFSDYQDLD 115
 DB 61 VIVVLLYIATSYTHLPSPCYLAMPYMAVQGCVCGLVIAHCGHAFSDYQDLD 120
 QY 116 IVGFVLSALLTPYPSWKYSHRNHNANTSLDNDEVYIPKRSKVITYSKLNNPPGRVF 175
 DB 121 TVGILHSALLVYPSWKYSHRRHNSNTGSLERDEVFVFKPSRVSYSKYLNNDLGRVI 180
 QY 176 TLVFRLLTGFLYLTLNLSGKKYGRFANHPDPSPIFNDREYOVLLSDFGLLAVFYAIK 235
 DB 181 TLVVTLLTGWPLYLFLFNVSGRPRYAFCHPDYGYVDRRLQIFISDAGIIVAVCTLY 240
 QY 236 LIVAAGAAWVINYVYIPVLGVSVFVLYITLHHTHLSLPHYDSEMMWIKALSTIDR 295
 DB 241 RVALVKGILAMLCYGVPLLVNGELVLTFLQHTHPSLPYDSEMMWIKALATVDRD 300
 QY 296 FGLNRFVHDVTHVTLHLISYIPHYAKKADAIKPVLGEEYKIDRTPIFKAMVREAK 355
 DB 301 YGVANKYFHNITDHYVTHLFTSMTHYAMETAKIKRILQYQFPGTPIYKAMREAK 360
 QY 356 ECIYIEPDESEHKGVFWY 374
 DB 361 ECIYIEPDESTPDKGFWY 379

RESULT 10
 Q8W2F0 . PRELIMINARY; PRT; 383 AA.
 AC Q8W2F0;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Delta-12 oleate desaturase (EC 1.3.1.35).
 GN FAD2-2.
 OS Helianthus annuus (Common sunflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Asterales; Asteroideae; Helianthaceae;
 OC Helianthus.
 NCBI_TaxID=4232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=HA89;
 RA Martinez-Rivas J.M., Sperling P., Lueths W., Heinz E.;
 RT "Spatial and temporal regulation of three different microsomal oleate
 desaturase genes (FAD2) from normal-type and high-oleic varieties of

RT sunflower (Helianthus annuus L.).";
 RL Mol. Breed. 8:159-168 (2001).
 DR EMBL; AF251843; AAL68982.1; -;
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 KW Oxidoreductase.
 SQ SEQUENCE 383 AA; 43991 MW; 7E143AB4E423BAF CRC64;

Query Match 66.8%; Score 1366.5; DB 10; Length 383;
 Best Local Similarity 63.4%; Pred. No. 4.7e-110;
 Matches 241; Conservative 60; Mismatches 72; Indels 7; Gaps 3;

QY 1 MGAGGRMSDPSGK-----NILERVPVD-PPFTLSLTKKALPTHCERSVIRSSYYVHD 54
 DB 1 MGAGGRMSNPVNGEKKRPDPLQRPVYQKPPFTGVDYKALIPHCERNVIRSSYYVVD 60
 QY 55 LIVAVFFYLYANTYIPLIPTLAYLAMPVYVFCQASILTGLMWIGHEGCHHAFSDYQDLD 114
 DB 61 LTIASIFYLYANNYIALPLSPLAYVAMPVYVFCQCVLTGVVIAHCGHAFSDYQDLD 120
 QY 115 DIVGFVLSALLTPYPSWKYSHRNHNANTSLDNDEVYIPKRSKVITYSKLNNPPGRV 174
 DB 121 DTGVLVHSALLVYPSWKYSHRRHNSNTGSLERDEVFVFKPSRVSYSKYLNNDLGRVI 180
 QY 175 FTLVFRLLTGFLYLTLNLSGKKYGRFANHPDPSPIFNDREYOVLLSDFGLLAVFYAI 234
 DB 181 LTLVTLTMGFLYLTLNLSGKKYGRFANHPDPSPIFNDREYOVLLSDFGLLAVFYAI 240
 QY 235 KLVAAAGAAWVINYVYIPVLGVSVFVLYITLHHTHLSLPHYDSEMMWIKALSTIDR 294
 DB 241 FRVAMTGLTFLVLTMYAGPLLVNGFLVLTFLQHTHPSLPYDSEMMWIKALATIDR 300
 QY 295 DFGFLNRFVHDVTHVTLHLISYIPHYAKKADAIKPVLGEEYKIDRTPIFKAMVREAK 354
 DB 301 DYGLNKKYFHNITDHYVTHLFTSMTHYAMETAKIKRILQYQFPGTPIYKAMRET 360
 QY 355 KECIYIEPDESEHKGVFWY 374
 DB 361 KECIYVDDEEVK-DGVYVY 379

RESULT 11
 Q8H2C3 . PRELIMINARY; PRT; 382 AA.
 AC Q8H2C3;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Delta-12 fatty acid desaturase.
 OS Persea americana (Avocado).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; magnoliids; Laurales; Lauraceae; Persea.
 NCBI_TaxID=3435;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. Puerte;
 RA Wang X., Lichter A., Prusky D.;
 RT "Isolation of a cDNA Clone Encoding an Avocado (Persea americana)
 RT Delta-12 Fatty Acid Desaturase.";
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY057406; AAL23676.1; -;
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 SQ SEQUENCE 382 AA; 43492 MW; 8323B053D86B3B8 CRC64;

Query Match 66.4%; Score 1360; DB 10; Length 382;
 Best Local Similarity 63.8%; Pred. No. 1.7e-109;
 Matches 241; Conservative 56; Mismatches 77; Indels 4; Gaps 3;

```

Qy 1 MGAGRMS--DPSEGNILERVV-DPPFTLSDLKKAIPTHCFERSVIRSSYYVVDL 57
Db 1 MGAGRMSVTPSVKXVDLERVPKAPPEFEGQLKKAIPKCFNRSIRSMSYVSDITI 60
Qy 58 AVFVYLYANTYPIPIPTPLAY-LAMPVYMFQASILTGLVIGHGCHHAASDYQI 116
Db 61 SSILYLYANTYPIPLPSPLSYFIAMPLWQGCVLTVWVIAHCGHHAASDYQI 120
Qy 117 VGFVLSALITPYFSWKYSHRNHNANTSLDNDEYVIPKRSKYIKYSLKNPPGRVFT 176
Db 121 VGLIHSALVLPYFSWKYSHRRHSNTGSLTSDEVFVKPSQMWPFKYLNNPGRILT 180
Qy 177 LVFRLTLPPLYLTLNIGSKYGRFANFPDMSPIFNDREYQVILSPFGLAVFYAIK 236
Db 181 LAFSLTLCMPPLAYLANVSGRKYDRFACHDPYGPYSRERLQILISDLGVLAVYCGLFR 240
Qy 237 LVAAGAAMVINMYAIPVLGVSFVFLITYLHHTHLSLPHYDSTEMNMIKALSTIDRF 296
Db 241 LVAACGLMVCVGVGFLVNLVNGFLVLTFLQHTHPSLPHYDSEMDWLKALATVDYDY 300
Qy 297 GFANRVPFDVTHVTHLHLSYIPHYHAKAADAIPVLGEYKIDRTPIFKAMRYAKE 356
Db 301 GVLMNVFNITDTYHAHLFSTMPHYHAMEATKARPILGDIYHSDGTPVYKAMRYAKE 360
Qy 357 CTYIEPDESEHKGVFWY 374
Db 361 CVYVEPDESGVKGVFWY 378

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RESULT 12

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ID 09SP28 PRELIMINARY; PRT; 383 AA.
AC 09SP28;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2002 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Delta-12 oleate desaturase (EC 1.3.1.35).
GN PAD2-2.
OS Vernonia galamensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Cichorioideae; Vernoniaeae;
OC Vernonia.
OC NCBI_TaxID=83960;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10759541;
RA Hage T.G., Seither C., Hildebrand D.;
RT "Isolation of two cDNAs from Vernonia galamensis (Cass.) Less.
RT encoding a microsomal oleate desaturase (PAD2) (accession nos.
RT AF188263 and AF188264) and functional expression in Saccharomyces
RT cerevisiae (PCR00-035).";
RL Plant Physiol. 122:1457-1457(2000).
DR EMBL, AF188264; AAF04094.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA_desat. fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
KW Oxidoreductase.
SQ SEQUENCE 383 AA; 44330 MW; 10D954DC084F7D41 CRC64;

```

Query Match 66.4%; Score 1359.5; DB 10; Length 383;
 Best Local Similarity 62.9%; Pred. No. 1.9e-109;
 Matches 239; Conservative 61; Mismatches 73; Indels 7; Gaps 3;

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Qy 1 MGAGRMSDPSEBK-----NILERVPD-PPTTSLDKKAIPTHCFERSVIRSSYYVVD 54
Db 1 MGAGRMSNPPDEKKAHEALQRPYOKPPTVDDIKKAIPPHCFNRSVIRSSYYVVD 60
Qy 55 LIVAVFYLYANTYPIPIPTPLAYLAMPVYMFQASILTGLVIGHGCHHAASDYQI 114
Db 61 LTISIFYLYANTYPIPLPSPLSYFIAMPLWQGCVLTVWVIAHCGHHAASDYQI 120

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Qy 115 DIVEVLSALITPYFSWKYSHRNHNANTSLDNDEYVIPKRSKYIKYSLKNPPGRV 174
Db 121 DTVGILHSALVLPYFSWKYSHRRHSNTGSLTSEDEVFVPLKKNVSTARYLNNPGR 180
Qy 175 FTVFRLTLPPLYLTLNIGSKYGRFANFPDMSPIFNDREYQVILSPFGLAVFYAI 234
Db 181 LTLVTLTGLMPLIMFVNSGRYDRFACHDPSPISNERRQIFISDGLAVFYGL 240
Qy 235 KLVAAGAAMVINMYAIPVLGVSFVFLITYLHHTHLSLPHYDSTEMNMIKALSTIDR 294
Db 241 FKLMAKGLTVLWLCYGGSPLLVNGFLVLTFLQHTHPSLPHYDTTENDMIRGALATIDR 300
Qy 295 DFGELNRPFDVTHVTHLHLSYIPHYHAKAADAIPVLGEYKIDRTPIFKAMRYEA 354
Db 301 DYGLNKVFNITDTYHAHLFSTMPHYHAMEATKARPILGEYQPDGTSIFAMRYET 360
Qy 355 KECYIEPDESEHKGVFWY 374
Db 361 KECYIYDKEVVK-DGVYVY 379

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RESULT 13

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ID 08W2E9 PRELIMINARY; PRT; 382 AA.
AC 08W2E9;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Delta-12 oleate desaturase (EC 1.3.1.35).
GN PAD2-3.
OS Helianthus annuus (Common sunflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae;
OC Helianthus.
OC NCBI_TaxID=4232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HA89;
RA Martinez-Rives J.M., Sperling P., Luehs W., Heinz B.;
RT "Spatial and temporal regulation of three different microsomal oleate
RT desaturase genes (PAD2) from normal-type and high-oleic varieties of
RT sunflower (Helianthus annuus L.).";
RL Mol. Breed. 8:159-168(2001).
DR EMBL; AF251844; AAL68983.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro; IPR005804; FA_desat. fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 2.
KW Oxidoreductase.
SQ SEQUENCE 382 AA; 44004 MW; 59B524A3593D624F CRC64;

```

Query Match 66.3%; Score 1357; DB 10; Length 382;
 Best Local Similarity 63.1%; Pred. No. 3.1e-109;
 Matches 239; Conservative 59; Mismatches 75; Indels 6; Gaps 3;

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Qy 1 MGAGRMSDPSEBK-----BGNILERV-VVDPPFTTSLDKKAIPTHCFERSVIRSSYYVVD 55
Db 1 MGAGRMSNPPDEKKAHEALQRPYOKPPTVDDIKKAIPPHCFNRSVIRSSYYVVD 60
Qy 56 IVAVFYLYANTYPIPIPTPLAYLAMPVYMFQASILTGLVIGHGCHHAASDYQI 115
Db 61 TIASIFYLYANTYPIPLPSPLSYFIAMPLWQGCVLTVWVIAHCGHHAASDYQI 120
Qy 116 IVGFVLSALITPYFSWKYSHRNHNANTSLDNDEYVIPKRSKYIKYSLKNPPGRVFT 175
Db 121 TVGILHSALVLPYFSWKYSHRRHSNTGSLTSEDEVFVPLKKNVSTARYLNNPGRILT 180
Qy 176 TLVFRLTLPPLYLTLNIGSKYGRFANFPDMSPIFNDREYQVILSPFGLAVFYAIK 235
Db 181 TLVTLTGLMPLIMFVNSGRYDRFACHDPSPISNERRQIFISDGLAVFYILF 240
Qy 236 LVAAGAAMVINMYAIPVLGVSFVFLITYLHHTHLSLPHYDSTEMNMIKALSTIDR 295

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Db      241 RLASTKGLVWVLTWYGCPLVNGFLVITFLQHTPSLPHYDSTEMDMKALATVDRD 300
Qy      296 FGLNRVHDVTHTHVHLHLSYIPHYAKKARDAIKPVLGKYYKIDRTPIFKAMYREAK 355
Db      301 YGLINKVPHNITDTHVHHLFSTMPHYAMKATKAIKPLGQYQFDGTSIFKAMYREBK 360
Qy      356 ECIYVPEDESEHKGVFWY 374
Db      361 ECIYVDKEDVK-DGVYMY 378

RESULT 14
QSP29  ID  QSP29  PRELIMINARY;  PRT;  383 AA.
AC      QSP29:
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB      Delta-12 oleate desaturase (EC 1.3.1.35).
GN      FAD2-1.
OS      Vernonia galamensis.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      Campanulids; Asterales; Asterales; Cichorioideae; Vernoniales;
OC      Vernonia.
OX      NCBI_TaxID=83960;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      PubMed=10759541;
RA      Hage T.G., Selcher C., Hildebrand D.;
RT      "Isolation of two cDNAs from Vernonia galamensis (Case.) Less.
RT      encoding a microsomal oleate desaturase (FAD2) (accession nos.
RT      AF188263 and AF188264) and functional expression in Saccharomyces
RT      cerevisiae (FER00-035).";
RL      Plant Physiol. 122:1457-1457(2000).
DB      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      InterPro; IPR005804; F:desat. fam.
DR      Pfam; PF00487; FA_desaturase; 1.
DR      Prodom; PD001081; FA_desat_fam; 2.
KW      Oxidoreductase.
SQ      SEQUENCE 383 AA; 44268 MW; C16B93B7F94DA80 CRC64;

Query Match      66.0%; Score 1350.5; DB 10; Length 383;
Best Local Similarity 62.4%; Pred. No. 1.2e-108;
Matches 237; Conservative 62; Mismatches 74; Indels 7; Gaps 3;

Qy      1  MGAGRMSDPSGK----NILERVPVD-PPTLSDLKKAIPTHCFERSVIRSSYYVND 54
Db      1  MGAGGRMSNPPEDEKKAHEALQRPVQKPPPTVDIKKAIIPKCLANSVSKSFYYVND 60
Qy      55 LIVAVFYLYANTYIPLIPTPLAYLAMPVYVFCQASILTGLWVIGHECGHAFSDYQLID 114
Db      61 LTISIFYYLYLTNTYIPLPHPLSYVAMPVYVFCQCVLTGLWVIAHECGHAFSDYQWMD 120
Qy      115 DIVGVVLSALLTPYFSWKYSHRNHNANTSLDNDEVYIPKRSKYKYSKLLNPPGRV 174
Db      121 DTVGILHSALLVPRFSWKYSHRRHSNTGSLERDEVFVPRKSKSVRSTARTLNPPGRV 180
Qy      175 FTLVRLTIGFPLYLITNISGKKYGRFANHPDPMSPIFNDRERVQVLSDFGLAVFYAI 234
Db      181 LTLVLTLTGLWPLVMPVSGRYDRFACHPDNPSPISSNERRAQIFISDGLIAVFGYGL 240
Qy      235 KLVAAKGAAMVINYAIPLVGVSVFVLITYLHHTHLSLPHYDSTENMWIKALSTIDR 294
Db      241 FKLMAKGLTAVLCMYGGRPLLVNGLVLTITFLQHTPSLPHYDTTMDWMLGALATIDR 300
Qy      295 DGFILNRVHDVTHTHVHLHLSYIPHYAKKARDAIKPVLGKYYKIDRTPIFKAMYREA 354
Db      301 DYGLINKVPHNITDTHVHHLFSTMPHYAMKATKAIKPLGQYQFDGTSIFKAMYRET 360
Qy      355 ECIYVPEDESEHKGVFWY 374

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Db      361 ECIYVDKEDVK-DGVYMY 379

RESULT 15
Q41305 ID  Q41305  PRELIMINARY;  PRT;  383 AA.
AC      Q41305:
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB      D12 oleate desaturase.
OS      Solanum commersonii (Commerson's wild potato).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC      Lamiales; Solanales; Solanales; Solanaceae; Solanum.
OX      NCBI_TaxID=4109;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Consiglio F., Amatruda M.R., Leone A., Costa A., Grillo S.;
RT      Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RL      EMBL; X92847; CAA63432.1; -.
DR      PIR; T10480; T10480.
DR      GO; GO:0016491; F:oxidoreductase activity; IEA.
DR      InterPro; IPR005804; FA_desat. fam.
DR      Pfam; PF00487; FA_desaturase; 1.
DR      Prodom; PD001081; FA_desat_fam; 2.
SQ      SEQUENCE 383 AA; 44101 MW; F17CFAE0C0CC5595 CRC64;

Query Match      65.9%; Score 1348.5; DB 10; Length 383;
Best Local Similarity 61.2%; Pred. No. 1.7e-108;
Matches 232; Conservative 65; Mismatches 77; Indels 5; Gaps 2;

Qy      1  MGAGRMSDPS----EGKILERVVD-PPTLSDLKKAIPTHCFERSVIRSSYYVNDL 55
Db      1  MGAGGRMSAPNGETEVKNPLQKVPKPPPTVDIKKAIIPKCFGRSLRISFSYYVNDL 60
Qy      56 IVAVFYLYANTYIPLIPTPLAYLAMPVYVFCQASILTGLWVIGHECGHAFSDYQLID 115
Db      61 ILVSIWVYANTYIHLDPICYITAMPYVLCQGCVCVGIWVNAHECGHAFSDYQWMD 120
Qy      116 IVGVVLSALLTPYFSWKYSHRNHNANTSLDNDEVYIPKRSKYKYSKLLNPPGRV 175
Db      121 TVGILHSALLVPRFSWKYSHRRHSNTGSLERDEVFVPRKSKSVRSTARTLNPPGRV 180
Qy      176 TLVRLTIGFPLYLITNISGKKYGRFANHPDPMSPIFNDRERVQVLSDFGLAVFYAIK 235
Db      181 SLITLTGLWPLYLAFVNSGRPYDRFACHPDYGPBYINNRRLQIFISDAGVLCYLYL 240
Qy      236 KLVAAKGAAMVINYAIPLVGVSVFVLITYLHHTHLSLPHYDSTENMWIKALSTIDR 295
Db      241 RIALVKGIAAMVINYAIPLVGVSVFVLITYLHHTHLSLPHYDSTENMWIKALSTICRD 300
Qy      296 FGLNRVHDVTHTHVHLHLSYIPHYAKKARDAIKPVLGKYYKIDRTPIFKAMYREAK 355
Db      301 YGLINKVPHNITDTHVHHLFSTMPHYAMKATKAIKPLGQYQFDGTSIFKAMYREAK 360
Qy      356 ECIYVPEDESEHKGVFWY 374
Db      361 ECIYVDKEDSEKGVFWY 379

Search completed: June 18, 2004, 17:37:54
Job time : 48 secs

```


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OM protein - protein search, using sw model

Run on: June 18, 2004, 17:29:57 ; Search time 59 Seconds
(without alignments)
1805.431 Million cell updates/sec

Title: US-10-069-772-2

Perfect score: 2047
Sequence: 1 MGAGGRMSDSEGNILERV.....IYIPDEDESEHKGVFWYHKM 377

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04.*

1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2047	100.0	377	4	AAB70946 C. offic
2	1636	79.9	375	2	AAW36793 Crepis al
3	1598.5	78.1	374	2	AAW79743 Crepis sp
4	1589.5	77.7	374	2	AAW79742 Crepis pa
5	1578.5	77.1	384	2	AAW83354 Vernonia
6	1396.5	68.2	383	2	AAW72825 Borago of
7	1332.5	65.1	383	4	AAE13421 Cotton ol
8	1331.5	65.0	387	7	AAE13427 Soybean m
9	1325.5	64.8	383	5	AAE13427 Soybean m
10	1323.5	64.7	383	5	AAE13427 Soybean m
11	1318	64.4	384	2	AAW86153 Protein B
12	1318	64.4	384	2	AAW94053 Protein B
13	1318	64.4	384	3	AAW70114 Brassica
14	1317	64.3	384	2	AAW27329 B. napus
15	1317	64.3	384	5	ABW80028 Rape m/cr
16	1313	64.1	384	2	AAW27330 B. napus
17	1312	64.1	384	2	AAW24997 Microsoma
18	1312	64.1	384	2	AAW94049 Amino aci
19	1312	64.1	384	3	AAW94457 Protein e
20	1312	64.1	384	5	ABG71327 Brassica
21	1311	64.1	384	8	AAW85752 Microsoma
22	1311	64.0	384	2	AAW86155 Protein B
23	1311	64.0	384	2	AAW94054 Amino aci
24	1311	64.0	384	2	AAW94051 Amino aci
25	1311	64.0	384	3	AAW70115 B. napus

26	1310	64.0	384	2	AAW94055 Amino aci
27	1310	64.0	384	3	AAW70116 B. napus
28	1308	63.9	384	5	ABG71326 Brassica
29	1307	63.8	384	2	AAW86154 Protein s
30	1307	63.8	384	2	AAW94052 Amino aci
31	1305	63.8	384	2	AAW24998 Microsoma
32	1305	63.8	384	2	AAW94050 Amino aci
33	1302.5	63.6	383	3	AAW1517 Arabidops
34	1301	63.6	384	2	AAW27331 B. napus
35	1300.5	63.5	383	2	AAW53697 Sequence
36	1300.5	63.5	383	3	AAW50097 Arabidops
37	1300.5	63.5	383	3	AAW70270 A. thalia
38	1300.5	63.5	383	3	AAW22053 Arabidops
39	1300.5	63.5	383	4	AAE13428 Arabidops
40	1300.5	63.5	383	5	ABW80027 Creas mic
41	1299	63.5	384	2	AAW24995 Microsoma
42	1299	63.5	384	2	AAW94047 Amino aci
43	1299	63.5	384	2	AAW94455 Protein e
44	1299	63.5	384	5	ABG71325 Brassica
45	1299	63.5	384	8	ADW85748 Microsoma

ALIGNMENTS

RESULT 1
AAB70946
ID AAB70946 standard; protein; 377 AA.

AC AAB70946;
DT 22-AUG-2001 (first entry)
XX C. officinalis calendulic acid desaturase.
XX
DE C. officinalis calendulic acid desaturase.
XX
KM Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;
KM triglyceride; transgenic plant.
XX
OS Calendula officinalis.
XX
PN DE19941609-A1.
XX
PD 08-MAR-2001.
XX
PF 01-SEP-1999; 99DE-01041609.
XX
PR 01-SEP-1999; 99DE-01041609.
XX
XX (IPBP-) IPB INST PFLANZENBIOCHEMIE.
XX Feussner I, Hornung E, Fritzsche K, Peitzsch N, Renz A;
PI WPI; 2001-283028/30.
XX N-PSDB; AAF86311.
XX
PT New nucleic acid sequence encoding Calendula officinalis calendulic acid
PT desaturase, useful for e.g. producing transgenic plants having oil with
PT an increased unsaturated fatty acid content.
XX
XX
PS Claim 1c; Page 15-16; 22pp; German.
XX
XX This invention describes a novel isolated nucleic acid sequence (I)
XX encoding a Calendula officinalis calendulic acid desaturase polypeptide.
XX The invention also describes (II) a process for producing unsaturated
XX fatty acids, comprising introducing at least one copy of (I) or (II) into
XX an oil-producing organism, growing the organism, isolating oil from the
XX organism and releasing fatty acids from the oil; (2) a process for
XX producing triglycerides with an increased unsaturated fatty acid content,
XX comprising introducing at least one copy of (I) or (II) into an oil-
XX producing organism, growing the organism and isolating oil from the
XX organism; (3) a process for producing saturated fatty acids, comprising
XX introducing at least one nonfunctional copy of (I) or (II) into an oil-
XX producing organism, growing the organism, isolating oil from the organism

CC and releasing fatty acids from the oil; (4) a process for producing
 CC triglycerides with an increased saturated fatty acid content, comprising
 CC introducing at least one nonfunctional copy of (i) or (ii) into an oil-
 CC producing organism, growing the organism and isolating oil from the
 CC organism; (5) an enzyme capable of converting a diunsaturated fatty acid
 CC of to a triunsaturated fatty acid. Transgenic organisms (especially
 CC plants) containing one or more copies of (i) are useful for producing
 CC oils with an increased unsaturated fatty acid content. Transgenic
 CC organisms (especially plants) containing one or more nonfunctional copies
 CC of (i) are useful for producing oils with an increased saturated fatty
 CC acid content. (i) and fragments of (i) are also useful for isolating
 CC genomic sequences by homology screening. This sequence represents the
 CC candellic acid desaturase described in the method of the invention
 CC
 XX

Sequence 377 AA;

Query Match 100.0%; Score 2047; DB 4; Length 377;
 Best Local Similarity 100.0%; Pred. No. 1.3e-200;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAGGRMSDPSEGNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVHDLIVAVY 60
 DB 1 MGAGGRMSDPSEGNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVHDLIVAVY 60
 QY 61 FYLLANTYIPLIPPLATLAMPVYVFCQASITGLMTVGHCGHAFSDYQOLIDIVGFV 120
 DB 61 FYLLANTYIPLIPPLATLAMPVYVFCQASITGLMTVGHCGHAFSDYQOLIDIVGFV 120
 QY 121 LHSALTPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSLNNPGRVFTLVER 180
 DB 121 LHSALTPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSLNNPGRVFTLVER 180
 QY 181 LTLGFPPLVLTNISKYGRFANHPDPMSPFNDREVOVLLSDGLLAVFYAIKLVA 240
 DB 181 LTLGFPPLVLTNISKYGRFANHPDPMSPFNDREVOVLLSDGLLAVFYAIKLVA 240
 QY 241 KGAANVIMYAIPLVGVSVFVLITYLHHTHLSLPHYSTENWTKALSTIDRDFGLN 300
 DB 241 KGAANVIMYAIPLVGVSVFVLITYLHHTHLSLPHYSTENWTKALSTIDRDFGLN 300
 QY 301 RVFHDVTHVLAHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 360
 DB 301 RVFHDVTHVLAHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 360
 QY 361 EPDEDESEKGVFWYHKM 377
 DB 361 EPDEDESEKGVFWYHKM 377

RESULT 2

AAW36793 standard; protein; 375 AA.

XX AC AAW36793;
 XX DT 25-MAR-2003 (revised)
 XX DT 20-APR-1998 (first entry)
 XX DE Crepis alpina delta 12 acetylase.
 XX KM Crepis alpina delta 12 acetylase; plant; yeast; acetylenic compound;
 XX KW fatty acid; coating; plastic; lubricant; oilseed.
 XX OS Crepis alpina.
 XX PN .MO9737033-A1.
 XX PD 09-OCT-1997.
 XX PF 14-FEB-1997; 97WO-SE000247.
 XX PR 29-MAR-1996; 96SE-00001236.
 XX

PA (BAFO/) BAFOR M.
 PA (BANVA/) BANAS A.
 PA (DAHL/) DAHLQVIST A.
 PA (GUMM/) GUMMESON P.
 PA (LEEM/) LEE M.
 PA (LENNM/) LENNAN M.
 PA (SJOE/) SJOEDAHN S.
 PA (STYM/) STYME S.
 PI Bator M, Banas A, Dahlqvist A, Gummeson P, Lee M, Lenman M;
 PI Sjoedahl S, Styne S;
 XX WPI, 1997-503117/46.
 DR N-PSDB; AAT95688.
 XX

Claim 7, Page 21, 33pp; English.

This is the Crepis alpina delta 12 acetylase. This is used in the
 CC production of acetylenic compounds. The process comprises treating C18
 CC fatty acids having a double bond at position delta 12 with an acetylase
 CC to form 12-ynoic acids. The acetylenic compounds can be produced by
 CC organisms such as oilseed plants, yeast and fungi which are transformed
 CC with the acetylase DNA. These organisms can accumulate these acetylenic
 CC compounds which are chemical feedstocks, particularly for coatings,
 CC plasticisers and lubricants. The process enables the production of these
 CC acetylenic compounds from a renewable resource with high purity and at
 CC reasonable cost. (Updated on 25-MAR-2003 to correct PA field.)
 XX

Sequence 375 AA;

Query Match 79.9%; Score 1636; DB 2; Length 375;
 Best Local Similarity 76.9%; Pred. No. 1.6e-158;
 Matches 289; Conservative 40; Mismatches 45; Indels 2; Gaps 1;

QY 1 MGAGGRMSDPSEGNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVHDLIVAVY 60
 DB 1 MGAGGRMSDPSEGNILERVVDPPEFTLSDLKKAIPTHCFERSVIRSSYYVHDLIVAVY 58
 QY 61 FYLLANTYIPLIPPLATLAMPVYVFCQASITGLMTVGHCGHAFSDYQOLIDIVGFV 120
 DB 59 FYFLADKYIPLIPPLATLAMPVYVFCQASITGLMTVGHCGHAFSDYQOLIDIVGFV 118
 QY 121 LHSALTPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSLNNPGRVFTLVER 180
 DB 119 LHSALTPYFSWKYSHRNHNANTNSLDNDVYIIPKRSKVKIYSLNNPGRVFTLVER 178
 QY 181 LTLGFPPLVLTNISKYGRFANHPDPMSPFNDREVOVLLSDGLLAVFYAIKLVA 240
 DB 179 LTLGFPPLVLTNISKYGRFANHPDPMSPFNDREVOVLLSDGLLAVFYAIKLVA 238
 QY 241 KGAANVIMYAIPLVGVSVFVLITYLHHTHLSLPHYSTENWTKALSTIDRDFGLN 300
 DB 239 KGAANVIMYAIPLVGVSVFVLITYLHHTHLSLPHYSTENWTKALSTIDRDFGLN 298
 QY 301 RVFHDVTHVLAHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 360
 DB 299 RVFHDVTHVLAHLISYIPHYHAKARDAIKPVLGEEYKIDRTPIFAMTREAECIYI 358
 QY 361 EPDEDESEKGVFWYHKM 376
 DB 359 EPDEDESEKGVFWYHKM 374

RESULT 3

AAW79743 standard; protein; 374 AA.

XX AC AAW79743;
 XX

DT 02-FEB-1999 (first entry)
 XX Crepis sp. delta-12-epoxygenase.
 XX Fatty acid epoxygenase; Crepx gene; delta-12-epoxygenase;
 KM mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;
 KM vegetable oil; oilseed.
 XX Crepis sp.
 XX Key location/Qualifiers
 FH Region 99. .104
 FT Region /note= "His-rich region"
 FT Region 135. .139
 FT Region /note= "His-rich region"
 FT Misc-difference 293
 FT Misc-difference 305 /note= "encoded by AGN"
 FT Region /note= "encoded by GTN"
 FT Region 309. .313
 FT Region /note= "His-rich region"
 XX MO9846762-A1.
 PN 22-OCT-1998.
 PD 09-APR-1998; 98WO-AU000246.
 XX 15-APR-1997; 97AU-00006223.
 PR 15-APR-1997; 97AU-00006226.
 PR 16-APR-1997; 97US-0043706P.
 PR 20-JUN-1997; 97US-0050403P.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (STYM/) STYMNE S.
 PA Styenne S, Green A, Singh S, Lenman M;
 PI WPI; 1998-568734/48.
 DR N-PSDB; AAV63102.
 XX New isolated fatty acid epoxygenase gene - used particularly for
 PT transforming plants for producing modified oils for use in, e.g.
 PT coatings, resins, glues, plastics, surfactants or lubricants.
 XX Claim 29; Page 84-86; 150pp; English.
 PS This is the amino acid sequence of a novel epoxygenase of a vernolic acid
 CC -containing Crepis sp. (not crepis palaestina). It was deduced from
 CC isolated cDNA clone Crepx (see AAV63102). The deduced sequence contains
 CC His-rich motifs (see AAW79752-54) that are characteristic of mixed
 CC function monooxygenases, and shows a high degree of homology to a novel
 CC delta-12-epoxygenase (see AAW79742) of C. palaestina. The invention
 CC relates generally to novel genetic sequences (see AAV63101-03) encoding
 CC fatty acid epoxygenases (see AAW79742-44), especially delta-12-
 CC epoxygenases or mixed function monooxygenases. These provide the means by
 CC which fatty acid metabolism can be manipulated in e.g. yeast, mould,
 CC bacteria, insects, birds, mammals and plants (especially oilseed plants
 CC such as flax), in particular to convert unsaturated fatty acids to
 CC epoxygenated fatty acids. The invention includes genetically modified oil
 CC -accumulating organisms and to the oils derived from them. These oils can
 CC be used in production of coatings, resins, glues, plastics, surfactants
 CC or lubricants
 XX Sequence 374 AA;
 SO
 Query Match 78.1%; Score 1598.5; DB 2; Length 374;
 Best Local Similarity 75.7%; Pred.No. 1.1e-154;
 Matches 286; Conservative 41; Mismatches 46; Indels 5; Gaps 3;
 QY 1 MGAGGRSDPSBGNILERPVPD-PPTLSLKLKAIPTCHREBSVYSSYVVDLIVAY 59
 DB 1 MGAGGR--GRTSEKSVMERVSVDPTFSLDKAIPHCPRSVIRSSYVVDLIVAY 58

QY 60 VFYLIANTYIPLIPTPLAYLAMPYVFCQASILGTGLWVIGHCCHHAFSDYQIIDIYGF 119
 DB 59 IFVFLANTYIIPNLPHPLAYLAMPYVFCQASVLGLWVIGHCCHHAFSNTVDDTYG 118
 QY 120 VLSGALLTPYRSKYSRHHNHAATNSLDNDVYIPKRSKXYISKLIANPPGRVFTLVF 179
 DB 119 IHSFLLTPYFSWYSHNHNHNTSSIDNDEVYIPKRSKXYIKLIANPPGRLLVLVI 178
 QY 180 RLTLGFPPLVLTNTSGKKYGRFANHPDPMSPIFNDRERVOLLSDFGLAIFYAIKLIVA 239
 DB 179 MFTLGFPLVLTNTSGKKYGRFANHPDPMSPIFYEREPVPLSDGLAIFYAIKAVA 238
 QY 240 AKGAAMVINYAIPLVGSVFEVLTLYLHTLSLPHYDSTENWIKGALSTIDRDFGL 299
 DB 239 NKGAAVAAQVGVPLGVFTFVDITPLHHTHQSPPHDSFEMMIRGALAIIDRDFGL 298
 QY 300 NRVPHDVTHTVHLHLISYIPHYAKARDAIKVLGYYIKIDRTPIKAMRYREKCY 359
 DB 299 NSVPHDVTHTVHMLHSYIPHYAKARDAIKPLIGFYWIDRTPIKAMRYREKCY 358
 QY 360 IEPDESEHKGVPWYHMK 377
 DB 359 IEP--DSKLGKGVWYHKL 374
 RESULT 4
 AAW79742
 ID AAW79742 standard; protein; 374 AA.
 XX AAW79742;
 AC 02-FEB-1999 (first entry)
 DT Crepis palaestina delta-12-epoxygenase.
 XX Fatty acid epoxygenase; Cpai2 gene; mixed function monooxygenase;
 KM delta-12-epoxygenase; epoxygenated fatty acid; transgenic plant;
 KM vegetable oil; oilseed.
 XX Crepis palaestina.
 OS
 XX Key location/Qualifiers
 FH Region 99. .104
 FT Region /note= "His-rich region"
 FT Region 135. .139
 FT Region /note= "His-rich region"
 FT Region 309. .313
 FT Region /note= "His-rich region"
 XX MO9846762-A1.
 PN 22-OCT-1998.
 PD 09-APR-1998; 98WO-AU000246.
 XX 15-APR-1997; 97AU-00006223.
 PR 15-APR-1997; 97AU-00006226.
 PR 16-APR-1997; 97US-0043706P.
 PR 20-JUN-1997; 97US-0050403P.
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (STYM/) STYMNE S.
 PA Styenne S, Green A, Singh S, Lenman M;
 PI WPI; 1998-568734/48.
 DR N-PSDB; AAV63101.
 XX New isolated fatty acid epoxygenase gene - used particularly for
 PT transforming plants for producing modified oils for use in, e.g.
 PT coatings, resins, glues, plastics, surfactants or lubricants.

PS Claim 29, Page 78-81; 150pp; English.

XX This is the amino acid sequence of a novel mixed function monooxygenase of
CC Crepis palaestina that is characterised as having delta-12-epoxygenase
CC activity. It was deduced from isolated full-length cDNA clone Cpai2 (see
CC AA63101). The deduced sequence contains His-rich motifs (see AA63101-52-
CC 54) that are characteristic of delta-12-desaturase enzymes. The Cpai2
CC gene was shown to be highly expressed in developing seeds, with no
CC expression detectable in leaves. The invention relates generally to novel
CC genetic sequences (see AA63101-03) encoding fatty acid epoxigenases (see
CC AA63101-03) encoding delta-12-epoxygenases or mixed function
CC monooxygenases. These provide the means by which fatty acid metabolism
CC can be manipulated in e.g. yeast, mould, bacteria, insects, birds,
CC mammals and plants (especially oilseed plants such as flax), in
CC particular to convert unsaturated fatty acids to epoxysaturated fatty
CC acids. The invention extends to genetically modified oil-accumulating
CC organisms and to the oils derived from them. These oils can be used in
CC production of coatings, resins, glues, plastic, surfactants or
CC lubricants

XX
XX Sequence 374 AA;

SO
Query Match 77.7%; Score 1589.5; DB 2; Length 374;
Best Local Similarity 75.4%; Pred. No. 9e-154; Indels 5; Gaps 3;
Matches 285; Conservative 40; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGAGGRMSDPSGKILRRVPDP-PFTLSDLKKAIPTHCFERSYIRSSYYVVDLIYAY 59
DB 1 MGAGGR--GRTSEKSVMERVSVDPTFSLSEKKAIPHCGRSIVIRSSYYVVDLIYAY 58
QY 60 VFYYLANTYIPLIPPLAYLAMPVYVFCOASTLTGLMWYIGHEGHAASDYLIDYGF 119
DB 59 IFYYLANTYIPLTPTSLAYLAMPVYVFCOASVLTGLMWIGHEGHAASNYTWFPDITVGF 118
QY 120 VLHSALILPYRSMKSHRNHNANTSLNDEYIIPKRSKVIYSKLLNPPGRVFTLVF 179
DB 119 ILHSALILPYRSMKSHRNHNANTSLNDEYIIPKRSKVIYSKLLNPPGRVFTLVF 178
QY 180 RLTLGFPYLLTNISGKKYGRFANFDPMSPIFNDRERVOVLLSDFGLLAVFYAKLLVA 239
DB 179 MFTLGFPYLLTNISGKKYGRFANFDPMSPIFKERERFOVLLSDGLLAVFYGIKVVAA 238
QY 240 AKGAAMVIMKTAIPVLGVSVFVLITLYLHHTLSLPHYDSTEMWIKGALSTIDDPGL 299
DB 239 NKGAAMVACMGVPLGVTFEPDVTITFLHHTHQSPPHYDSTEMWIRGALSIDDPFGL 298
QY 300 NRVFHDVHTVLAHHLISYIPHYHAKBARDAIKPVLGEYKIDRTPIFKAMVREAKECIY 359
DB 299 NSVFHDVHTVLAHHLISYIPHYHAKBARDAIKPVLGEYKIDRTPIFKAMVREAKECIY 358
QY 360 IEPDESEHKGVFWYHKM 377
DB 359 IEP--DSKLKGVYVYHKL 374

RESULT 5
AAW83354
ID AAW83354 standard; protein; 384 AA.
XX AAW83354;
XX
XX 27-AUG-2003 (revised)
DT 10-FEB-1999 (first entry)
XX
XX Vernonia galamensis fatty acid epoxidising enzyme.
DE
XX Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;
KW expression; chimeric gene; recombinant enzyme.
XX
XX Vernonia galamensis.
XX
XX US5846784-A.

PD 08-DEC-1998.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX 11-JUN-1997; 97US-00872302.
PR
XX (DDPO) DU FONT DE NEMOURS & CO E I.
PA
XX
XX Hitz WD;
PI
XX WPI; 1999-059065/05.
DR N-PSDB; AAV72550.
XX
XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid
PT epoxidising enzyme - used to alter levels of expression of the enzymes in
PT transformed host cells or to produce recombinant enzymes.

PS Claim 5; Col 29-32; 21pp; English.

XX
XX The present sequence is Vernonia galamensis fatty acid epoxidising
CC enzyme. The present invention also describes: (i) Vernonia galamensis
CC fatty acid desaturase; (ii) chimeric genes comprising the fragments
CC linked to regulatory sequences; and (iii) transformed host cells
CC containing the chimeric genes. The DNA's from the present invention can
CC be used to alter levels of expression of the enzymes in transformed host
CC cells or to produce the recombinant enzymes by transformation of
CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)

XX
XX Sequence 384 AA;

SO
Query Match 77.1%; Score 1578.5; DB 2; Length 384;
Best Local Similarity 76.5%; Pred. No. 1.2e-152; Indels 3; Gaps 2;
Matches 280; Conservative 39; Mismatches 44; Indels 3; Gaps 2;

QY 15 NILERVPVD-PFTLSDLKKAIPTHCFERSYIRSSYYVVDLIYAYVYFYLANTYIPLIP 73
DB 19 NINERAPVDAAPFSLSDLKKAIPHCGRSIVIRSSYYVVDLIITFLTYLANSYIPLIP 78
QY 74 TPLAYLAMPVYVFCOASTLTGLMWYIGHEGHAASDYLIDYGFVLHSALILPYRSMK 133
DB 79 PFLPYLAMPVYVFCOASTLTGLMWYIGHEGHAASVQWVDNVTGFLHSFLTFYFSWK 138
QY 134 YSHRNHNANTSLNDEYIIPKRSKVIYS--KLLNPPGRVFTLVRLTGLPFLYLLT 191
DB 133 YSHRNHNANTSLNEEYIIPKRSQILNYSNFFLDNTPRITFLTLMTLGEPFLYLLT 198
QY 192 NISGKKYGRFANFDPMSPIFNDRERVOVLLSDFGLLAVFYAKLLVAKGAAMVIMNYA 251
DB 199 NISGKKYGRFANFDPMSPIFSERERIOVLSVDGLINAVFGKFLVAKGFGWMRYG 258
QY 252 IPIVGVSVFVLITLYLHHTLSLPHYDSTEMWIKGALSTIDDPGFLNRYVHDVTHV 311
DB 259 APVVGANFIMITYLHHTLSLPHYDSTEMWIKGALTITIDRFGFLNRYVHDVTHV 318
QY 312 LHLISYIPHYHAKBARDAIKPVLGEYKIDRTPIFKAMVREAKECIYIEPDESEHKGV 371
DB 319 LHLIFPYIPHYHAKBARDAIKPVLGEYKIDRTPIFKAMVREAKECIYIEPDESKGKGV 378
QY 372 FMYHKM 377
DB 379 YMYHKM 384

RESULT 6
AAV72825
ID AAV72825 standard; protein; 383 AA.
XX AAV72825;
XX
XX 31-MAY-2001 (first entry)
DT
XX
XX Borage officinalis fatty acid hydroxylase enzyme.
DE
XX

KM Borage; fatty acid hydroxylase; conjugated double bond; delta-9;
 XX delta-12; transgenic plant; seed oil.
 XX Borago officinalis.
 XX WO200112800-A2.
 XX 22-FEB-2001.
 XX 15-AUG-2000; 2000WO-US022371.
 XX 16-AUG-1999; 99US-0149050P.
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX Canoon EB, Hiltz WD, Ripp KG;
 XX WPI; 2001-218351/22.
 XX
 XX Novel nucleic acid fragment encoding plant fatty acid modifying enzyme
 PT associated with modification of delta-9 position of the fatty acid,
 XX useful for creating transgenic plants having altered lipid profiles.
 XX Disclosure; Fig 2; 96pp; English.
 XX
 XX The present invention relates to nucleic acid fragments encoding plant
 CC fatty acid modifying enzymes associated with conjugated double bond
 CC formation, comprising a modification of delta-9 position or a delta-12
 CC position of fatty acids. The nucleic acid fragments are useful for
 CC creating chimeric gene which is useful for creating transgenic plants
 CC having altered lipid profiles. They are also useful for producing seed
 CC oil containing fatty acids comprising a modification at delta-9 position
 CC or delta-12 position. The seed is useful for improving the carcass
 CC quality of an animal by supplementing a diet of the animal with animal
 CC feed. The nucleic acid fragments are useful for isolating nucleic acid
 CC fragments encoding homologous fatty acid modified enzymes from the same
 CC or other plant species. The present sequence is Borago officinalis fatty
 CC acid hydroxylase enzyme. It is a fatty acid modifying enzyme associated
 CC with conjugated double bond formation
 XX
 XX Sequence 383 AA:
 SQ
 Query Match 68.2%; Score 1396.5; DB 4; Length 383;
 Best Local Similarity 63.9%; Pred. No. 5.4e-134;
 Matches 242; Conservative 62; Mismatches 70; Indels 5; Gaps 2;
 QY 1 MGAGGRMSDBSEK---NILERPVVD-PPTTSLDKKALPTHCERSVIRSSYYVHDL 55
 DB 1 MGGGGRMPVPPTKGGKSKSDVFRVSEKRPPTVGDLLKVIIPPHCFORSVLHSFSYVVDL 60
 QY 56 IVAVVFYLLANTYIPLPTPLAYLAMPVYFCQASITLGLMVTGHEGCHAFSDYQLIDD 115
 DB 61 VIHALFTYTSRHYHLOPHPLSYAMPJYAMPLWFCQSVLGVAVIAHEGCHAFSDYQWIDD 120
 QY 116 IVGFVLHSALLTPYFSWKYSHRNHNANTNSLDNDEVYIPKSKSKVYISKLIANPPGRVF 175
 DB 121 TVGILLHSALLVFPFSWKYSHRNHNANTNSLDNDEVYIPKSKSGISMSSEYLIANPPGRVYL 180
 QY 176 TLVRLTLGFPYLLTNIISGKKYGRFANHPDPSPIFNDRERRVOLLSDFGLLAVFAIK 235
 DB 181 VTLVQLTGWPLVYLMFVNSGRPRYDFACHFDPKSPYVDRERLQIYISDAGIVAVMYGLY 240
 QY 236 LTVAKAAMVYINNYAPVGVSVFVLYITLHHTHLSLPHYDSTENWIMGALSTDRD 295
 DB 241 RLTVAKAGAMVVCYGGPPLVANGGLVITLQHTQPLPHYDSSEWMLGALATVDRD 300
 QY 296 FGLIARVHDVTHVTLHLISYIPHYAKKARDAIKEVLAGYYKIDRTPIFKAMVREAK 355
 DB 301 YGFLANKLHNITDTHVHHLFSTWPHYAMKATKAIKRIIDYIQCORTPIFKAMVREVK 360
 QY 356 ECIYIEPDESEHKGVFMY 374
 DB 361 ECIVVEADEGDNKKGVFMY 379

RESULT 7
 AAE13421
 ID AAE13421 standard; protein; 383 AA.
 XX
 XX AAE13421;
 XX
 XX 12-FEB-2002 (first entry)
 XX
 XX Cotton oleoyl-PC delta12-desaturase (ghPAD2-2) protein.
 DE Cotton; delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;
 KM linoleic acid; stearic acid; oleic acid; transgenic plant;
 KM cotton seed oil; oleoyl-PC delta12-desaturase; FAD2-2.
 XX
 XX Goesypium hirsutum.
 OS
 XX WO200179499-A1.
 XX
 XX 25-OCT-2001.
 XX
 XX 18-APR-2001; 2001WO-AU000436.
 XX
 XX 18-APR-2000; 2000US-0198124P.
 XX
 XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA
 XX Green A, Singh S, Liu Q,
 XX WPI; 2001-602932/68.
 DR N-PSDB; AAD22380.
 XX
 XX Modifying endogenous oil of cotton plants, to produce cotton seed oil
 PT with reduced palmitic and/or linoleic acid content, involves producing
 PT transgenic plants containing a fatty acid biosynthesis gene in a
 PT construct.
 XX
 XX Example 8; Fig 6; 201pp; English.
 XX
 XX The invention relates to a method for modifying the endogenous oil of a
 CC cotton plant, to produce cotton seed oil. The method comprises producing
 CC a transgenic cotton plant having a gene construct which includes a fatty
 CC acid biosynthesis gene operably linked to a promoter sequence capable of
 CC conferring expression of the delta9-desaturase (delta9 stearoyl-ACP
 CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-
 CC desaturase) gene in the seed of a cotton plant. The invention is useful
 CC for producing cottonseed oil with reduced palmitic and/or linoleic acid
 CC content, and increased stearic and/or oleic acid content. The present
 CC sequence is cotton oleoyl-PC delta12-desaturase (ghPAD2-2) protein
 CC related to the invention
 XX
 XX Sequence 383 AA:
 SQ
 Query Match 65.1%; Score 1332.5; DB 4; Length 383;
 Best Local Similarity 60.7%; Pred. No. 1.9e-127;
 Matches 230; Conservative 70; Mismatches 74; Indels 5; Gaps 2;
 QY 1 MGAGGRMSDBSEK---NILERPVVD-PPTTSLDKKALPTHCERSVIRSSYYVHDL 55
 DB 1 MGGGGRMSVPTSPKPPFNLSIKRVYKRPPTTSLSEIKALIPPHCFORSVLHSFSYLLVDF 60
 QY 56 IVAVVFYLLANTYIPLPTPLAYLAMPVYFCQASITLGLMVTGHEGCHAFSDYQLIDD 115
 DB 61 ILSLFFHVATNYEPNIPQALSNVAMPJYAMOCITLGVAVIAHEGCHAFSDYQWIDD 120
 QY 116 IVGFVLHSALLTPYFSWKYSHRNHNANTNSLDNDEVYIPKSKSKVYISKLIANPPGRVF 175
 DB 121 TVGILLHSALLVFPFSWKYSHRNHNANTNSLDNDEVYIPKSKSLRWAKGFNPPGRFL 180
 QY 176 TLVRLTLGFPYLLTNIISGKKYGRFANHPDPSPIFNDRERRVOLLSDFGLLAVFAIK 235
 DB 181 SITQLTGWPLVYLAFAVAGRPYDRFACHYDPYGFIFSDRERLQIYISDAGVLAVALY 240

Qy	236	LLVAAKGAAMVNNMVAIPPLGVSVEFVLIITYLHHTLSPHYDSTGEMNNIKGALSTIDRD	295
Db	241	RLVLAKGGWALSVGVGLVNVNALLVMYLIQHTHPSLPHYDSSMDWRGALSTVDRD	300
Qy	296	FGFLNRVPHDVTHTVTHLHLLISYIPHYAKEARDAIKPVLGEYXKIDRTPTIFKAMYLEAK	355
Db	301	YGIINKVPHNITIDTVVAHLLFSTMPHYHAMVATKAIKPLIGEYYQGDGMPPVYKALIREAK	360
Qy	356	ECITYEPDEDSERKGVFWT 374	
Db	361	ECLYVEPDEGDKDKGVFWF 379	
RESULT 8			
ID	ADE40489	standard; protein; 387 AA.	
XX	AC	ADB40489;	
XX	DT	29-JAN-2004 (first entry)	
DE	P.	granatum delta-12-desaturase PuFAD12 protein.	
XX	KW	desaturase; transgenic; plant; oil; triglyceride; unsaturated fatty acid;	
KW	KW	food; animal feed; cosmetic; pharmaceutical; pomegranate;	
XX	KW	delta-12-desaturase; PuFAD12; enzyme.	
XX	OS	Punica granatum.	
XX	XX		
FH	Key	Location/Qualifiers	
FT	Misc-difference	155	
FT		/note= "Unidentified residue"	
FT	Misc-difference	162	
FT		/note= "Unidentified residue"	
FT	Misc-difference	227	
FT		/note= "Unidentified residue"	
XX	PN	DE10134660-A1.	
XX	XX		
PD	06-FEB-2003.		
XX	XX		
PF	20-JUL-2001; 2001DE-01034660.		
XX	XX		
PR	20-JUL-2001; 2001DE-01034660.		
XX	XX		
PA	(BAD1) BASF PLANT SCI GMBH.		
XX	XX		
PI	Feussner I, Hornung E, Pernstich C;		
XX	XX		
DR	WPI; 2003-722899/69.		
DR	N-PSDB; ADB40488.		
XX	XX		
PS	Claim 11; SEQ ID NO 6; 38pp; German.		
XX	XX		
CC	This invention describes a novel nucleic acid encoding a polypeptide with		
CC	desaturase activity. The products of the invention are used in the		
CC	construction of constructs, vectors, organisms and transgenic plants		
CC	containing the desaturase. The invention also describes methods for		
CC	preparing oils or triglycerides with increased content of unsaturated		
CC	fatty acids; oils, fats and fatty acid mixtures and a novel nucleic acid		
CC	encoding a protein able to convert a fatty acid to a more highly		
CC	unsaturated acid. The products of the invention are used to produce		
CC	transgenic plants (or other organisms) that produce oils and fats with		
CC	increased contents of unsaturated fatty acids, useful in preparation of		
CC	foods, animal feeds, cosmetics and pharmaceuticals and in homology		
CC	screening for isolation of genomic sequences. This sequence represents		
CC	the Punica granatum (pomegranate) delta-12-desaturase PuFAD12 described		
CC	in the disclosure of the invention.		

xx	Sequence	387 AA;
sq	Query Match	65.0%; Score 1331.5; DB 7; Length 387;
	Beet Local Similarity	59.7%; Pred. No. 2.5e-127;
	Matches 230; Conservative	65; Mismatches 81; Indels 9; Gaps 2
QY	1 MGAGGRMDPS-----EGKNLEERP-VDPPTLSDLKKAIPTHCFERSVIRSSYYV	51
DB	1 MGAGGRMTVPENKBEGDEGKSOQYQRPSPAKPPTTLEIKKALPDPHCFKSLKSPSYV	60
QY	52 VHDLIYAVFYFYLTANTYIPLIPTPLAYLAMPVYWCQASITGLVIGHECGHAFSDYQ	111
DB	61 LYDYLVAIFYYVATTYIDALPGPLRYAAMPYVMAQGCVLITGVWVIAHECGHAFSDYQ	120
QY	112 LIDDIYGVNLHSALITPYFSWKYSHRNHANTNSLIDNEVYIPKRSKYKTIYSKLLANPP	171
DB	121 WYDDCVGVLHSALIVPYFSWKYSHRHSHNSYGSXERBEVYKPKSKSKMPWFSKTLANPP	180
QY	172 GRVFLTVRLTLGFLYLTLTNISGKCYGRFANHPDPMSPIFNDRERVOVLISDFGLAVF	231
DB	181 GRVMTLLITLTGLMPLYLALNVSGMPYRFACHDPYPPIYDRRKOYIYSDVGIMAT	240
QY	232 YAIKLLVAAKGAAMWNNYAIAPVLGVSVFYVLTITYLHHTHSLPHYDSIENWNMIGALST	291
DB	241 YLYKLTAAARGLAWVCYGVGPIILVNNFLVITITLQHTTHPALPHYDSIENWMLGALAT	300
QY	292 IDRDGFLNRFVHDVTHTVTLHHLLSYLPHYAKARDAIKRPVLGEYKKIDRTPLFKAMV	351
DB	301 ADRDYGILNKVFHNITDTHVAHHFLFTSPMPHAMAEATKAIRKPIILDYQFDGTPVYKAMW	360
QY	352 REAKECIYEPDEDESHGCVFPMYHK	376
DB	361 REARECLTYEPDGANSKGVETMYK	385

Key	Location/Qualifiers
FT	105..110
FT	/note="Histidine binding motif"
FT	141..145
FT	/note="Histidine binding motif"
FT	315..319
FT	/note="Histidine binding motif"
PN	WO200179499-A1.
XX	
PD	25-OCT-2001.
XX	
PF	18-APR-2001; 2001WO-AU000436.
XX	
PR	18-APR-2000; 2000US-0198124P.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX	
PI	Green A, Singh S, Liu Q;
XX	
DR	WPI; 2001-602932/68.

XX Modifying endogenous oil of cotton plants, to produce cotton seed oil
 PT with reduced palmitic and/or linoleic acid content, involves producing
 PT transgenic plants containing a fatty acid biosynthesis gene in a
 PT construct.

XX Example 8, Fig 7, 201pp; English.

XX The invention relates to a method for modifying the endogenous oil of a
 CC cotton plant, to produce cotton seed oil. The method comprises producing
 CC a transgenic cotton plant having a gene construct which includes a fatty
 CC acid biosynthesis gene operably linked to a promoter sequence capable of
 CC conferring expression of the delta9-desaturase (delta9 stearyl-ACP
 CC desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-
 CC desaturase) gene in the seed of a cotton plant. The invention is useful
 CC for producing cottonseed oil with reduced palmitic and/or linoleic acid
 CC content, and increased stearic and/or oleic acid content. The present
 CC sequence is soybean microsomal omega-6 desaturase, gmfAD2-2 protein
 CC related to the invention

XX Sequence 383 AA;

Query Match 64.8%; Score 1325.5; DB 4; Length 383;
 Best Local Similarity 61.3%; Pred. No. 1e-126;
 Matches 233; Conservative 62; Mismatches 80; Indels 5; Gaps 2;

QY 1 MGAGGRMSDSESGK---NLEERVVD--PPTLSDLKKAIPYHCFERSVIRSSYYVVDL 55
 Db 1 MGAGGRMDVPANKKSEVDLPKRVPEKQFSLGKIKKAIIPHCFGRSVIRSSYYVVDL 60
 QY 56 IVAVVFFYLLANTYPLIPLPLAYLAMPVYVFCQASILTGLVWIGHGCHHAFFSDYQLID 115
 Db 61 TIACLVYVAHYHFLPLPGPLSFRGMALYMAVQGCILGVWVIAHCGHHAFFSDYQLID 120
 QY 116 IVGVLSALLTPYFSWKSHRNHNANTSLDNDVYIPIKRSKKTYSKILNPPGRV 175
 Db 121 IVGLILSHALLVPFSWKSHRNHNANTSLDNDVYIPIKRSKKTYSKILNPPGRV 180
 QY 176 TLVRLTLGFPYLLTNISGKKYGRFANHPDMSPIFNDREVOVLSDFGLLAVFYAIK 235
 Db 181 TLAVTLTLGMPYLLTNANSGRYPDRFACHYDPGYISDRERLQIYIDAGVLAFFYELF 240
 QY 236 LIVAAGAAVYINNVYALPVLGVSVFVLITYLHHTLSLPHYSTENWIKGALSTIDR 295
 Db 241 RLAAKGLAAVYVGVPLVNVGFLVLTFLQHTHPALPHYTSEMDWMLGALATVDRD 300
 QY 296 FGFLANRVHDVTHVLAHLISYIPHYAKAARDAIKPVLGSEYKIDTPIFKAMRYEAK 355
 Db 301 YGILNKVFHNITDTHVAHLFSMTMHPYHAMEATKAIKPIIDGYRFFDETPEVKAMREAR 360
 QY 356 ECIYIEPDESEHKGVFYWH 375
 Db 361 ECIYIEPDESEHKGVFYWH 380

RESULT 10
 AAG80695
 ID AAG80695 standard; protein; 383 AA.

XX AAG80695;
 AC
 DT 08-MAR-2002 (first entry)

XX C. officinalis Cofad2 protein.

XX Cofad2, linoleic acid, conjugated fatty acid; plant; cosmetic;
 KM pharmaceutical; lubricant.

XX Calendula officinalis.

OS WO200185968-A2.

XX 15-NOV-2001.
 PD

XX 09-MAY-2001; 2001WO-IB001059.
 PF
 XX 09-MAY-2000; 2000US-0203027P.
 PR
 XX (BIOR-) BIORIGINALE FOOD & SCI CORP.
 PA
 XX Qiu X;

DR WPI; 2002-089796/12.
 DR N-PSDB; AA169486.

PT Nucleic acids which encode a conjugase and its related enzyme a delta
 PT desaturase to be used for the large scale production of conjugated
 PT linoleic acid and linolenic acid in plants.

PS Claim 3; Fig 1; 49pp; English.

XX This invention describes a novel polypeptide, Cofad2, capable of
 CC catalyzing the formation of two conjugated double bonds. The products of
 CC the invention can be used for the large scale production of conjugated
 CC linoleic acids. The composition may be used for cosmetic or
 CC pharmaceutical purposes. The conjugated linoleic acids may be used for
 CC coating, painting or cold weather ester-type lubricant purposes. There is
 CC not a natural source which is rich in conjugated linoleic acids and
 CC chemical processes result in a mixture of several isomers. Plant
 CC biotechnology is cost-effective and renewable with little side effects.
 CC This sequence represents the Calendula officinalis Cofad2 protein

XX Sequence 383 AA;

Query Match 64.7%; Score 1323.5; DB 5; Length 383;
 Best Local Similarity 61.3%; Pred. No. 1.6e-126;
 Matches 233; Conservative 57; Mismatches 83; Indels 7; Gaps 2;

QY 1 MGAGGRMSDSESGKILERVVD-----PPTLSDLKKAIPYHCFERSVIRSSYYVVD 54
 Db 1 MGAGGRMODPTNGKNTPEPIQRPHEKPEFTGDIKKAIPHCFNRSVIRSSYYVVD 60
 QY 55 LIVAVVFFYLLANTYPLIPLPLAYLAMPVYVFCQASILTGLVWIGHGCHHAFFSDYQLID 114
 Db 61 LTIASILYIANNTYSTLPSPPLAYLAMPVYVAVGCVLTVGVWVIAHCGHHAFFSDYQLID 120
 QY 115 DIVGVLSALLTPYFSWKSHRNHNANTSLDNDVYIPIKRSKKTYSKILNPPGRV 174
 Db 121 DTGVLVLSHPLVYFSWKSHRNHNANTSLDNDVYIPIKRSKKTYSKILNPPGRV 180
 QY 175 FTLVRLTLGFPYLLTNISGKKYGRFANHPDMSPIFNDREVOVLSDFGLLAVFYAI 234
 Db 181 LTLVTLTLGMPYLLTNANSGRYPDRFACHYDPGYISDRERLQIYIDAGVLAFFYELF 240
 QY 235 KLVVAAGAAVYINNVYALPVLGVSVFVLITYLHHTLSLPHYSTENWIKGALSTIDR 294
 Db 241 FRLAMTKGLTWVLTMYGSPPLVNVGFLVLTFLQHTHPALPHYTSEMDWMLGALATVDR 300
 QY 295 DFGFLANRVHDVTHVLAHLISYIPHYAKAARDAIKPVLGSEYKIDTPIFKAMRYEAK 354
 Db 301 DYGLNKVFHNITDTHVAHLFSMTMHPYHAMEATKAIKPIIDGYRFFDETPEVKAMRET 360
 QY 355 KECIYIEPDESEHKGVFYWH 374
 Db 361 KECIYVDKDEEVK-DGVYWH 379

RESULT 11
 AAW86153
 ID AAW86153 standard; protein; 384 AA.

XX AAW86153;

XX 04-MAR-1999 (first entry)

XX Protein sequence of F form of wild-type Fad2 gene.
 DE

Query Match	64.4%	Score 1318	DB 2	Length 384
Best Local Similarity	61.2%	Pred. No. 5,9e-126		
Matches 233	Conservative 61	Mismatches 81	Indels 6	Gaps 4
QY	1 MGAGGRM--SDPSEGG--NILERRVPVD--PPFLTSDIKKRIIPTHCEPBRSVIRSSYYVYVHDL	55		
DB	1 MGAGGRMOVSPSPKSKSETDTIKRVPETPTFVGEIKKAIIPHCIFPFRSIPRSYSYLIWDI	60		
QY	56 IVAAYFFYYLANIYPIPLIPTPLAYLAMPVYVFCOASILITGLVNIHGRCGHAFSDYOLIDD	115		
DB	61 IIASCFYVATYTFPLPHPLPLSYFAMPPLYMAGCGCYLTGVMYIAHCGHAFSDYOLIDD	120		
QY	116 IVGFVLHSAALLTPYRSWKYSHRNHNHANTNSLDNDEVYIIPKRSKVKIYKSLNNPGRYVF	175		
DB	121 TVGLIFHSFLVLPYFSWKYSHRHSHSNTSLEBDEVFVPEKKSIDIKWYGYLIANNPGRYVF	180		
QY	176 TLVFLTLTGFRPLYLTNTISGKKY--GRFANHDPMSIIPNDRERVOYLTDGFLAIFYAI	234		
DB	191 MLTVQFTGLGMPLYLAFNVSGRPDGDFACHFPHNATIYNDRELOIYISDAGLIACYGI	240		
QY	235 KLLVAAGKAAYINMAYIPVLGVSVEFVILITYLHHTLSLPHYDSTENMWIKGALSTIDR	294		
DB	241 FRYAAGGVSASVNCFCYGVGLVINGVLVILITYQHTHPSLPHYDSEEMWIKGALSTIDR	300		
QY	295 DFGFLNRFVHDVTHTHVLAHLISYIPHYAKAKARDAIKFVLGEYKIKDRTPIFKAMYREA	354		
DB	301 DYGILINKVFHNITDTHVAHLFTSTMBHYAMEATKAIKILGEYQFDGTPVVKAMWREA	360		
QY	355 KECITYEPDEDEBHKGVFMYH	375		

DB 361 KECIYVEPDRQEKKGVEFWYN 381

RESULT 12
AAW94053
ID AAW94053 standard; protein; 384 AA.
XX
AC AAW94053;
XX
DT 06-APR-1999 (first entry)
DE Amino acid sequence of Brassica wild-type Fad2-F gene product.
XX
KM Fatty acid desaturase; FAD; Brassicaceae; Helianthus; mutation;
fatty acid; oleic acid; linoleic acid; Fad2 gene.
XX
OS Brassica napus.
PN W09856239-A1.
PD 17-DEC-1998.
PF 11-JUN-1998; 98WO-US012332.
PR 12-JUN-1997; 97US-00874109.
PA (CRGI) CARGILL INC.
PI Debonte LR, Zhegong F, Loh WH, Shorrosh BS;
DR MPI; 1999-059929/05.
N-PSDB; AAX06619.

PT New isolated mutant fatty acid desaturase genes - obtained by mutation of
Brassicaceae or Helianthus plants, used for producing plants or seeds
having altered fatty acid compositions.

Example; Page 73-75; 116pp; English.

The invention relates to fatty acid desaturases (FAD) from Brassicaceae
or Helianthus, where the FAD genes comprise at least one mutation in
their sequences. The mutation is in a region encoding the His-Xaa-Xaa-Xaa-
His motif of the delta-12 or delta-15 fatty acid desaturases. The
invention also provides methods for producing the FAD mutant genes and
gene products. The products can be used for producing plants and seeds
which have altered fatty acid compositions, e.g. an elevated oleic acid
content, a decreased, stabilised linoleic acid content, both elevated
oleic acid and decreased, stabilised linoleic acid content or a
decreased, stabilised level of alpha-linolenic acid and increased level
of linoleic acid. The plants may be e.g. soybean, rapeseed, sunflower,
safllower, castor bean or corn. The present sequence represents the amino
acid sequence of the Brassica wild-type Fad2-F gene product

Sequence 384 AA;

Query Match 64.4%; Score 1318; DB 2; Length 384;
Best Local Similarity 61.2%; Pred. No. 5,9e-126;
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4

1 MGAGGRM--SDPSSEK--NIILRVVD--PPFTLSDLKKRIPTHCPERSVIRSSYYVVHDL 55
1 MGAGGRMOVSPSKSKEJTTIRKVCETPEFPVVGELKKRIIPHCFRKS.IPRSSSYLIWDI 60
56 IVAAYFYFLIANTYIPLIPTLAYLAMPVVMFCOASITGLTAVIIGHGCHHAFFSDYLIDD 115
61 IIASCFYVATYTPFLPHRLPSLYFMALPYMAOCQCVLTGVWVIHAHGCHHAFFSDYIMDD 120
116 IVGFVLHSALLTPYSWMKSHRNHNANTNSLDNDVEYIIPKRSKVKIYSKLNNPGRRVF 175
121 TVGLIFHSFLIVPYFSWKSHRRHSNSTSLERDEVFVPKKSDIKMYGYKLNNPLGRTV 180
176 TLVFLTLTGFPYLYLTNTISGKY-GRFANHPDMSPINFDNRERVQVLLDQGLLAIFYAI 234

Db 181 MLTVQFTLGMPLAFAVNSGPRPDGCFACHPNAPIYNDERLQIYISDAGILAVCYGL 240
 QY 235 KLVAAKGAAMVIMMYAIPVLGVSVFVLITYLHHTHLSLPHYDSTENWIKGALSTDR 294
 Db 241 FRVAAAGVASMVCFCYGPLIVNGFLVLTLYLQHTHPSLPHYDSEMDLRGALATVDR 300
 QY 295 DFGFLNRVFDVTHVTHVLAHLISYIPIHYAKARDAIKPVLGEEYKIDRTPIFRAMREA 354
 Db 301 DYGILNKVFHNITDTHVAHHLFSTMPHYHMEATKAIKPIIGEYYQFDGTPVAVAMREA 360
 QY 355 KECIYIEPDEDESHKGVFWYH 375
 Db 361 KECIYIEPDEROGEEKGVFWYN 381
 RESULT 13
 ID AAY70114 standard; protein; 384 AA.
 XX AAY70114;
 AC AAY70114;
 DT 05-JUN-2000 (first entry)
 XX Brassica napus wild type Delta-12 fatty acid desaturase-F (Fad2-F).
 XX Long chain monounsaturated fatty acid; erucic acid; oleic acid;
 KM delta-15 fatty acid desaturase; Fad3; linoleic acid; vegetable oil;
 KM industrial oil; lubricant; hydraulic oil; delta-12 fatty acid desaturase;
 KM Fad2; Fad2-F; rapeseed.
 XX Brassica napus.
 OS
 FH Key location/Qualifiers
 FT Region 165..180
 FT /label=Conserved_region
 FT MO200007433-A1.
 PD 17-FEB-2000.
 XX 03-AUG-1999; 99WO-US017645.
 XX 03-AUG-1998; 98US-00128602.
 XX (CRGI) CARGILL INC.
 XX Kodali D, Fan Z, Debonte LR;
 PI WPI; 2000-223937/19.
 DR N-PSDB; AAZ51120.
 XX New Brassica plants and seeds having elevated long chain monounsaturated
 PT fatty acid content, for industrial uses, e.g. engine lubricants.
 XX Disclosure; Page 104-105; 117pp; English.
 PS The patent discloses Brassica plants and seeds having a long chain
 CC monounsaturated fatty acid (FA) content of at least 8% and an erucic
 CC acid content of at least 15% based on total FA composition. The patent
 CC further relates to genes encoding delta-12 and delta-15 fatty acid
 CC desaturases (Fad2 and Fad3 respectively). Mutations in these genes result
 CC in useful alterations in the fatty acid compositions of the seed oil e.g.
 CC mutation in Fad2 gene confers elevated oleic acid content and decreased
 CC linoleic acid content. The Brassica seeds are useful source for vegetable
 CC oil and industrial oils such as engine lubricants, transmission fluids
 CC for diesel engines and hydraulic oil. The present sequence is that of
 CC Brassica napus microsomal wild type delta-12 fatty acid desaturase-F
 CC (Fad2-F)
 XX Sequence 384 AA;
 SQ
 Query Match 64.4%; Score 1318; DB 3; Length 384;
 Best Local Similarity 61.2%; Pred. No. 5.9e-126;

Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;
 QY 1 MGAGRM-SDPSECK-NLIERVPVD-PPTLSDLKKAIPTHCFERSVIRSSYYVHDL 55
 Db 1 MGAGRMQVSPPSKKSSTDTIKRVPCTPPTVSELKKAIPPHCFKSIIPRSSTYLLWDI 60
 QY 56 IVAVFYFLANTYIPLIPTPLAYLAMPVYWCQASILTLGVLVIGHEGCHAFSDYQLID 115
 Db 61 IIAACFYVATNTYPLPLPHPLSYFAMPLVMACQGCGLTVGVAVIAHEGCHAFSDYQLIDD 120
 QY 116 IVGFVLHSAITLPYFSKYSHRNHNANTNSLNDDEVYIPKRSKVKYISKLANPPGHVF 175
 Db 121 TVGLIFHSFLVLPYFSKYSHRNHNANTNSLNDDEVYIPKRSKVKYISKLANPPGHVF 180
 QY 176 TLVFRLLTGLPFLYLTLNIGSKKY-GRFANHPDPMSPIFNBERVQVLSLDFGLAVFAI 234
 Db 181 MLTVQFTLGMPLAFAVNSGPRPDGCFACHPNAPIYNDERLQIYISDAGILAVCYGL 240
 QY 235 KLVAAKGAAMVIMMYAIPVLGVSVFVLITYLHHTHLSLPHYDSTENWIKGALSTDR 294
 Db 241 FRVAAAGVASMVCFCYGPLIVNGFLVLTLYLQHTHPSLPHYDSEMDLRGALATVDR 300
 QY 295 DFGFLNRVFDVTHVTHVLAHLISYIPIHYAKARDAIKPVLGEEYKIDRTPIFRAMREA 354
 Db 301 DYGILNKVFHNITDTHVAHHLFSTMPHYHMEATKAIKPIIGEYYQFDGTPVAVAMREA 360
 QY 355 KECIYIEPDEDESHKGVFWYH 375
 Db 361 KECIYIEPDEROGEEKGVFWYN 381
 RESULT 14
 ID AAY27329 standard; protein; 384 AA.
 XX AAY27329;
 AC AAY27329;
 DT 15-NOV-1999 (first entry)
 XX B. napus delta-12 fatty acid desaturase 2 (FAD2) D form.
 XX Fatty acid; delta-12 desaturase; fatty acid desaturase; FAD; enzyme;
 KM linoleic acid; alpha-linolenic acid; mutant; nutritional value;
 KM genetic mapping; plant breeding.
 XX Brassica napus.
 OS
 FH EP945514-A1.
 PD 29-SEP-1999.
 XX 26-MAR-1998; 98EP-00302322.
 XX 26-MAR-1998; 98EP-00302322.
 XX (DUPLO) DU PONT DE NEMOURS & CO E I.
 PI Broglie RM, Miao G, Debonte LR, Reiter RS, Hiltz WD;
 DR WPI; 1999-530050/45.
 DR N-PSDB; AAX91076.
 XX Altering fatty acid profiles in plant seeds, useful for changing
 PT nutritional value of seeds.
 XX Example; Page 19-21; 44pp; English.
 XX The invention relates to a method for altering the fatty acid composition
 CC in plant seeds and comprises transforming a plant with a nucleic acid
 CC construct (I) comprising a seed-specific regulatory sequence linked to
 CC either a mutant delta-12 or delta-15 fatty acid desaturase (FAD) gene
 CC encoding a protein with a mutation in a His-(Asp/Glu)-Cys-(Gly/Ala)-His
 CC amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15

CC FAD. Expression of this construct in plants decreases the level of
 CC activity of these enzymes in the cells of the plant i.e. the construct
 CC acts as a dominant negative. The construct comprising a mutant delta-12
 CC gene is used to decrease the level of linoleic acid in the seeds of
 CC plants to (soybean, rapeseed, sunflower, oil palm, coconut palm, flax,
 CC castor and peanut). Similarly a construct comprising a mutant delta-15
 CC gene is used to decrease the levels of alpha-linolenic acid in the seeds
 CC of plants, especially Brassica canola. The new method may also be used to
 CC transform a plant with both (i) comprising DNA encoding mutant delta-12
 CC and (i) comprising DNA encoding mutant delta-15 FAD genes, to decrease
 CC the levels of both linoleic and alpha-linolenic acid simultaneously in
 CC their seeds. These methods alter the nutritional value of the seeds of
 CC plants which have been transformed. (i) may also be used as DNA
 CC diagnostic markers in plant genetic mapping and plant breeding programs.
 CC In addition (i) may be used to isolate other related FAD genes. The
 CC present sequence represents a Brassica napus wild type D form of
 CC microsomal delta-12 fatty acid desaturase 2 (FAD2)
 XX
 SQ Sequence 384 AA;
 Query Match 64.3%; Score 1317; DB 2; Length 384;
 Best Local Similarity 61.3%; Pred. No. 7.5e-126;
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;
 QY 1 MGAGGRM-----SDPSGKNILERVVD-PEPTLSDLKKAIPTHCFERSVIRSSYTVVD 54
 DB 1 MGAGGRMOVSPSKSETDNI-KRVPCEPPTFYGELKKAIPHCFKSIRSFSTYLIWD 59
 QY 55 LIVAVFVYLLANTYIPLIPTPLAYLAMPVWFCQASILITGLMVI GHEGHHAFSDYOLID 114
 DB 60 IILASCFYVATYTFPLLPPLPLSTFAMPLVWACQCVLTIGWVIAHEGHHAFSDYOLID 119
 QY 115 DIVGFVLHSAALTTPYFSWKYSHRNHANTNSLNDDEVYIPKRSKVYKLSKLNPPGRV 174
 DB 120 DTVGILFHSPFLVYFWSKYSHRHNSHTGSLERDEVEVPKKKSDIKMYGKYLNPPGRT 179
 QY 175 FTLVFRLTLGFPPLVLTNLSGKKY-GRPAHFDMSPFNDREVOVLISDFGLAVFYA 233
 DB 180 VMLTVQFTLGMPLVLAFFVNSGRPYDGGPACHFNPAPIYNDREKLIQIYISAGILAVCYG 239
 QY 234 IKLVAAGAAMVINMVAIPLVGSVFVLTLYLHTHTLSLPHYDSTEMNMIKALSTID 293
 DB 240 LYRAAAGVAVASWCFYGVPLIYNGFLVLTLYLOHTHPSLPHDSSMDWLKGLATVD 299
 QY 294 RDFGLNRVFDVTHVTLHLISYIPHYAKAADAIPVLGSEYKIDRTPIFKAMTYRE 353
 DB 300 RDYGI LNKVFHNITDTVHAHLFSTMPHYAMEATKAIKPILGSEYQDGTPIVYVAMWRE 359
 QY 354 AKECIYIEPDEDESEHKGVFWTH 375
 DB 360 AKECIYVEPDRQGEKKGVFWYN 381
 RESULT 15
 ABB80028 ID ABB80028 standard; protein; 384 AA.
 XX AC ABB80028;
 XX DT 26-JUN-2002 (first entry)
 DE Rape microsomal delta-12 desaturase amino acid sequence.
 XX KW Rape; microsomal delta-12 desaturase; delta-12 hydroxylase;
 KM delta-12 fatty acid hydroxylase; enzyme; plant; vegetable oil; seed oil;
 KM fat; oil; heart disease.
 XX OS Brassica napus.
 XX US6372965-B1.
 XX 16-APR-2002.
 PD XX

PF 14-AUG-1998; 98US-00133962.
 XX PR 17-NOV-1992; 92US-00977339.
 PR 15-OCT-1993; 93WO-US009987.
 PR 20-JUN-1994; 94US-00262401.
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA Lightner JE, Okuley JJ, Hitz W, Kinney AJ, Perez-Grau L;
 PI Yadav NS;
 XX DR N-PSDB; ABL58600.
 XX WPI; 2002-392229/42.
 PR New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or
 PT delta-12 fatty acid hydroxylase for creating transgenic plants and
 PT producing seed oil with altered levels of unsaturated fatty acids.
 XX Example 3; Col 75-76; 54pp; English.
 PS The invention relates to an isolated nucleic acid fragment encoding or
 CC comprising a sequence encoding a plant enzyme that is a delta-12
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.
 CC Chimeric genes comprising nucleic acids of the invention are used to
 CC create transgenic plants with altered levels of unsaturated fatty acids,
 CC and can modify plant lipid composition. Nucleic acids of the invention
 CC can be used as hybridization probes to isolate or amplify nucleotide
 CC sequences encoding other fatty acid desaturases or fatty acid desaturase-
 CC related enzymes. They can also be used in restriction fragment length
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in
 CC seed oil of oil producing plant species. They can also be used to produce
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic
 CC acids of the invention can combine the high oleate trait of transformed
 CC seeds with mutations for altered fatty acid compositions to obtain new
 CC total acid compositions and/or improved agronomy. A vegetable oil low in
 CC fatty saturates and high in monounsaturates would provide significant
 CC health benefits to consumers (reduced risk of coronary heart disease) as
 CC well as economic benefits to oil processors. The current sequence
 CC represents a rape microsomal delta-12 desaturase amino acid sequence
 XX
 SQ Sequence 384 AA;
 Query Match 64.3%; Score 1317; DB 5; Length 384;
 Best Local Similarity 61.3%; Pred. No. 7.5e-126;
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;
 QY 1 MGAGGRM-----SDPSGKNILERVVD-PEPTLSDLKKAIPTHCFERSVIRSSYTVVD 54
 DB 1 MGAGGRMOVSPSKSETDNI-KRVPCEPPTFYGELKKAIPHCFKSIRSFSTYLIWD 59
 QY 55 LIVAVFVYLLANTYIPLIPTPLAYLAMPVWFCQASILITGLMVI GHEGHHAFSDYOLID 114
 DB 60 IILASCFYVATYTFPLLPPLPLSTFAMPLVWACQCVLTIGWVIAHEGHHAFSDYOLID 119
 QY 115 DIVGFVLHSAALTTPYFSWKYSHRNHANTNSLNDDEVYIPKRSKVYKLSKLNPPGRV 174
 DB 120 DTVGILFHSPFLVYFWSKYSHRHNSHTGSLERDEVEVPKKKSDIKMYGKYLNPPGRT 179
 QY 175 FTLVFRLTLGFPPLVLTNLSGKKY-GRPAHFDMSPFNDREVOVLISDFGLAVFYA 233
 DB 180 VMLTVQFTLGMPLVLAFFVNSGRPYDGGPACHFNPAPIYNDREKLIQIYISAGILAVCYG 239
 QY 234 IKLVAAGAAMVINMVAIPLVGSVFVLTLYLHTHTLSLPHYDSTEMNMIKALSTID 293
 DB 240 LYRAAAGVAVASWCFYGVPLIYNGFLVLTLYLOHTHPSLPHDSSMDWLKGLATVD 299
 QY 294 RDFGLNRVFDVTHVTLHLISYIPHYAKAADAIPVLGSEYKIDRTPIFKAMTYRE 353
 DB 300 RDYGI LNKVFHNITDTVHAHLFSTMPHYAMEATKAIKPILGSEYQDGTPIVYVAMWRE 359
 QY 354 AKECIYIEPDEDESEHKGVFWTH 375
 DB 360 AKECIYVEPDRQGEKKGVFWYN 381

Thu Jun 24 08:51:45 2004

us-10-069-772-2.rag

Page 11

Search completed: June 18, 2004, 17:36:25
job time : 61 secs

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2047	100.0	1152	8 CQF245938	AX245938 Calendula
2	2047	100.0	1285	6 AX089471	AX089471 Sequence
3	1922	93.9	1419	8 AY166773	AY166773 Helianthu
4	1644	80.3	979	8 AY166776	AY166776 Rudbeckia
5	1629	79.6	1435	8 CAY16285	Y16285 Crepis alpi
6	1607	78.5	979	8 AY166778	AY166778 Helichrys
7	1596	78.0	979	8 AY166777	AY166777 Dimorphot
8	1592.5	77.8	1312	6 AR367438	AR367438 Sequence
9	1592.5	77.8	1312	6 AX031162	AX031162 Sequence
10	1592.5	77.7	1312	6 BD061165	BD061165 Plant fat
11	1589.5	77.7	1358	6 AR367437	AR367437 Sequence
12	1588.5	77.7	1358	6 AX031160	AX031160 Sequence
13	1588.5	77.7	1358	6 BD061164	BD061164 Plant fat
14	1589.5	77.7	1358	6 CPY16283	Y16283 Crepis pala
15	1578.5	77.1	1364	6 AR064128	AR064128 Sequence
16	1541.5	75.3	1406	8 AY462108	AY462108 Stokesia
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18	1387.5	67.8	1516	8 AF525534	AF525534 Vernonia
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22	1360	66.4	1250	8 AY057406	AY057406 Persaea am
23	1359.5	66.4	1507	8 AF188264	AF188264 Vernonia
24	1357	66.3	1259	8 AF251844	AF251844 Helianthu
25	1350.5	66.0	1475	8 AF188263	AF188263 Vernonia
26	1348.5	65.9	1472	8 SCD120LDS	X92847 S.commerbon
27	1347.5	65.8	1401	8 AY178447	AY178447 Punica gr
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29	1337.5	65.3	1350	8 PCR437139	AX373739 Punica gr
30	1337.5	65.3	1398	6 AX700111	AX700111 Sequence
31	1336	65.3	1447	8 PCUR6072	UB6072 Petroselinu
32	1336	65.3	1627	8 AB094415	AB094415 Sinapiac
33	1336	65.3	7914	8 AF331163	AF331163 Gossypium
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36	1325.5	64.8	1536	8 SOYMO6DA	L43921 Glycine max
37	1323.5	64.7	1411	6 AX301157	AX301157 Sequence
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39	1321.5	64.6	1452	8 AY083163	AY083163 Olea euro
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41	1318	64.4	1155	6 BD261361	BD261361 Plants, s
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45	1317	64.3	1155	6 AR184295	AR184295 Sequence

RESULT 1

ALIGNMENTS

CORF245938		1152 bp	mRNA	linear	PLN 22-DEC-1999
LOCUS	CORF245938				
DEFINITION	Calendula officinalis partial mRNA for (8,11)-linoleoyl desaturase (des8.11 gene).				
ACCESSION	AJ245938.1	GI:6634079			
VERSION		(8,11)-linoleoyl desaturase			
KEYWORDS					
SOURCE	Calendula officinalis				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Calenduleae; Calendula.				
REFERENCE	1 Fritzsche,K., Hornung,E., Peitzsch,N., Renz,A. and Feussner,I.				
AUTHORS	Isolation and characterization of a calendic acid producing				
TITLE	(8,11)-linoleoyl desaturase				
JOURNAL	FEBS Lett. 462 (3), 249-253 (1999)				
MEDLINE	20086417				
PUBMED	10622705				
REFERENCE	2 (bases 1 to 1152)				
AUTHORS	Feussner,I.				
TITLE	Direct Submission				
JOURNAL	Submitted (02-SEP-1999) Feussner I., Hormonforschung, Institut fuer Pflanzenbiochemie, Weinberg 3, D-06120 Halle/Saale, GERMANY				
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Score:	2047.00	Matches:	377		
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Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
DB:	8	Gaps:	0		
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Db	1 ATGGGTCTGGTGTCGGATGTCGATCACTCGAGGAAAAAAATCTTGAACGTGYG	60			
OY	21 ProValAPProproPhetheThieuSeRaSpLeuLySLySaLaIlleProThZhiSeCySpHe	40			
Db	61 CCAAGTCATCCACCCTTCAACGTTAACCATCTGAAGAAAGCATTCCTTAACCATTCCTTT	120			
OY	41 GluArgSeArVallleArgSeSerTyTrYValVaHlaHisApLeuIlleValalaTyVal	60			

LOCUS	AX089471	1285 bp	DNA	linear	PAT 21-MAR-2001
DEFINITION	Sequence 1 from Patent WO0115362.				
ACCESSION	AX089471	GI:13443732			
VERSION	AX089471.1	GI:13443732			
Db	121	GAGGAGTCTGTCATCCGGTATCATTAATCTGTTATATATCATATGCTATGTTGGCTATGTC	180		
Qy	61	PheTyrTyrIleuAlaenThrTyrIleProIleuIleProThrProIleuAlaTyrIleuAla	80		
Db	181	TTCTACTACTCTGGCAAAACAGCTAATATCCCTCTTATTCCTACACCTCGGCTTACCTGACA	240		
Qy	81	ThrProValTyrTrpPheCysGlnAlaSerIleIleuThrGlyLeuTrpValIleGlyHis	100		
Db	241	TGGCCCGCTTATCTGGTTTGTCAAGCTACAGCATCTTCAACGGCTCTCGGTCATCGGTAC	300		
Qy	101	GluCysGlyHisIleAlaPheSerAspTyrGlnIleuIleAspAspIleValGlyPheVal	120		
Db	301	GAATGTGTCTACCATGATTTAGGGACTACCAAGTGAATGATGATGATTTGGATTGGTGTG	360		
Qy	121	LeuHisSerAlaLeuLeuThrProTyrPheSerTrpIleTyrSerHisIleArgAsnHis	140		
Db	361	CTCCATTCGGCTCTCTCCACCCCTAATTTCTCTGGAATATATACCAACAGAAATACACAC	420		
Qy	141	AlaIleThrAsnSerIleuAspAsnAspGlnValTyrIleProValArgIleSerIleVal	160		
Db	421	GCACAACCAAAATTCACCTGATACGAAGAATTTACATCTCTTAAACGTAAGTCCAAAGTC	480		
Qy	161	LysIleTyrSerIleuIleuAsnAsnProProGlyArgValPheThrIleuValPheArg	180		
Db	481	AAGATTATTCCAAACTTCTTAACAATCCACCCGGGGAAGTGTTCACCTTGGTGTTCGG	540		
Qy	181	LeuThrIleuGlyPheProLeuTyrIleuLeuThrAsnIleSerGlyIleTyrGlyArg	200		
Db	541	TTGACTTTAGGATTTCCGTTATACCTCTTAACTAATATCTCGGCAAGAAATACGGGAGG	600		
Qy	201	PheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgIleuArgValGlnVal	220		
Db	601	TTTCCCAACCACTTTGATCCCATAGTCCCAATTTTCAACGATCTGTGAACGGGTTCAGATT	660		
Qy	221	LeuIleuSerAspPheGlyIleuLeuAlaValPheTyrAlaIleIleuLeuValAla	240		
Db	661	TTGCTATCCGATTTCCGTTCTTCTCGCTGATTTTATGCAATCAAGCTTCTTGTAGCACA	720		
Qy	241	LysGlyAlaAlaIleProValIleAsnMetTyrAlaIleProValIleuGlyValSerValPhe	260		
Db	721	AAAGGGGAGCTTGGATATCAATGACATGACGCAATTCAGATCTAGGTGTGAAGCGGTGTC	780		
Qy	261	PheValIleuIleThrTyrLeuHisIleThrIleIleuSerLeuProHisTyrAspSerThr	280		
Db	781	TTCTGTTTGAACATATTTGACACCAACCCATCTTCACTCCCTCATTTGATTCACAC	840		
Qy	281	GluTrpAsnTrpIleIleGlyAlaIleuSerThrIleAspArgAspPheGlyPheLeuAsn	300		
Db	841	GAATGAACTGTGATCAAAAGCGCCTTATCAACAATCAATAGGATTCGCGGTCTCTAAT	900		
Qy	301	ArgValPheHisAspValThrIleThrHisIleValIleuHisIleuIleSerTyrIlePro	320		
Db	901	CGGGTTTCCACGACGTTACACACATCTCAGCTCTTGATCATTTGATCTCATATATCCA	960		
Qy	321	HisTyrHisAlaIleGlyAlaArgAspAlaIleIleuProValIleuGlyIleuTyrTyrLys	340		
Db	961	CATTATCATGCAAGAAAGCAAGGAGATGCAATCAACGACAGTGTGGCGAGTACTATATAA	1020		
Qy	341	IleAspArgThrProIlePheIleAlaMetTyrArgGlnAlaIleGlyGlnCysIleTyrIle	360		
Db	1021	ATTCACACGAGCTCCAAATTTTCAAGCAATGATAGAAAGGTAAAGAAATGATTTAATC	1080		
Qy	361	GluProAspGluAspSerGlnHisIleGlyValPheTyrTyrHisIleMet	377		
Db	1081	GAAGCCCATGAGATGAGATGAGACGACCAAAAGGTGTGTCTTCTGTATCCCAAGATG	1131		

Db 462 GCCAACACAAATTCACCTCGATAACGATGAAGTTACAT

Db	42	ATGGGTGCTGGTGGTCGGATGTGGATTCATCGAGGGAAAAAACAATCCTTGAAACGTGTG	101
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Oy	41	GluArgSerValIleArgSerSerTyrTyrValaHisAspLeuIleValaTyrVal	60
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Oy	81	TrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGlyHis	100
Db	282	TGGCCCGTTTACTGGTTTGTCAAGCTAGATCTCTACCGCGCTCTGGGTCATCGGTCAC	341
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Oy	121	LeuHisSerAlaLeuLeuThrProTyrPheSerTrpTyrTyrSerHisArgAsnHis	140
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ORIGIN

Alignment Scores:

Pred. No.:	3.89e-171	Length:	1419
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Best Local Similarity:	91.78%	Mismatches:	14
Query Match:	93.89%	Indels:	0
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US-10-069-772-2 (1-377) x AY166773 (1-1419)

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OY 41 GluArgSerValIleArgSerSerTyTYrValValHisAspLeuIleValAlaIYrVal 60
Db 189 GAAGATCTGCATCGTTCACTTACTATGTTGTTCACTGACCTGATTTGGCCATGTC 248
OY 61 PheTYrTYrLeuAlaSerThrTYrIleProLeuIleProThrProLeuAlaTYrLeuAla 80
Db 249 TTTTACTTCCTTCCACACATATATCCCTCTTCACTACCCCTGGGCTTACTTACCA 308
OY 81 TrpProValTYrTrpPheCysGluAlaSerIleLeuThrGlyIleTrpValIleGlyHis 100
Db 309 TGGCGGGTTTACTGCTTTTGTCAAGCTTCACTCTCACTGGGCTATGGGCTATCGGTAC 368
OY 101 GluCysGlyHisHisAlaPheSerAspTYrGluLeuIleAspAspIleValGlyPheVal 120
Db 369 GAATGTGGTCAACAAGCTTATGATGATCAACAAATTGATGATGATTTGGGTTGCTC 428
OY 121 LeuHisSerAlaIleLeuThrProTYrPheSerTYrPlyTYrSerHisArgAsnHis 140
Db 429 CTCCAATTAGCTCTTATACCCCTTATTTCTTGGAAATACAGCCATCGGAACACAC 488
OY 141 AlaSerThrAsnSerLeuAspAsnAspGluValTYrIleProLYrArgLYrSerLYrVal 160
Db 489 GCCAACAAGATTCGCTTGAATGATGATGAAGTTTACTTCTTAAGCGAAGCCAAATT 548
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OY 181 LeuThrLeuGlyPheProLeuTYrLeuLeuThrAsnIleSerGlyLYrLYrGlyArg 200
Db 609 TTAACCTCAAGGTTTCTTTGTACTCTTGTGACTTAACATTTCTGGCAAAATATACGGG 668
OY 201 PheAlaAsnHisAspAspProMetSerProIlePheAsnAspArgGluArgValGlnVal 220
Db 669 TTTCGCAACCACTTTGATTCACATAGTCGATTTTCACTGACGCGTGAAGAGTACGGTT 728
OY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTYrAlaIleLYrLeuLeuValAlaAla 240
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OY 281 GluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeuAsn 300
Db 909 GAAAGCAACTGAGACAGAGGGGCAATTTCGCAATTGATGAGGATTTTGGATTCCTGAT 968

OY 301 ArgValPheHisAspValIleThrHisThrHisValLeuHisHisLeuIleSerTYrIlePro 320
Db 969 AGGCTTTCATGATAGTACCACTCACTGCTTGCATCTGATCTCTTCAATTTCA 1028

OY 321 HisTYrHisAlaLysGluAlaArgAspAlaIleLysProValIleuGlyGluTYrTYrLys 340
Db 1029 CATTTATCATGCAAAAGAGGCAAGAGACGCAATCAAGCAAGCTTGGGATTTTATAG 1088

OY 341 IleAspArgTrpProIlePheLysAlaMetTYrArgGluAlaLysGlyIleTYrIle 360
Db 1089 ATCGATAGAACCCCTATTTCACAGCGATGCGAGAGGCGCAAGATGATCTACATC 1148

OY 361 GluProAspGluAspSerGluHisLysGlyValPheTrpTYrHisLysMet 377
Db 1149 GAACCGATGAGATGAGTACGAAACAAAGGCAATATTGGTATCAATAATG 1199

RESULT 4
AY166776 979 bp DNA linear PLN 02-JUN-2003
LOCUS
DEFINITION Rudbeckia hirta delta12-fatty acid acetylase gene, partial cds.
ACCESSION AY166776
VERSION AY166776.1 GI:31322140
KEYWORDS
SOURCE
ORGANISM
Rudbeckia hirta
Rudbeckia hirta
Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Rudbeckia.
1 (bases 1 to 979)
Cahoon, B. B., Schnurr, J. A., Huffman, B. A. and Minto, R. B.
Fungal responsive fatty acid acetylases occur widely in
evolutionarily distant plant families
Plant J. 34 (5), 671-683 (2003)
2 (bases 1 to 979)
Cahoon, B. B.
Direct Submission
Submitted (19-OCT-2002) Crop Genetics, Dupont, Bldg. 402
Experimental Station, Wilmington, DE 19880-0402, USA
Location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.:	3.39e-145	Length:	979
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Qy      41 GluArgSerValaalleArgSerSerTyrrValValaIleAspLeuIleValaIleTyrrVal 60
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Qy      301 ArgValPheHisAspValThriIleThriIleValIleuHisIleLeuIleSerTyrrIlePro 320
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Qy      321 HisTyrrHisAlaLeuGlyAlaArgAspAlaIleIleAspProValleuGlyGluTyrrTyrr 340
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DEFINITION
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Gaps: 0
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Qy      92 LeuThrglyLeuTrpValalleglyHisGlyCysGlyHisIleAlaPheSerAspTyrrGln 111
Db      181 CTMAACGGTTATAGGTGATCGGTCAAGAAATGTGKACCAATGCTTTATGATGATCAAG 240
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 Db 481 AATGTTCCGGGAAGAAATACGAAAGTTTGGCAACCACTTGTATCCGTGATGCCGATT 540
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 Db 541 TTCACCGGCGCGAAGCAATTCAGTTGTCTATCGATCTTGGTATCATGCTGTATT 600
 Qy 232 TyrlleAlaIleValSerLeuValAlaAlaIleGlyAlaAlaIleProValIleAsnMetTyrlle 251
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 LOCUS Dimorphotheca sinuata delta12-fatty acid acetylase gene, partial
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 ACCESSION AY166777
 VERSION AY166777.1 GI:31322142
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 SOURCE Dimorphotheca sinuata (African daisy)
 ORGANISM Dimorphotheca sinuata
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Calenduleae; Dimorphotheca.
 1 (bases 1 to 979)
 REFERENCE
 CAHON, E.B., SCHNUR, J.A., HUFFMAN, E.A. and MINTO, R.E.
 Fungal responsive fatty acid acetylases occur widely in
 evolutionarily distant plant families
 Plant J. 34 (5), 671-683 (2003)
 JOURNAL
 2 (bases 1 to 979)
 CAHON, E.B.
 Direct Submission
 TITLE Submitted (19-Oct-2002) Crop Genetics, Dupont, Bldg. 402
 AUTHORS
 JOURNAL

FEATURES
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 Experimental Station, Wilmington, DE 19880-0402, USA
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 Alignment Scores:
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 Score: 1596.00 Matches: 286
 Percent Similarity: 94.48% Conservative: 22
 Best Local Similarity: 87.73% Mismatches: 18
 Query Match: 77.97% Indels: 0
 DB: 8 Gaps: 0
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 Qy 72 IleProThrProLeuAlaIleTyrlleValIleProValTyrllePheCysGlnAlaSerIle 91
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Qy 80 ALaTrpProValIYrTrpPheCysGlnAlaSerIleuThrGlyLeuTrpValIleGly 99

REFERENCE 1

AUTHORS Green, A., Singh, S., Stymer, S. and Lenman, M.
TITLE Plant fatty acid epoxigenase genes and uses therefor
JOURNAL Patent: WO 9846762-A 3 22-OCT-1998;
 GREEN ALLAN (AU); SINGH SURINDER (AU); COMM SCIENT IND RES ORG
 (AU); STYMER STEN (SE); LENMAN MARIT (SE)

FEATURES Location/Qualifiers

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ORIGIN

Alignment Scores:

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Pred. No.: 3,44e-140 Length: 1312
Score: 1592.50 Matches: 285
Percent Similarity: 86.24% Conservative: 41
Best Local Similarity: 75.40% Mismatches: 47
Query Match: 77.80% Indels: 5
DB: Gaps: 3

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US-10-069-772-2 (1-377) x AX031162 (1-1312)

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QY 21 ProValAspPro---ProPheThrLeuSerAspLeuValAlaIleProThrHisGly 39
DB 80 TCAGTTATTCACGTAACCTTCTCACTGATGATTTGAAGACAGACATCCCTCCACATTCG
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DB 260 GCTTGGCGGCTTTCCTGCTTGTCAAGCTAGCGCTCCACATGGGTTATVGATCCTCGC
QY 100 HisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAspIleValGlyPhe 119
DB 320 CATTAATGTGTCAACATGCTATAGCACTACATGAGGTGACGACACTGTGGGCTTC
QY 120 ValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrTyrSerHisArgAsnHis 139
DB 380 ATCATTCATTCATTTCTCTCCACCCCGATTTCTCTTGAATAACAGTCAACCGGATCAC
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DB 440 CATTCACAACAAAGTTCATGATTAACATGAAGTTTACATTCGAAAGAACAGTCCAAA
QY 160 ValIleTyrSerIleValLeuAspAspProProGlyArgValPheThrLeuValPhe 179
DB 500 CTCAAGGCTATCTATAACTTCTTAACACCACTGATGATCTGTGGTTTGGTTATC
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RESULT 10

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LOCUS BD061165 1312 bp DNA linear PAT 27-AUG-2002
DEFINITION Plant fatty acid epoxigenase genes and uses therefor.
ACCESSION BD061165
VERSION BD061165.1 GI:22606771
KEYWORDS JP 2001518797-A/2.

SOURCE

ORGANISM Crepis sp.
REFERENCE 1 (bases 1 to 1312)
 Stymer, S., Green, A., Singh, S. and Lenman, M.
 Plant fatty acid epoxigenase genes and uses therefor
 Patent: JP 2001518797-A 2 16-OCT-2001;
 COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION, STEN
 STYMER

COMMENT

OS Crepis sp.
PN JP 2001518797-A/2
PD 16-OCT-2001
PF 09-APR-1998 JP 1998543302
PR 15-APR-1997 AU PO 6223,15-APR-1997 AU PO 6226 PR
 16-APR-1997 US 60/043706 20-JUN-1997 US 60/050403 PI STEN
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CT Topology: Linear;
FT Key CDS Location/Qualifiers
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ORIGIN /db_xref="taxon:137775"

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 Best Local Similarity: 75.40% Mismatches: 47
 Query Match: 77.80% Indels: 5
 DB: 6 Gaps: 3

US-10-069-772-2 (1-377) x BD061165 (1-1312)

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 Qy 180 ArgLeuThrLeuGlyPheProleuTyTyTyLeuThrAsnIleSerGlyLysTyTyGly 199
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 Db 680 GTCCTCTTGGGATCTTGTCTCTTCTGCTGTTTAAAGATTTAAAGTTGGCTTACCA 739
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RESULT 11
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 DEFINITION Sequence 1 from patent US 6329518.
 ACCESSION AR367437
 VERSION AR367437.1 GI:3460636
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 Unclassefied.
 1 (bases 1 to 1358)
 REFERENCES
 Green, A., Singh, S., Lemman, M. and Styenne, S.
 TITLE Plant fatty acid epoxigenase genes and uses therefor
 JOURNAL Patent: US 6329518-A 11-DEC-2001;
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ORIGIN /mol_type="genomic DNA"

Alignment Scores:

Pred. No.: 6.88e-140 Length: 1358
 Score: 1589.50 Matches: 285
 Percent Similarity: 85.98% Conservative: 40
 Best Local Similarity: 75.40% Mismatches: 48
 Query Match: 77.65% Indels: 5
 DB: 6 Gaps: 3

US-10-069-772-2 (1-377) x AR367437 (1-1358)

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 Db 84 TCAGTGTATCCAGTAACCTTCTCACTAGTAGATTTGAAGCAAGCAATCCCTCCCATTC 143
 Qy 40 PheGluArgSerValIleArgSerSerTyTyTyValValHisAspLeuIleValAlaTyx 59
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 Db 264 GCTTGGCCGCTTACTGTGTCTGTCAGCTAGCTGCTCATCTGCTTATGATGATGATGAT 323
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 Db 324 CACGAATGTGTCAACATGCTTATGACATACATGATGATGATGATGATGATGATGATGAT 383
 Qy 120 ValLeuHisSerAlaLeuLeuThrProTyTyTyPheSerTyTyTySerHisArgAsnHis 139
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Score:	1589.50	Matches: 285
Percent Similarity:	85.98%	Conservative: 40
Best Local Similarity:	75.40%	Mismatches: 48
Query Match:	77.65%	Indels: 5
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US-10-069-772-2 (1-377) x AX031160 (1-1358)		
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 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; Crepis.
 REFERENCE 1
 AUTHORS Lee, M., Lemman, M., Banas, A., Bafar, M., Singh, S., Schweizer, M.,
 Nilsson, R., Liljenberg, C., Dahlqvist, A., Gummesson, P., Sjoedahl, S.,
 Green, A. and Stymer, S.
 TITLE Identification of non-heme diiron proteins that catalyze triple
 bond and epoxy group formation
 JOURNAL Science 280 (5365), 915-918 (1998)
 MEDLINE 98239771
 PUBMED 9572738
 REFERENCE 2 (bases 1 to 1358)
 AUTHORS Lemman, M.E.
 TITLE Direct Submission
 JOURNAL Submitted (21-JAN-1998) M.E. Lemman, Dept of Plant Breeding
 Research, SLU, Herman Ehles V 2-4, 26831 Svalov, SWEDEN
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 ORIGIN
 Alignment Scores:
 Pred. No.: 6.88e-140 Length: 1358
 Score: 1589.50 Matches: 285
 Percent Similarity: 85.98% Conservative: 40
 Best Local Similarity: 75.40% Mismatches: 48
 Query Match: 77.65% Indels: 5
 Gaps: 3
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 DB 144 TTCAGAGATCTGTAAATCCGCTCATCTTAATGTGTTCAAGATCATATATGCGCTAC 203

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 DB 864 ACTAAATGGAATGATCAAGAGGGGCTTGTCAACCAATCGATAGGACTTGTGATTCCTG 923
 QY 300 AsnArgValPheHisAspValThrHisIleValLeuHisIleLeuIleSerTyIle 319
 DB 924 AATAGTGTTCATGATGATTTTACACACATCATGATCATGATCATGATCATGATCATGAT 983
 QY 320 ProHisTyHisAlaIYsGlyAlaArgAspAlaIleIYsProValLeuGlyGluTyTy 339
 DB 984 CCACTATCATGTGCAAGAGAGGCAAGGATCATATCAAGCAATCTTGGCGCATTTTAT 1043
 QY 340 LysIleAspArgThrProIlePheIYsAlaMetTyArgGluAlaIYsGluCysIleTy 359
 DB 1044 ATGATGACAGAGACTCCAAATTTTAAAGCAATGTGAGAGAGGCGAGGAGTGTGATGAC 1103
 QY 360 IleGluProAspGluAspSerGluHisIYsGlyValPheTrpTyHisIYsMet 377
 DB 1104 ATCGAGCT-----GATAGCAAGCTCAAGAGTATTATGATCATTAATTTG 1151
 RESULT 15
 LOCUS AR064128 1364 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 3 from patent US 5846784.
 ACCESSION AR064128
 VERSION AR064128.1 GI:5993436
 SOURCE unknown.

ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1364)
Hitz, W.D.
TITLE Fatty acid modifying enzymes from developing seeds of *Veronica galamensis*
JOURNAL Patent: US 5846784-A 3 08-DEC-1998;
FEATURES Location/Qualifiers
source 1. 1364
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.:	7,49e-139	Length:	1364
Score:	1578.50	Matches:	280
Percent Similarity:	87.16%	Conservative:	39
Best Local Similarity:	76.50%	Mismatches:	44
Query Match:	77.11%	Indels:	3
DB:	6	Gaps:	2

US-10-069-772-2 (1-377) x AR064128 (1-1364)

QY 15 AsnIleLeuGluValProValAsp--ProProPheThrLeuSerAspLeuLys 33
DB 157 AATATAAACGAACGACCGGTTGATCGGCACCATTCGTAAAGCATTAAGAA 216
QY 34 AlaIleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValHis 53
DB 217 GCATTCCTCCGCAATGCTTCAGAGATCTCCATCCCTTATCGTACGTCTTCAG 276
QY 54 AspLeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIlePro 73
DB 277 GATCTCATTAATACCTCTTATACAGCGCTCGGCACCTTACATTCCTCTCTCT 336
QY 74 ThrProLeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThr 93
DB 337 CCTCCTTACCTTCTTGAATGCGCTGTTTACGTTTGCATTCGATTCGATCTCACT 396
QY 94 GLeuTyrValIleGluHisGluCysGluHisHisAlaPheSerAspTyrGlnLeuIle 113
DB 397 GGTATATGGCTCATTTGGCCATGAATGTGCCATCATCTTATAGAGATCAAGGGTT 456
QY 114 AspAspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrLys 133
DB 457 GATAACACCGTTGATCATCTCCATTCCTTCTTCAACACCTTCTTCTTGGAAA 516
QY 134 TyrSerHisArgAsnHisHisAlaAsnThrAsnSerIleuAspAspGluValTyrIle 153
DB 517 TACAGCCATCGAAGACCAACGCAACGAAATTCATCGAAGACGAGAGTTTACAT 576
QY 154 ProLysArgLysSerLysValLysIleTyrSer-----LysLeuLeuAsnAspProPro 171
DB 577 CTTAAAGCCAGTCCCACTCAGGAATTCCTCAATTCTTCAATTCTTGACACACCCCT 636
QY 172 GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThr 191
DB 637 GGTGGAATCTCATTTGCTATCATGTGACCTTGCGCTTCTTATACCTTGAC 696
QY 192 AsnIleSerGlyLysGlyTyrGlyArgPheAlaAsnHisPheAspProMetSerProIle 211
DB 697 AATATTCAGGCAAGAAATACCAAGGTTTGCACACCTTGATCCGTTGAGCCCATC 756
QY 212 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe 231
DB 757 TTCAGTGAAGCGTAACGAATCCAGTCTGCTATCGATGCGGTCTCATCTGCTGT 816
QY 232 TyrAlaIleLysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAla 251
DB 817 TACGGGCTTAAGTTCTTGTAGCAAAAGAGGTTGCGGTGAGTATCGCATGTAACGA 876
QY 252 IleProValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHis 271

DB 877 GCCCCAGTGGTGGCTGAATGCTTCAATAATGATCACTTATCTCCACACACCAT 936
QY 272 LeuSerLeuProHisTyrAspSerThrGluTyrAsnTyrIleLysGlyAlaLeuSerThr 291
DB 937 CTGCTTGGCTCATTTAGATTCGACCGAATGAACTGSAATCAAGAGCCTTGATCA 996
QY 292 IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisVal 311
DB 997 ATCGATGAGATTTGCGGTCTCGAATAGGGTGTTCATGACGCTACACACACACG 1056
QY 312 LeuHisIleLeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIle 331
DB 1057 TTGCATCATTTGTTCCCGTACATTCACATTAATCATCGAAGAGGCGAGGACGATA 1116
QY 332 LysProValLeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyr 351
DB 1117 AAGCCGGTGTAGGGAGATCGAGATGATCGATGATCGATGATCGATGATCGATGAT 1176
QY 352 ArgGluAlaLysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyVal 371
DB 1177 AGAGAGGCGAAGGAATGATCTCATCGACGATGAAAGTAAGAACACAAAGGTGTA 1236
QY 372 PheTyrTyrHisLysMet 377
DB 1237 TATGTATCCATTAATG 1254

Search completed: June 23, 2004, 16:53:19
Job time : 3312 secs

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OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:50:48 ; Search time 425 Seconds
(without alignments)
12844.552 Million cell updates/sec

Title: US-10-069-772-1
Perfect score: 1285
Sequence: 1 aaagcctcctctctctga.....aaaaaaaaaaaaaaaa 1285

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002s:*\n7: geneseqn2003as:*\n8: geneseqn2003bs:*\n9: geneseqn2003cs:*\n10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1285	100.0	1285	4	AAF88311
2	718.6	55.9	1128	2	AAT95688
3	715.8	55.7	1358	2	AAV63101
4	705.4	54.9	1312	2	AAV63102
5	699.8	54.5	1364	2	AAV72550
6	455.6	35.5	1369	6	ABL58599
7	455.6	35.5	1372	2	AAO66068
8	455.6	35.5	1372	3	AAZ51315
9	455.6	35.5	1411	3	AAZ51315
10	454.4	35.4	1476	2	AAV72549
11	454	35.3	1152	2	AAZ32636
12	454	35.3	1451	3	AAZ32636
13	454	35.3	2973	2	AAO66074
14	454	35.3	2973	6	ABL58607
15	453.6	35.3	1451	3	AAZ32636
16	453.4	35.3	1390	3	AAZ32636
17	453.4	35.3	1580	7	ABZ22026
18	450.8	35.1	1152	2	AAZ32637
19	445.8	34.7	1422	5	AAZ22380
20	444.8	34.6	1411	5	AAZ22379
21	436.8	34.0	1411	5	AAZ22379
22	436	33.9	1662	2	AAT88864
23	432	33.6	1423	6	ABL58600

24	432	33.6	1464	2	AAZ91076
25	431.8	33.6	1216	4	AAZ89457
26	431	33.5	1155	2	AAV84678
27	431	33.5	1155	2	AAZ06617
28	431	33.5	1155	2	AAZ51118
29	429.4	33.4	1155	2	AAV84677
30	429.4	33.4	1155	2	AAV84676
31	429.4	33.4	1155	2	AAZ06618
32	429.4	33.4	1155	2	AAZ51119
33	427.8	33.3	1155	2	AAZ06619
34	427.8	33.3	1155	2	AAZ51120
35	426.8	33.2	1164	7	ABZ58386
36	426.2	33.2	1155	2	AAZ91077
37	426.2	33.2	1155	2	AAZ06620
38	426.2	33.2	1155	2	AAZ06621
39	426.2	33.2	1155	3	AAZ51121
40	426.2	33.2	1155	3	AAZ51122
41	425.2	33.1	1155	2	AAZ5846
42	425.2	33.1	1155	2	AAZ06613
43	425.2	33.1	1155	3	AAZ27144
44	425.2	33.1	1155	6	ABZ55809
45	425.2	33.1	1155	10	ABZ85747

ALIGNMENTS

RESULT 1	AAZ88311	AAZ88311 standard; DNA; 1285 BP.
XX	AC	AAZ88311;
XX	DT	22-AUG-2001 (first entry)
XX	DE	C. officinalis calendulic acid desaturase encoding DNA.
XX	KW	Calendula; calendulic acid desaturase; unsaturated fatty acid; oil;
XX	OS	triglyceride; transgenic plant; de.
XX	XX	Calendula officinalis.
XX	FM	Key
XX	FT	Location/Qualifiers
XX	FT	42..1175
XX	FT	/*tag= a
XX	FT	/product= "calendulic acid desaturase"
XX	PD	DE19941609-A1.
XX	PD	08-MAR-2001.
XX	PD	01-SEP-1999; 99DE-01041609.
XX	PR	01-SEP-1999; 99DE-01041609.
XX	PA	(IPB-) IPB INST PFLANZENBIOCHEMIE.
XX	PI	Feussner I, Hornung E, Fritsche K, Peitzsch N, Renz A;
XX	DR	WPI; 2001-283028/30.
XX	DR	P-PSDB; AAB70946.
XX	PT	New nucleic acid sequence encoding Calendula officinalis calendulic acid
XX	PT	desaturase, useful for e.g. producing transgenic plants having oil with
XX	PT	an increased unsaturated fatty acid content.
XX	PS	Claim 1b; Page 13-15; 22pp; German.
XX	CC	This invention describes a novel isolated nucleic acid sequence (i)
XX	CC	encoding a Calendula officinalis calendulic acid desaturase polypeptide.
XX	CC	The invention also describes (ii) a process for producing unsaturated
XX	CC	fatty acids, comprising introducing at least one copy of (i) or (ii) into
XX	CC	an oil-producing organism, growing the organism, isolating oil from the

organism and releasing fatty acids from the oil; (2) a process for producing triglycerides with an increased unsaturated fatty acid content, comprising introducing at least one copy of (I) or (II) into an oil-producing organism, growing the organism and isolating oil from the organism; (3) a process for producing saturated fatty acids, comprising introducing at least one nonfunctional copy of (I) or (II) into an oil-producing organism, growing the organism, isolating oil from the organism and releasing fatty acids from the oil; (4) a process for producing triglycerides with an increased saturated fatty acid content, comprising introducing at least one nonfunctional copy of (I) or (II) into an oil-producing organism, growing the organism and isolating oil from the organism; (5) an enzyme capable of converting a diunsaturated fatty acid of to a triunsaturated fatty acid. Transgenic organisms (especially plants) containing one or more copies of (I) are useful for producing oils with an increased unsaturated fatty acid content. Transgenic organisms (especially plants) containing one or more nonfunctional copies of (I) are useful for producing oils with an increased saturated fatty acid content. (I) and fragments of (I) are also useful for isolating genomic sequences by homology screening. This sequence encodes the calendulic acid desaturase described in the method of the invention

Sequence 1285 BP; 364 A; 294 C; 253 G; 374 T; 0 U; 0 Other;

Query Match 100.0%; Score 1285; DB 4; Length 1285;
Best Local Similarity 100.0%; Pred. No. 1.2e-306;
Matches 1285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAAAGCTCACTCTCTGTGAGGGTAATATATCAACAATGAGTCTGGTGTCCGA 60
1 AAAAGCTCACTCTCTGTGAGGGTAATATATCAACAATGAGTCTGGTGTCCGA 60
61 TGTGGATTCATCTGAGGAAAAAATCCTTTGAACGTGTGCGATCCATCCGTTCA 120
61 TGTGGATTCATCTGAGGAAAAAATCCTTTGAACGTGTGCGATCCATCCGTTCA 120
121 CGTTAAGGATCTGAAGAAAGGATTCCTACCATTTGCTTGAGGAGTCTGCAACGGT 180
121 CGTTAAGGATCTGAAGAAAGGATTCCTACCATTTGCTTGAGGAGTCTGCAACGGT 180
181 CATCATATGATGTTGATGATGATCTCATTTGTTGCTTATGCTTACATCTTGAAACA 240
181 CATCATATGATGTTGATGATGATCTCATTTGTTGCTTATGCTTACATCTTGAAACA 240
241 CGTATATCCCTTATATCTTACACCTCTGCTTACCTTACATGCTTCTTACATCTTGAAACA 300
241 CGTATATCCCTTATATCTTACACCTCTGCTTACCTTACATGCTTCTTACATCTTGAAACA 300
301 GTCAAGTAGATCCTCAACGGGCTCTGGGTCATGCTCAAGAAATGAGTCAACCATGAT 360
301 GTCAAGTAGATCCTCAACGGGCTCTGGGTCATGCTCAAGAAATGAGTCAACCATGAT 360
361 TTAAGGACTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
361 TTAAGGACTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
421 CCCCGATTTCTTCTGGAATATAGCCACAGGAATACCAAGCCAAACAATTTCACTCG 480
421 CCCCGATTTCTTCTGGAATATAGCCACAGGAATACCAAGCCAAACAATTTCACTCG 480
481 ATTAAGATGAAGTTTACATCTTAAACGTAAGTCAAGATTTATTTCAAACTTC 540
481 ATTAAGATGAAGTTTACATCTTAAACGTAAGTCAAGATTTATTTCAAACTTC 540
541 TTAACATTCACCCGGGCGAGTTCACCTTGTGTTCGTTGACTTTAGATTTCCGT 600
541 TTAACATTCACCCGGGCGAGTTCACCTTGTGTTCGTTGACTTTAGATTTCCGT 600
601 TATACCTTTAATCTATCTGCGGCAAGAAATACGGAAGTTTCCACCATTTGATC 660
601 TATACCTTTAATCTATCTGCGGCAAGAAATACGGAAGTTTCCACCATTTGATC 660
661 CCATGAGTCAATTTTGAAGATGTTGAAGCGTTTCAAGTTTGTATCCGATTTCCGTC 720
661 CCATGAGTCAATTTTGAAGATGTTGAAGCGTTTCAAGTTTGTATCCGATTTCCGTC 720

DB 661 CCATGAGTCAATTTTGAAGATGTTGAAGCGTTTCAAGTTTGTATCCGATTTCCGTC 720
QY 721 TTTCTGCTGATTTTATGATCAATCAAGCTTTGTGACGCAAAAGGGCAGCTGGGTAA 780
DB 721 TTTCTGCTGATTTTATGATCAATCAAGCTTTGTGACGCAAAAGGGCAGCTGGGTAA 780
QY 781 TCAACATGATGCAATTCAGTACTAGTGTAAAGCGTGTCTTGTGATTCATATTT 840
DB 781 TCAACATGATGCAATTCAGTACTAGTGTAAAGCGTGTCTTGTGATTCATATTT 840
QY 841 TGACACACACCATCTCTCACTCCCTCATATGATTCACCGAATGAAATGATCAAAAG 900
DB 841 TGACACACACCATCTCTCACTCCCTCATATGATTCACCGAATGAAATGATCAAAAG 900
QY 901 GCGCCTTATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
DB 901 GCGCCTTATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY 961 CACACACTCAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 961 CACACACTCAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1021 CAAGGATGCAATCAAGCAGTGTGGCGAGTACTATTAATGACAGACATCCATTT 1080
DB 1021 CAAGGATGCAATCAAGCAGTGTGGCGAGTACTATTAATGACAGACATCCATTT 1080
QY 1081 TCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 TCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 AGCACAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 AGCACAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 TGTATGCTTATTAAGTTGTTAACTTTCTATTCGTTAATTAATTAATTAATTAAGAA 1260
DB 1201 TGTATGCTTATTAAGTTGTTAACTTTCTATTCGTTAATTAATTAATTAATTAAGAA 1260
QY 1261 AAAAAAAAAAAAAAAAAAAAAA 1285
DB 1261 AAAAAAAAAAAAAAAAAAAAAA 1285

RESULT 2
AAT95688
ID AAT95688 standard; DNA; 1128 BP.
AC AAT95688;
DT 25-MAR-2003 (revised)
DT 20-APR-1998 (first entry)
XX Crepis alpina delta 12 acetylase encoding DNA.
XX Crepis alpina delta 12 acetylase; Plant; Yeast; acetylenic compound;
XX fatty acid; coating; plastic; lubricant; oilseed; ss.
OS Crepis alpina.
XX
XX
FH Key Location/Qualifiers
FT 1..1128
FT CDS /*tag= a
FT /product= "Crepis alpina delta 12 acetylase"
PD MO9737033-A1.
XX
XX
XX 09-OCT-1997.
XX
XX
XX 14-FEB-1997; 97MO-SE000247.
PF 29-MAR-1996; 96SE-00001236.
XX
XX
XX (BAFO/) BAFOR M.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (STYM/) STYME S.

PI Stymer S, Green A, Singh S, Lenman M;

DR WPI; 1998-568734/48.

DR P-PSDB; AAW79742.

PT New isolated fatty acid epoxysenase gene - used particularly for transforming plants for producing modified oils for use in, e.g. coatings, resins, glues, plastics, surfactants or lubricants.

PS Claim 15; Page 78-81; 150pp; English.

This full-length cDNA clone, designated Cpai2, codes for a novel mixed function monooxygenase (see AAM79742) of *Crepis palustris* that is characterised as having delta-12-epoxygenase activity. It was isolated from a *C. palustris* cDNA library using a Crepis alpina acetyltransferase partial gene sequence (see AAM73104) as probe. The encoded protein contains His-rich motifs (see AAM79752-54) that are characteristic of mixed function monooxygenases. The Cpai2 gene was shown to be highly expressed in developing seeds, with no expression detectable in leaves. The invention relates generally to novel genetic sequences (see AAM73101-03) encoding fatty acid epoxygenases (see AAM79742-44), especially the means by which fatty acid metabolism can be manipulated in e.g. yeast, mould, bacteria, insects, birds, mammals and plants (especially oilseed plants such as flax), in particular to convert unsaturated fatty acids to epoxygenated fatty acids. The invention extends to genetically modified oil-accumulating organisms and to the oils derived from them. These oils can be used in production of coatings, resins, glues, plastics, surfactants or lubricants

SQ Sequence 1358 BP; 358 A; 308 C; 278 G; 414 T; 0 U; 0 Other;

Query Match	Score	DB 2;	Length
55.78;	715.8;		1358;

Matches 903; Conservative 0; Mismatches 237; Indels 15;

Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;

OY	29	TTATATCAAA	CATGGGCTG	TGCTGGAT	GTGCGAT	TCATCGAGG	AAAAA	CA	88
Db	17	ATCATTTAT	CAACATGGG	TGCCGG	CGGTG	-----TGGTGG	CAATCG	AAAAATCGGT	70
OY	89	CCTTGAACG	TGTCAGT	CGATCC	---ACGGT	TCAAGT	TAAAGCAT	CTGAAGAACGAT	145
Db	71	CATGAACGT	GTCTCAGT	TGATTC	AGTAAC	CTTCTC	ACTGAAGAT	TGAAGCAAGAT	130
OY	146	TCCTAACCA	TGCTTTAG	CGCATCT	GTCAATCGG	TCATCAAT	ACTAATGTT	GTTCATATCT	205
Db	131	CCCTCCCA	TGCTTCC	AGAGATCT	GTATTCGG	CTCATCTTA	CTACTA	TGTTGTCAAATCT	190
OY	206	CATTGTGCT	ATATGCTT	CTACTAC	CTTGCAAA	CAAGTATAT	CCCTTA	TTCTCTACAC	265
Db	191	CATTATGCT	CAATCTTCT	TACTCTCT	TCCCAACA	CATATATCT	CTTCTCT	CTAC	250
OY	266	TCTGGCTTA	CCAGCATGG	CCCGTT	ACTGTTT	GTCAAGCT	AGCATCCT	CAACGGCT	325
Db	251	TCTAGCTTA	CTAGCTGG	CCGGTT	ACTGTTCT	GTCAAGCT	ATAGGCT	CCTCACTGGCTT	310
OY	326	CTGGGTCA	TGGGTCA	AGGATGT	GTGCACCA	TGATTTAG	GGACTAC	CAAGTTGATGA	385
Db	311	ATGATATCC	TGGGCAC	AGATGTGG	TGCACCAT	GTCTTAT	CAACTAC	CAATGTGTTAGCA	370
OY	386	CATTGTGGA	TGCGTCC	ATTCGG	CTCCCA	CCCGATTT	CTTTG	GAATATAG	445
Db	371	CAGTGGCTT	CACTCTCA	CTCACTAT	TCTCC	CAACCCG	ATTTCT	CTTGGAAATTCAG	430
OY	446	CCACAGAT	TCACCA	CGCCACA	CAAAAT	CACTCGAT	TAAAGATGA	ATTACATCTTA	505
Db	431	TCACCGGA	TACCAAT	TCACA	CAAGTT	CGATGTAT	TAAAGATGA	AGTTTACATTCGAA	490
OY	506	ACGTATGTC	GAAGGTCA	GAATTTAT	TCCAA	CTTTCA	CAATCCA	CCCGGCGAGTGT	565

[illegible]

PR 15-APR-1997; 97AUG-00006223.
 PR 15-APR-1997; 97AUG-00006226.
 PR 16-APR-1997; 97AUG-0043706P.
 PR 20-JUN-1997; 97JUN-0050403P.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (STYM/) STYMNE S.
 PI Scymne S, Green A, Singh S, Lenman M;
 PI MPI: 1998-556734/48.
 DR P-PSDB; AAM79743.
 XX
 PT New isolated fatty acid epoxigenase gene - used particularly for
 PT transforming plants for producing modified oils for use in, e.g.
 PT coatings, resins, glues, plastics, surfactants or lubricants.
 XX
 PS Claim 16; Page 84-86; 150pp; English.
 XX
 CC This cDNA clone, designated Crepx, codes for a novel epoxigenase (see
 CC AAM79743) of a Crepis sp. (not Crepis palaestina) that has a high
 CC vernolic acid content. The Crepx gene shows a high degree of homology to
 CC the novel Crep12 delta-12-epoxigenase gene (see AAV63101) of C.
 CC palaestina. Crepx cDNA was isolated from a Crepis sp. cDNA library using
 CC a Crepis alpina acetyltransferase partial gene sequence (see AAV63104) as
 CC probe. The invention relates generally to novel genetic sequences (see
 CC AAV63101-03) encoding fatty acid epoxigenases (see AAM79742-44).
 CC especially delta-12-epoxigenases or mixed function monooxygenases. These
 CC provide the means by which fatty acid metabolism can be manipulated in
 CC e.g. yeast, mould, bacteria, insects, birds, mammals and plants
 CC (especially oilseed plants such as flax), in particular to convert
 CC unsaturated fatty acids to epoxigenated fatty acids. The invention
 CC extends to genetically modified oil-accumulating organisms and to the
 CC oils derived from them. These oils can be used in production of coatings,
 CC resins, glues, plastics, surfactants or lubricants
 XX
 SQ Sequence 1312 BP; 347 A; 301 C; 263 G; 399 T; 0 U; 2 Other;
 Query Match 54.9%; Score 705.4; DB 2; Length 1312;
 Best Local Similarity 78.6%; Pred. No. 8,76-164;
 Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;
 QY 77 GGGAAAAAATCTTGAAGCTGTGCAAGTCGATCC--ACCGTTACGTTAAGCGATCT 133
 DB 55 GGAATAAGTCGTCATGAGAGCTGTCTCAGTTCATGATCAAGTAACTTTCATGATGATTT 114
 QY 134 GAAGAAAGCGATCTCTACCCATTGCTTGAAGCATCTGTATCCGGTCATATCTATGT 193
 DB 115 GAAGCAAGCAATCCCTCCATCTTCCAGCCGATCTGTATCCGTTTCTATTTAAGT 174
 QY 194 TGTTCATGATCTCATGTGTGCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 253
 DB 175 TGTTCATGATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 234
 QY 254 TATTCCTACACCTCTGCTTACCTAGCATGCGCGTTTACTGTTTGTCAAGCTAGCAT 313
 DB 235 TCTCCCTCATCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 294
 QY 314 CTTCAACCGGCTCTGCTGCTATCGCTCAAGATGTGTGTCACATGATTTTACGACTTCA 373
 DB 295 CTTCACTGGGTATGATCTCTGCGCATGATGTGTGTCACATGATTTTACGACTTCA 354
 QY 374 GTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 433
 DB 355 ATGGGTTGAGACACCTGTGGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 414
 QY 434 TTGAAATATATAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 493
 DB 415 TTGAAATATATAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 474
 QY 494 TTATCTTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 553
 DB 475 TTATCTTCTTAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 534

QY 554 CGGCGAGTGTTCATTTGGTGTTCGTTGATCTTATGATTTCCGTATACCTTTAAC 613
 DB 535 TGTGTGACCTGTGTGTTTGGTTATCATGTTTCACTTGAATTTCTTTATATCCTTTGAC 594
 QY 614 TATATCTCGGCGAAGAAATACGAGAGTTTGGCAACCACTTTGATCCATGATGCAAT 673
 DB 595 AATATATTTCCGGCAAGAAATACGATGATTTGGCAACCACTTTGATCCATGATGCAAT 654
 QY 674 TTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 733
 DB 655 TTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 714
 QY 734 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 793
 DB 715 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 774
 QY 794 AATTCAGTACTAGTGTAAAGCGTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 853
 DB 775 AGTTCGGGTGCTAGCGTATTTTACCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 834
 QY 854 TCTTCACTCCCTCATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 913
 DB 835 TCACTGCTGCTCATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 894
 QY 914 AATGATAGGATTTTCGGGTTCTGAAATCGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 973
 DB 895 AATGATAGGATTTTCGGGTTCTGAAATCGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCT 954
 QY 974 CTTGATCATTTTGTATCTATCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1033
 DB 955 CATCATCATTTTGTATCTATCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1014
 QY 1034 CAACCCAGTGTGGCGAGATCTTAAATGCAAGAGATCCATTTTCAAGAGATGTA 1093
 DB 1015 CAACCCAGTGTGGCGAGATCTTAAATGCAAGAGATCCATTTTCAAGAGATGTA 1074
 QY 1094 TAGAGAGCTTAAAGATGATCTTACATCGAGCCGATGAGATGAGATGAGATGAGATG 1153
 DB 1075 GAGAGAGGAGAGATGATCTTACATCGAGCC-----TGATGCAAGATGCAAGATG 1128
 QY 1154 GTTCTGTACCAAGATGATCAAA 1180
 DB 1129 TTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1155
 RESULT 5
 AAV72550
 ID AAV72550 standard; cDNA; 1364 BP.
 XX
 AC AAV72550;
 XX
 DT 27-AUG-2003 (revised)
 DT 10-FEB-1999 (first entry)
 XX
 DE Vernonia galamensis fatty acid epoxidising enzyme encoding cDNA.
 XX
 KM Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;
 KM expression; chimeric gene; recombinant enzyme; ss.
 OS Vernonia galamensis.
 XX
 FH Key Location/Qualifiers
 FT CDS 103..1257
 FT /*tag= a
 XX
 PN US5846784-A.
 XX
 PD 08-DEC-1998.
 XX
 PF 11-JUN-1997; 97JUN-00872302.
 XX
 PR 11-JUN-1997; 97JUN-00872302.

XX (DUPO) DU PONT DE NEMOURS & CO E I.
 XX Hiltz WD;
 XX WPI, 1999-059065/05.
 DR P-PSDB; AAM83354.
 XX
 PT DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid
 PT epoxidising enzyme - used to alter levels of expression of the enzymes in
 PT transformed host cells or to produce recombinant enzymes.
 XX
 PS Claim 6, Col 25-29, 21pp; English.
 XX
 CC The present sequence encodes Vernonia galamensis fatty acid epoxidising
 CC enzyme. The present invention also describes: (i) Vernonia galamensis
 CC fatty acid desaturase; (ii) chimeric genes comprising the fragments
 CC linked to regulatory sequences; and (iii) transformed host cells
 CC containing the chimeric genes. The DNA's from the present invention can
 CC be used to alter levels of expression of the enzymes in transformed host
 CC cells or to produce the recombinant enzymes by transformation of
 CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 1364 BP; 391 A; 305 C; 280 G; 388 T; 0 U; 0 Other;
 Query Match 54.5%; Score 699.8; DB 2; Length 1364;
 Best Local Similarity 75.8%; Pred. No. 2.1e-162;
 Matches 894; Conservative 0; Mismatches 277; Indels 8; Gaps 2;

QY 112 CACCGTTCACGTTAAGCATCTGAAGAAAGGATTCCTACCCATGCTTGAAGCATCTG 171
 DB 188 CACATCTCTGTTAAGCATCTGAAGAAAGGATTCCTACCCATGCTTGAAGCATCTG 247
 QY 172 TCATCCGGTTCATCTATGTTGTCATGATCTCATGTTGCTTACCTTCTTACTAC 231
 DB 248 CCAATCCGTTCTGTCATCTGTTGTCATGATCTCATGTTGCTTACCTTCTTACTAC 307
 QY 232 TTGCAACACGTTATATCCCTTATCTTACACCTCTGCGTTACCTAGCATGCGCGTTT 291
 DB 308 TCGCAACTCTTATATCTCTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367
 QY 292 ACTGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 351
 DB 368 ACTGTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 427
 QY 352 ACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
 DB 428 ATCATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 487
 QY 412 CTCTCTCAACCCGTTATCTCTTGAATATGATGATGATGATGATGATGATGATGATG 471
 DB 488 TTCTCTCAACCCGTTATCTCTTGAATATGATGATGATGATGATGATGATGATGATG 547
 QY 472 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
 DB 548 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 607
 QY 529 ---ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 585
 DB 608 CCAATTTCAATTTCTTGAACACCCCTGATGATGATGATGATGATGATGATGATGATG 667
 QY 586 CTTTAGATTTCCGTTATATCTCTTAACTAATATCTGAGGAGAAATACGGAGGTTTG 645
 DB 668 CTTTAGATTTCCGTTATATCTCTTAACTAATATCTGAGGAGAAATACGGAGGTTTG 727
 QY 646 CCAACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 705
 DB 728 CCAACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 787
 QY 706 TATCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 765
 DB 788 TATCGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 847

QY 766 GGGGAGCTTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 825
 DB 848 GGTTCGGTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 907
 QY 826 TTTGATCATATTTTGCACACACCATCTCTCATCTCTCATATGATGATGATGATG 885
 DB 908 TATGATCATATTTTGCACACACCATCTCTCATCTCTCATATGATGATGATGATG 967
 QY 886 GGAATGGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATG 945
 DB 968 GGAATGGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATG 1027
 QY 946 TTTTCCACAGCTTACACACACCTCATCTCTCATCTCTCATATGATGATGATG 1005
 DB 1028 TGTTCATGACGTCTACACACACCTCATCTCTCATCTCTCATATGATGATGATG 1087
 QY 1006 ATCATGCAAAAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATG 1065
 DB 1088 ATCATGCAAAAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATG 1147
 QY 1066 ACAGAGCTTCAATTTTCAAGCAATGATGATGATGATGATGATGATGATGATG 1125
 DB 1148 ATAGAGCTTCCGTTTATCAAAAGCAATGATGATGATGATGATGATGATGATG 1207
 QY 1126 CCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1185
 DB 1208 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1267
 QY 1186 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1245
 DB 1268 GTACGT--AGTACGTTGATGATGATGATGATGATGATGATGATGATGATG 1325
 QY 1246 TTATCATTAAG 1284
 DB 1326 ATGAAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1364

RESULT 6
 ABL58599
 ID ABL58599 standard; cDNA; 1369 BP.
 XX
 AC ABL58599;
 DT 26-JUL-2002 (first entry)
 XX
 DE Crees microsomal delta-12 desaturase cDNA.
 XX
 KW Crees; microsomal delta-12 desaturase; delta-12 hydroxylase;
 KW delta-12 fatty acid hydroxylase; enzyme; plant; vegetable oil; seed oil;
 KW fat; oil; heart disease; gene; de.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key location/Qualifiers
 FT CDS 93..1244
 FT /"tag= a
 FT /product= "microsomal delta-12 desaturase"
 XX
 PD US6372965-B1.
 PD 16-APR-2002.
 PF 14-AUG-1998; 98US-00133962.
 PF 17-NOV-1992; 92US-00977339.
 PR 15-OCT-1993; 93WO-US009987.
 PR 20-JUN-1994; 94US-00262401.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Lightner JE, Okuley JJ, Hiltz W, Kinney AJ, Perez-Grau L;
 PI Yadav NS;
 XX

DR WPI; 2002-392229/42.
 DR P-PSDB; ABB80027.
 XX New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or
 PT delta-12 fatty acid hydroxylase for creating transgenic plants; and
 PT producing seed oil with altered levels of unsaturated fatty acids.
 XX
 PS Claim 1; Col 65-70; 54pp; English.
 XX
 CC The invention relates to an isolated nucleic acid fragment encoding or
 CC comprising a sequence encoding a plant enzyme that is a delta-12
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.
 CC Chimeric genes comprising nucleic acids of the invention are used to
 CC create transgenic plants with altered levels of unsaturated fatty acids,
 CC and can modify plant lipid composition. Nucleic acids of the invention
 CC can be used as hybridisation probes to isolate or amplify nucleotide
 CC sequences encoding other fatty acid desaturase or fatty acid desaturase-
 CC related enzymes. They can also be used in restriction fragment length
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in
 CC seed oil of oil producing plant species. They can also be used to produce
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic
 CC acids of the invention can combine the high oleate trait of transformed
 CC seeds with mutations for altered fatty acid compositions to obtain new
 CC fatty acid compositions and/or improved agronomy. A vegetable oil low in
 CC total saturates and high in monounsaturates would provide significant
 CC health benefits to consumers (reduced risk of coronary heart disease) as
 CC well as economic benefits to oil processors. The current sequence
 CC represents a cress microsomal delta-12 desaturase cDNA
 XX
 SQ Sequence 1369 BP; 324 A; 358 C; 302 G; 385 T; 0 U; 0 Other;
 Query Match 35.5%; Score 455.6; DB 6; Length 1369;
 Best Local Similarity 63.9%; Pred. No. 3.4e-102;
 Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

QY 109 ATCCACCGTTTCACTTAAAGCATGTAAGAAAGGATTCCTACCATTTCTTTAGCGAT 168
 DB 175 AACCGCTTTCTCGGTGAGATCTGAAGAAAGCATCCCGCATTTGTTCAAGCCT 234
 QY 169 CTGTCATCCGGTATCATATCATGTGTGATGATGATGATGATGATGATGATGATGAT 228
 DB 235 CAATCCCTCGCTCTTCTCTCACTTACATGATGATGATGATGATGATGATGATGATGAT 294
 QY 229 ACCTTGCAACACGATATATCCCTTATTTCTTACACCTCTGGCTTACCTATGACGCGG 288
 DB 295 ACGTGGCAACAATTAATCT 354
 QY 289 TTATAGTGTGTTGCAAGCTAAGATCTTACCGGCTCTGGGTCAATCGGTCAAGATGTG 348
 DB 355 TCTATGCGGCTGTCAAGGCTGTCTCTTACTGATCTGGGTCAATGCGCAAGATGCG 414
 QY 349 GTACCCATGATTTAAGGACATCAAGTGTATGATGATGATGATGATGATGATGATGAT 408
 DB 415 GTACACGAGATTTAGGACATCAAGTGTATGATGATGATGATGATGATGATGATGATGAT 474
 QY 409 CGGCTCTCTCAACCCGATTTCTTCTGGAATATATAGCAAGAAATCAACGCGCAACA 468
 DB 475 CTTTCT 534
 QY 469 CAATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
 DB 535 CTGGATCCCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
 QY 529 ATTCCAAATCTTAAAGATCAACCGGCGAGTTCATCTTGGTGTGTTGGTTGACTT 588
 DB 595 ACGGGAATATCTTAACAACCTCTTGAAGCATCAATGATGATGATGATGATGATGATGAT 654
 QY 589 TAGGATTCGGTATATCTTAACTAATATCTCGGCAAGAAATACGAGGATTTGCA 648
 DB 655 TCGGCTGCGCTTCTTACTGACCTTTAAGCTCTCTGCAAGCGTATGACGGGTTGCTT 714
 QY 649 ACCACTTTGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708

DB 715 GCCATTTCTTCCCAACGCTCCCATCTAATGACCAAGAACGCTCCAGATATACCTCT 774
 QY 709 CCGATTTGCGTCTCTCGCTGATATTTATGCAATCAAGCTTCTGTAGACGAAAGGCG 768
 DB 775 CTGATGGGGGATTTCTAGCCGTCTGTTGGTCTTTACCGTTAGCGTGTGCAAGGGA 834
 QY 769 CAGCTTGGGTATCAACATGATGACCAATTCAGTACTAGTGTAAAGGCTTCTTGGTT 828
 DB 835 TGGCTCGATGATCTGCTCTTACGAGATACCGCTTCTGATGATGATGATGATGATGATGAT 894
 QY 829 TGATCAATATTTGACACCAACCATCTCTTCACTCCCTCATTAATGATTAACGAAATGA 888
 DB 895 TGATCACTTACTTTCAGACACATCTATCCCTCTGCTTCACTAGATTCATCAAGATGCG 954
 QY 889 ACTGATCAAAAGGCGCTTATCAACAATGATGATGATGATGATGATGATGATGATGATGAT 948
 DB 955 ACTGGCTCAGGAGGCTTTGGCTACCGTATGACAGATGATGATGATGATGATGATGATGAT 1014
 QY 949 TCCAGACGTTTACACACATCTACGCTTGTGATCAATTTGATCTCAPACATTCACATTATC 1008
 DB 1015 TCCACACATTAACAGACACACACGCTGCTATCTGCTTCTGACATGCGCATTTATA 1074
 QY 1009 ATGCAAGGAAGCAAGGATGATCAATCAAGCAGTGTGGGAGATATATTAATTCAGCA 1068
 DB 1075 ACGCAATGGAAGCTTCAAAAGCGATTAAGCCAAATTCGAGACTATTAACAGTTGATG 1134
 QY 1069 GGACTCCAAATTTTCAAGCATGATATGAGAGGCTTAAGGATGATGATGATGATGATGATGAT 1128
 DB 1135 GAACACCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194
 QY 1129 ATGAGATAGGACACAAAGGTGTGTTGTTGTTACCAAGATGATTAACAAAGGTG 1186
 DB 1195 ACAGGAGAGGATGACAAAGAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 1252

RESULT 7
 AA066068
 ID AA066068 standard; cDNA; 1372 BP.
 XX
 AC AA066068;
 XX
 DT 25-MAR-2003 (revised)
 DT 09-NOV-1994 (first entry)
 XX
 DE Sequence encoding microsomal delta-12 desaturase.
 XX
 KM Fatty acid; desaturase; lipid; unsaturated; transgenic plant; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT CDS 93..1244
 FT /*tag= a
 PN W09411516-A1.
 XX
 PD 26-MAY-1994.
 XX
 PF 15-OCT-1993; 93MO-US009987.
 XX
 PR 17-NOV-1992; 92US-00977339.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Lightner JE, Okuley JU;
 XX
 DR WPI; 1994-183515/22.
 DR P-PSDB; AAR53697.
 XX
 PT Genes for fatty acid desaturase enzymes - permit alteration of plant
 PT lipid composition.
 XX
 PS Claim 3; Page 112-114; 147pp; English.

XX The gene corresp. to AA066068 was isolated by screening Arabidopsis
CC genomic DNA library using radiolabeled pSF2b cDNA insert, purifying
CC positively-hybridizing plaque, and subcloning a 6kb Hind III insert
CC fragment from the phage DNA in pluescript vector. Comparison of the
CC sequences of the gene (AA066074) and the cDNA (AA066068) revealed the
CC presence of a single intron of 1134 bp at a posn. between nucleotides 88
CC and 89 of the cDNA, which is 4 nucleotides 5' to the initiation codon.
CC The cDNA is contained in clone AAP92103. Plasmid AAP92103 was deposited
CC on October 16, 1992 with the ATCC and bears accession number ATCC 69095.
CC An isolated nucleic acid fragment where in the nucleic acid identity is
CC 90% or greater to AA066068 or AA066074 is claimed. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 1372 BP, 324 A, 358 C, 303 G, 387 T, 0 U, 0 Other;
Query Match 35.5%; Score 455.6; DB 2; Length 1372;
Best Local Similarity 63.9%; Pred. No. 3.4e-102;
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;
QY 109 ATCCAGCGTTACGTTAAGCATCTGAAGAAAGGATTCCTACCCATTGCTTTAGAGCAT 168
DB 175 AACCGCTTCTCGGTGGAGATCTGAAGAAAGCATCCCGCATTTGTTCAAGCGCT 234
QY 169 CTGTGATCCGCTCATCATATGTTGTTGATGATGATGATGATGATGATGATGATGAT 228
DB 235 CAATCCCTGCTCTTCTCTTACCTTATGATGATGATGATGATGATGATGATGATGAT 294
QY 229 ACCTTGCAACAGCATATATCCCTCTTATCTTACACCTCTGCTTACCTTACCTTACCTG 288
DB 295 ACGTGGCAACAATTAATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 354
QY 289 TTTAAGTGTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 348
DB 355 TCFATGGGCTGTGCAAGGCTGTGTCTTACCTGATCTGATGATGATGATGATGATGATG 414
QY 349 GTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 408
DB 415 GTCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 474
QY 409 CGGCT 468
DB 475 CTTCT 534
QY 469 CAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
DB 535 CTGATCCCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 594
QY 529 ATTCCAATCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 588
DB 595 ACGGAATATCTTAACCAACCTCTGGAAGATGATGATGATGATGATGATGATGATGAT 654
QY 589 TAGGATTCCTGTTATCTTAACTAATATCTCGGCAAGAAATACCGGAGGTTTGCA 648
DB 655 TCGGATGCTCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
QY 649 ACCATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
DB 715 GCCATTTCTTCCCAACGCTCCCATCTCAATGATGATGATGATGATGATGATGATGAT 774
QY 709 CGGATTCGCTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 768
DB 775 CTGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
QY 769 CAGCTGGGATATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 828
DB 835 TGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 894
QY 829 TGATTCATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 888
DB 895 TGATTCATATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 954
QY 889 ACTGATCAAGAGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATG 948

DB 955 ACTGCTCAAGGAGGCTTTGGCTTACCTAGACAGACTACGATCTTGAAACAAGGCT 1014
QY 949 TCACAGAGTTACACACACTACGCTTTGATCATATTTGATCTTACATTTCCATTATC 1008
DB 1015 TCACACATTTACAGACACACAGCTGCTCATCTGCTTCTGACATGCGGATTA 1074
QY 1009 ATGCAAGGAAGCAAGGATGATCAAGCCAGTGTGGCGGATCTATTAATTCACA 1068
DB 1075 ACGGATGGAAGCTTCAAGGCGATTAAGCCATTTGGAAGATTTTACCAAGTTG 1134
QY 1069 GAATCCAAATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATG 1128
DB 1135 GAACACCTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194
QY 1129 ATGAGATAGGAGACACAAAGGTGTTCTGTGATCAACAAGATTAATCAAAAAGTG 1186
DB 1195 ACAGGAAGGTGACAAAGAAAGTGTACTGTATCAACAATTAAGTTATGAGCATGATG 1252
RESULT 8
AAZ51315
ID AAZ51315 standard; DNA, 1372 BP.
XX
XX AAZ51315;
AC
XX 06-JUN-2000 (first entry)
DT
XX
XX A. thaliana FAD2 gene encoding delta12-desaturase.
XX
XX Arabidopsis FAD2 gene; delta12-desaturase; yeast delta-9 desaturase;
KW pl-olel gene; transgenic plant; oil plant; mono-unsaturated fatty acid;
KW foodstuff; ss.
XX
XX Arabidopsis thaliana.
OS Synthetic.
OS
FH Key Location/Qualifiers
FT CDS 93..1244
FT /tag= a
FT /product= "delta12 desaturase"
PN MO200011012-A1.
XX
XX 02-MAR-2000.
PD
XX
XX 24-AUG-1999; 99WO-US019443.
PF
XX
XX 24-AUG-1998; 98US-0097586P.
PR
XX
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
PA
XX
XX Martin CE, Mitchell A;
PI
XX
XX WPI; 2000-237610/20.
DR P-PSDB; MAY70270.
PT
XX
XX New synthetic desaturase gene, useful to obtain transgenic plants that
PT produce a higher yield of unsaturated fatty acids, is customized for
PT expression in a plant cytoplasm.
XX
XX Example 4; Page 72-73; 77pp; English.
XX
XX The present sequence is Arabidopsis thaliana FAD2 gene encoding delta12
CC desaturase. Substitution of N-terminal Ole1 protein coding sequences with
CC the N-terminal sequence derived from the Arabidopsis FAD2 gene is done to
CC optimise gene expression, membrane targeting and ER (endoplasmic
CC reticulum) retention of the chimeric enzyme. Modified yeast delta-9
CC desaturase pl-olel gene comprising a desaturase domain and a cyr b5
CC domain, is customized for expression in a plant cytoplasm. This gene is
CC modified for expression in Arabidopsis and related species to obtain
CC transgenic plants that produce a higher yield of unsaturated fatty acids.
CC Transgenic plants, especially oil plants, are produced by this method

CC which have increased amounts of unsaturated, particularly mono -
CC unsaturated fatty acids, to obtain foodstuff that is more healthy and has
CC improved flavour

XX Sequence 1372 BP; 324 A; 358 C; 303 G; 387 T; 0 U; 0 Other;

Query Match 35.5%; Score 455.6; DB 3; Length 1372;
Best Local Similarity 63.9%; Pred. No. 3.4e-102;
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

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QY 109 ATCCAGCGTTCAAGCTTAAGCATGTAAGAAAGGATTCCTACCATTCCTTTAGCAT 168
DB 175 AACCGCTTTCTCGGAGGATCTGAAGAAAGATCCCGCATTTGTTCAAGCGT 234
QY 169 CTGTCATCCGGTCACTCATCTATCTGTTGTCATGATCTCATTTGTCCTTACT 228
DB 235 CAATCCCTGCTCTTCTCTCACTTATCATGATCATATTAAGCTTCTTACT 294
QY 229 ACCTTGCAACACGTAATATCCCTTATTCCTACACCTTGGCTTACCTAGACGCCG 288
DB 295 ACGTCGACCAATTAATTAATCTCTCTCTCCTCAGCCTCTCTTACTTGGCTGGCAC 354
QY 289 TTTACTGTTTTCGACGTAAGCATCTCAACCGGCTTGGGTGATCGGTCAAGAAATG 348
DB 355 TCTATTGGGCTGCAAGGCTGTGTCTCACTGTAATCTGGTATAGCCGCAAGATGCG 414
QY 349 GTCCACATGATTTAGGACTACAGTATGATGATGATGATGATGATGATGATGATG 408
DB 415 GTACACACGATTAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 474
QY 409 CGGCTCTCTCAACCCGTAATTTCTTGGAAATATAGCCACAGAAATCACAGCCACA 468
DB 475 CTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 534
QY 469 CAATTCACGTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
DB 535 CTGATCTCTCGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATG 594
QY 529 ATTCCAATCTTCAATCAATCCCGGAGATGATGATGATGATGATGATGATGATGAT 588
DB 595 ACGGAAATACCTCAACACCTCTTGAAGCATGATGATGATGATGATGATGATGATG 654
QY 589 TAGATTTCCGTAATACCTCTTAACTAATCTCGGCAAGAAATACGGAAGTTGCCA 648
DB 655 TCGGATGAGCTTGTACTGATGATGATGATGATGATGATGATGATGATGATGATG 714
QY 649 ACCACTTGAATCCATGATGATGATGATGATGATGATGATGATGATGATGATG 708
DB 715 GCCATTTCTTCCCAAGCTTCCATCAATGACGAAAGCGCTCCAGATATACCTCT 774
QY 709 CCGATTTCCGTAATACCTCTTAACTAATCTCGGCAAGAAATACGGAAGTTGCCA 768
DB 775 CTGATGAGGATTTATGAGCGCTCTTAACTAATCTCGGCAAGAAATACGGAAG 834
QY 769 CAGCTTGGTATATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 828
DB 835 TGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 894
QY 829 TGAATCAATTTGACACACACCATCTCTCACTCTCTCATTTATGATTCACGAAATGA 888
DB 895 TGAATCAATTTGACACACACCATCTCTCACTCTCTCATTTATGATTCACGAAATGA 954
QY 889 ACTGATCAAGAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGAT 948
DB 955 ACTGATCAAGAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGAT 1014
QY 949 TCCACGAGCTTACACACATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
DB 1015 TCCACGAGCTTACACACATGATGATGATGATGATGATGATGATGATGATGATGAT 1074
QY 1009 ATGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1068
DB 1075 ACGCAATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1134
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QY 1069 GAATCCAAATTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATG 1128
DB 1135 GAACACCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1194
QY 1129 ATGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1186
DB 1195 AAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1252

RESULT 9
ID AAC35456 standard; DNA; 1411 BP.
XX AAC35456;
AC AAC35456;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 10262.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
PN EP1033405-A2.
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
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Query Match 35.5%; Score 455.6; DB 3; Length 1411;
Best Local Similarity 63.9%; Pred. No. 3.4e-102;
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;
09 ATCCACGTTACGTTAAGCATCTGAAGAAGGATTCACCATGCTTTGACGAT 168

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Db 243 AACCGCTTTCTCGTGGAGATCTGAAGAAAGCAATCCGCCGANTTTTCAAGCCT 302
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Db 303 CAATCCCTCGCTTTTCTTCTTACTTATCATGTGATCATATTAAGCTTCTTACT 362
Qy 229 ACCTTGGAAACAGTATATCCCTTTATTCCTACACCTTGGCTTACCTTACGAGCCG 288
Db 363 ACGTCGCAACAATTAATCTTCTCTCCCTCCTCAGCCCTCTCTTACTTGGCTGGCAC 422
Qy 289 TTTATCTGTTTGTCAAGCTAGCATCTCACCGGCTCTGGGTCTACGCTACGAATGTG 348
Db 423 TCTATGGGCTGTCAAGGCTGTGTCTTACTGTGTATCTGGGTCTATGCTCCACAATGCG 482
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Qy 529 ATTCAAACTCTTAAACATCAACCCGAGAGTTCATTTGTGTGTGTGTGTGTGTGTGT 588
Db 663 ACGGAAATTAATCAACCTCTTGGAGCATGATGATGATGATGATGATGATGATGATGAT 722
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Db 723 TCGGGTGGCCCTTGTATAGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTT 782
Qy 649 ACCACTTGTATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
Db 783 GCCATTTCTTCCCAAGCTCTCCATCTAATGACCGGAAAGCTCTCCATGATGATGAT 842
Qy 709 CCGATTCGCTCTCTGCTGATTTTATGCAATCAAGCTCTTGTAGCAGCAAAAGGG 768
Db 843 CTGATGGGGATATCTAGCCCTGTTTGTGCTTAACTTAACTTAACTTAACTTAACTT 902
Qy 769 CAGCTTGGTATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
Db 903 TGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 962
Qy 829 TGATCAATTTTGAACCAACCACTCTCTCACTCTCTCACTTATGATGATGATGATGAT 888
Db 963 TGATCACTTATCTTGCAGACACTCATCTCTGCTCTCACTGATGATGATGATGATGAT 1022
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Db 1263 ACGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320

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RESULT 10
AAV72549

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ID AAV72549 standard; cDNA; 1476 BP.
XX
AC AAV72549;
XX
DT 27-AUG-2003 (revised)
DT 10-FEB-1999 (first entry)
XX
DE Vernonia galamensis fatty acid desaturase enzyme encoding cDNA.
XX
KW Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;
KW expression; chimeric gene; recombinant enzyme; ss.
XX
OS Vernonia galamensis.
XX
FH
FT Key location/Qualifiers
FT CDS 134..1282
FT /*tag= a
XX
XX US5846784-A.
XX
PD 08-DEC-1998.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX 11-JUN-1997; 97US-00872302.
XX
PR 11-JUN-1997; 97US-00872302.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E. I.
XX
PI Hitz WD;
XX
XX WPI; 1999-059065/05.
XX
DR P-PSDB; AAW83353.
XX
XX
XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid
XX epoxidising enzyme - used to alter levels of expression of the enzymes in
XX transformed host cells or to produce recombinant enzymes.
XX
PS Claim 2; Col 21-24; 21pp; English.
XX
CC The present sequence encodes Vernonia galamensis fatty acid desaturase.
CC The present invention also describes: (i) Vernonia galamensis fatty
CC acid epoxidising enzyme; (ii) chimeric genes comprising the fragments
CC linked to regulatory sequences; and (iii) transformed host cells
CC containing the chimeric genes. The DNA's from the present invention can
CC be used to alter levels of expression of the enzymes in transformed host
CC cells or to produce the recombinant enzymes by transformation of
CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 1476 BP; 373 A; 337 C; 346 G; 420 T; 0 U; 0 Other;
XX
Query Match 35.4%; Score 454.4; DB 2; Length 1476;
Best Local Similarity 64.2%; Pred. No. 6.8e-102;
Matches 683; Conservative 0; Mismatches 381; Indels 0; Gaps 0;
Qy 109 ATCCACGCTTACAGCTTAAGGATCTGAAGAAAGCAATTCCTACCATCTTGAAGCAT 168
Db 213 AACCTCTTACCATCAGGAGCACTCAAAAAGCAATTCCTCCCACTGTTCCAGGCT 272
Qy 169 CTGTCATCCGGTCAATCACTATGTTGTTCAATGATCTCATGATGATGATGATGATGAT 228
Db 273 CCTTATCCGTTCTCTTATGCTTATGATGATGATGATGATGATGATGATGATGATGAT 332
Qy 229 ACCTTGAACAGCTATATCCCTTTATTCCTTACACCTTGGCTTACTTACGAGGCCG 288
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Db 453 GTACCAATGATTAAGGACTATCAATGATGATGATGATGATGATGATGATGATGATGAT 512

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Oy		CGGCTCTCCTCAACCCCGATATTTCTCTTGAAATAATAGCACAGGAATACACACGCCAACA	468
Db		513 CGGTTCATCTTGTCTCTTCTTTTCATGMAANTACAGTCAICGTGTGACACCACCTCCACA	572
Oy		469 CAATATCACTCGATAACGATGAAAGTTTACATCTCTTAACTGTAAGTCGAAGGTCAAGATT	528
Db		573 CCGATCATCTCGAGGTGATGAAAGTCTTGTGCCAAAACCGAGATCGAAAAATCCCTGGT	632
Oy		529 ATTCCAACCTCTTAAACAATCCACCCGGGCGAGTGTTCACTTGTGGTTCGTTGACTT	588
Db		633 ACTCAAAATPACTTTAACAACGACCTGGCCCGATGATGATGATGTTCACACCCCTAACTC	692
Oy		589 TAGATTTCCGTTATACCTCTTAACTAATATCTCGGCAAGAATAACGGAGTTTGCCA	648
Db		633 TAGGTGGCCCTTGTACTTGTGTTTTCAATGATATCAGGAGAACCTATGACCGTTTTGCT	752
Oy		649 ACCACTTTGATCCAGTAGTCATTTTCAAAGATGTGAACGGCTTCAAGTTTGTCTAT	708
Db		753 GCCACTTTTCTCTTAAACAGCCCTATATCAAGAACGATGAGGTCTCAAAATATGGCTTT	812
Oy		709 CCGATTTGGTCTCTCTCGCTGATTTTATGCAATCAACTCTTGTGTACACAAAGGG	768
Db		813 CGGATTTAGGATGATCAACATGTCCTTATCTTTATCTGTGTGCTGTAGCAAAAGGTG	872
Oy		769 CAGCTTTGGGTATCAACATGTACGCAATTCAGTACTAGTGTGAAGCTGTCTTCTGTT	828
Db		873 TGGCTTGGGTAAATGCAATGTATGGGAATCCCGCTACTGATTTGTGAACGGATTTCCGTGA	932
Oy		829 TGATCAATATTTGCACCAACCCATCTCTCACTCCCTCATTTATGATTTCAAACCGAATGA	888
Db		933 CGATCACCTTACCTTCACAACACTCACCCCTTCAATGCCCCACTATGATAGCTCAGAGTGG	992
Oy		889 ACTGGATCAAGGGCGCTTATCAACAATCGAATAGGGAATTTGGGTTCTGATGGGGTT	948
Db		993 ACTGGCTAAGGGAGCAATATGGCAAGGTGACCGTGACTATGTGTGCTCAACAAGGTAT	1052
Oy		949 TTCAAGAGCTTACACACACTCAGTCTTTCGATCATTTGTATCTCATATTCACATTTATC	1008
Db		1053 TTCATPATCATCAAGATACACACGATGTGACACATTTGTTCGACGATGCTCATTTATA	1112
Oy		1009 ATGCAAGAGAACAGAGGATGCATCAACCAAGTGTGGCGAGTACTATATAAATGCACA	1068
Db		1113 ACGCATATGAGGCAACGAAGCAGTGAAGCCTTTCCTTGGGGAGTATATCATGTTTGACG	1172
Oy		1069 GGACTTCCAAATTTTCAAGCAATGTATPAGAGGGCTTAAGAAATGCATCTACATCGAGCCG	1128
Db		1173 GGACTTCCGTTTACCTAGCAATATGAGAGAGGCAAAAGATGTCTGTTCGTGATCCAG	1232
Oy		1129 ATGAGATAGCGAGCAAAAGGTGTCTTCTGTATCACAAGATG	1172
Db		1233 ATGAGGGGAGGCTCAGGAGGATGTCTTTGGTACAAGATTAAG	1276
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ID	AAZ32636	standard; cDNA; 1152 BP.	
XX	AAZ32636;		
DT	19-JAN-2000	(first entry)	
DE	Arabidopsis thaliana wild-type fatty acyl desaturase FAD2 cDNA.		
KM	Fatty acyl dehydrogenase; FAD2, fatty acyl hydroxylase; LPAH12, homology;		
KW	evolutionarily conserved; wild-type; mutation; oleic acid; linoleic acid;		
KM	unsaturated fatty acid; ricinoleic acid; oil; wax;		
XX	hydroxylated fatty acid; lubricant; nylon; mutant; mutation; ds.		
OS	Arabidopsis thaliana.		
Key	Location/Qualifiers		
FT	CDS	1..1152	

[illegible]

Db 323 GTACACGAGTTCAGGAGTCAACAAAGGCTGATGACACAGTGGTCTTATCTTCATT 382
Qy 409 CGGCTCTCTCAACCCGATTTCTTGGAAATATAGCCAGGAATCAACGACGCAACA 468
Db 383 CTTTCTCTCTGTCCTTACTTCTCGAAGTATAGTCATGCGCTGATCAATTCACACA 442
Qy 469 CAATTCATCTGATAGAGTGAAGTTACATTCCTAAAGTAAGTCGAAAGGTCAGATTT 528
Db 443 CTGATCTCTGAAAGATGATGATTTGTCCAAAGCAAAATCAAGCAATCAAGTGT 502
Qy 529 ATTCAACTCTTAAATCAATCCACCCGGGAGTGTCACTTGTGTGTGTGATTT 588
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Qy 589 TAGATTTCCGTTATACCTTAACTAATATCTGGGCAAGAAATACGAGGTTTCCCA 648
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Qy 1129 ATGAGATTAGGAGACCAAAAGGTGTCTGTGACCAAGATGTAATCA 1178
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RESULT 12
AAC39493
ID AAC39493 standard; DNA; 1451 BP.

AC AAC39493;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 24835.

XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EPI033405-A2.

PD 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
PF 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
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PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
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PR 02-JUL-1999; 99US-0142055P.

PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
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PR 19-JUL-1999; 99US-0144352P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 35.3%; Score 454; DB 3; Length 1451;
Best Local Similarity 63.8%; Pred. No. 8.5e-102;
Matches 688; Conservative 0; Mismatches 390; Indels 0; Gaps 0;

QY 109 ATCCACCGTTCACCTTAAGGATGTGAAGAAAGCATTCCTACCATTCCTTTAGGAT 168
DB 235 AACCGCTTCTCCGTGGAGATCGAAGAAAGCAATCCGCCCATTTGTTCAACGCT 294
QY 169 CTGTACCCGGTATCATATGATGTGATCATGTATCATTCATTCATTCATTCATTCAT 228
DB 295 CAATCCCTGCTCTTCTCTCACTTATCATGTACATCATATTAAGCCTCATGCTTCTACT 354
QY 229 ACCTTGAAACACGTATATCCCTTATTCCTACACCTCTGCTTACCTACATGCGCG 288
DB 355 ACGTGGCAACAATTAATCTCTCTCTCCCTGACCTCTCTCTTAATGCTTGGCGAC 414
QY 289 TTAATGATTTGTCAAGCTAGCATCTCACCGCTCTGGGTATGGTACGAATGTG 348
DB 415 TCTATTTGGCTGTCAAGGCTGTGTCTTAATCTGTATCTGGGTATGCCCCAAGTGGC 474
QY 349 GTCAACGATCTTAAGGACATCAAGTGAATGATGATTCATTTGGATGGTGTCCATT 408
DB 475 GTCAACGATCTTAAGGACATCAAGTGAATGATGATTCATTTGGATGGTGTCCATT 534
QY 409 CGGCTCTTCACCCCGATTTCTTTGAAATATAGCAGAGATTCACGACGCAACA 468
DB 535 CTTCTCTCTGCTCTTACTTCTCTGGAAGTATGATGATGCGCGATTCACATTCACA 594
QY 469 CAAATTCATCTGATPAAGATGAATTAATCTCTTAACGTAAGTCGAAGTCAAGATT 528
DB 595 CTGATCCCTCGAAGAGATGAATTAATTTGTCCAAGACAGAAATACGAATCAAGTGT 654
QY 529 ATTCAAACTTAACAATCCACCGCGGAGTTCACCTTGTGGTTGATTCCT 588

Db 655 ACGGAAATACCTCAACACCCCTTGGACGATGANTGTAAACCGTTCAGTTTGTCC 714
 Qy 589 TAGATTTCCGTTATACCTTTATATATCTCGGCAAGAAATACGAGGATTTGCA 648
 Db 715 TCGGCTGGCCCTTCTTACCTTAAACGCTCTCGGCAAGCCGATGACGGGTTGGCTT 774
 Qy 649 ACCACTTGTATCCATGATGCAATTTTCAAGATCGTGAACGGCTTCAAGTTTGTAT 708
 Db 775 GCACTTTCTTCCCAACGCTCCCATCTACATGACCGGAAGCGCTCCAGATATACCTCT 834
 Qy 709 CCGATTTCCGCTCTCTGCTGTATTTATGCAATCAAGCTCTGTATGACGAAAGGG 768
 Db 835 CTATGCGGGGATTTAGCCGCTGTTTGGCTTACCGTACGCTGCTGCAAGGGA 894
 Qy 769 CAGCTTGGTATCAATGATGACCAATTCAGTACTAGGTAGCGTGTCTTCTGTT 828
 Db 895 TGGCTTGAATGATGCTCTCTACGAGTACCGCTTGTATGATGATGATGATGATGAT 954
 Qy 829 TGATGACATTTTTCACACACCCATCTCTGCTCTGATTTATGATTTCAACGATGGA 888
 Db 955 TGATCACTTCTTACGACACACTCATCCCTGTTGCTCTGATGATGATGATGATGATG 1014
 Qy 889 ACTGATCAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATG 948
 Db 1015 ACTGCTCAGGGAGCTTTGGCTACGATGACAGATGATGATGATGATGATGATGATG 1074
 Qy 949 TCCACGACGTTACACACACTGCTTGTGATGATGATGATGATGATGATGATGATGATG 1008
 Db 1075 TCCACGACGTTACACACACTGCTTGTGATGATGATGATGATGATGATGATGATGATG 1134
 Qy 1009 ATGCAAGGAAAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1068
 Db 1135 ACGCAATGGAAGTACCAAGGCGATTAAGCCATTTCTGGAGATGATGATGATGATGATG 1194
 Qy 1069 GGAATCCATTTTCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 1128
 Db 1195 GAAACCGTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1254
 Qy 1129 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1186
 Db 1255 ACAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1312
 RESULT 13
 ID AA066074 standard; DNA: 2973 BP.
 AC AA066074;
 DT 25-MAR-2003 (revised)
 DT 09-NOV-1994 (first entry)
 DE Sequence of microsomal delta-12 desaturase gene.
 KM Fatty acid; desaturase; lipid; unsaturated; transgenic plant; ss.
 OS Arabidopsis thaliana.
 FH Key Location/Qualifiers
 FT exon 433..520
 FT intron 521..1654
 FT /tag= a
 FT /tag= b
 PN M09411516-A1.
 PD 26-MAY-1994.
 PF 15-OCT-1993; 93WO-US009987.
 PR 17-NOV-1992; 92US-00977339.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX Lightner JE, Okuley JU;
 XX WPI; 1994-183515/22.
 DR
 XX Genes for fatty acid desaturase enzymes - permit alteration of plant
 PT lipid composition.
 PS Claim 3; Page 136-138; 147p; English.
 CC The gene corresp. to AA066068 was isolated by screening Arabidopsis
 CC genomic DNA library using radiolabeled pSf2b cDNA insert, purifying
 CC positively-hybridizing plaque, and subcloning a 6kb Hind III insert
 CC fragment from the phage DNA in pBluescript vector. Comparison of the
 CC sequences of the gene (AA066074) and the cDNA (AA066068) revealed the
 CC presence of a single intron of 1134 bp at a posn. between nucleotides 88
 CC and 89 of the cDNA, which is 4 nucleotides 5' to the initiation codon.
 CC The cDNA is contained in clone AAP92103. Plasmid AAP92103 was deposited
 CC on October 16, 1992 with the ATCC and bears accession number ATCC 69095.
 CC An isolated nucleic acid fragment where in the nucleic acid identity is
 CC 90% or greater to AA066068 or AA066074 is claimed. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 XX Sequence 2973 BP; 762 A; 637 C; 569 G; 1005 T; 0 U; 0 Other;
 SQ
 Query Match 35.3%; Score 454; DB 2; Length 2973;
 Best Local Similarity 63.8%; Pred. No. 1e-101;
 Matches 688; Conservative 0; Mismatches 390; Indels 0; Gaps 0;
 Qy 109 ATCCACGCTTACGTTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 168
 Db 1741 AACGCGCTTCTCGGTGGAGATCTGAAGAAAGCAATCCGCGCATTTGTTCAAGGCT 1800
 Qy 169 CTGTCATCCGGTATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 228
 Db 1801 CAATCCCTCGCTCTTCTCTCTTCACTTATGATGATGATGATGATGATGATGATGATGATG 1860
 Qy 229 ACCTTGCAACAGATATATCCCTTATTCCTACACCTCTGCTGATCTTATGATGATGATG 288
 Db 1861 ACGTGGCAACCAATATATCT 1920
 Qy 289 TTTACTGTTTTGTCAAGTACATCTCTCAACCGGCTCTGATGATGATGATGATGATGATG 348
 Db 1921 TCTATGGGCTGTGCAAGGCTGTGTCTCTACTGATGATGATGATGATGATGATGATGATG 1980
 Qy 349 GTCAACATGATTTAGGATCTACAGTATGATGATGATGATGATGATGATGATGATGATG 408
 Db 1981 GTCAACATGATTTAGGATCTACAGTATGATGATGATGATGATGATGATGATGATGATG 2040
 Qy 409 CGGCTCTCTCAACCGGCTATTTCTTGTGAATATAGCAAGGATCAACGCAACA 468
 Db 2041 CTTTCT 2100
 Qy 469 CAATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
 Db 2101 CTGGATCCCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
 Qy 529 ATTCCAACTTTTAAATATCAACCGGCGGAGATGATGATGATGATGATGATGATGATGATG 588
 Db 2161 ACGGAAATATCTTCMAAACCTCTTGAGCATGATGATGATGATGATGATGATGATGATG 2220
 Qy 589 TAGATTTCCGTTATACCTTTTATATATCTCGGCAAGAAATACGAGGATTTGCA 648
 Db 2221 TCGGCTGGCCCTTCTTACCTTAAACGCTCTCGGCAAGCCGATGACGGGTTGGCTT 2280
 Qy 649 ACCACTTGTATCCATGATGCAATTTTCAAGATCGTGAACGGCTTCAAGTTTGTAT 708
 Db 2281 GCCATTTCTTCCCAACGCTCCCATCTACATGACCGGAAGCGCTCCAGATATACCTCT 2340
 Qy 709 CCGATTTCCGCTCTCTGCTGTATTTATGCAATCAAGCTCTGTATGACGAAAGGG 768
 Db 2341 CTATGCGGGGATTTAGCCGCTGTTTGGCTTACCGTACGCTGCTGCAAGGGA 2400

QY 769 CAGCTGGGTAAATGCAATGTAAGCAATTCAGTAAGTGTAAAGCTGTTCTGCTT 828
 Db 2401 TGGCTCGATGATCTGCTCTCAAGAGTACGCTTGTAGTAAATGCTTCTGCT 2460
 QY 829 TGATCAATATTTGACACCAACCATCTCTCACTCCCTCATTTATGATCAACCAATGA 888
 Db 2461 TGATCACTTACTTGACAGCACTCATCTCTGTTGCTTCCATGATTCATCAAGTGG 2520
 QY 889 ACTGGATCAAGGCGCTTATCAACATGATGATGATTTGGGTTCTGTAATCGGCTT 948
 Db 2521 ACTGGCTCAAGGAGGCTTGGCTACCGTAGACAGAGTACGGAATCTTGAACAAGGTGT 2580
 QY 949 TCCGACAGTTCACACACTAGCGCTTGATGATTTGATGATCAATTCATCAATATC 1008
 Db 2581 TCCACAAATTAACAGACACACAGCGCTCATCACTGTTCTTCACAAATGCGCATTTATA 2640
 QY 1009 ATGCAAGAAGACAGGATGATCAATCAAGCGATGTTGGCGAGTACTATAAATGACAA 1068
 Db 2641 ACGCAATGGAAGCTACAAAGCGATTAAGCCAAATTCGGAGACTATTACAGTTCCATG 2700
 QY 1069 GGAATCCAAATTTCAAGCAATGTATAGAGAGGCTAAGAAATGCAATTCATCAAGCCCG 1128
 Db 2701 GAACACCGTGTATGTGCGATGTATAGGAGGCAAGAGTGTATGTATAGAACCGG 2760
 QY 1129 ATGAGATAGGAGACAAAGTGTGTCTGTATCAACAAATGTAAATCAAAAAGTGT 1186
 Db 2761 AAGGGAAGGTGACAAAGAAAGTGTGTATCTGTATCAACAAATGTATAGAGATGATG 2818

RESULT 14

ABL58607 standard; DNA; 2973 BP.

ABL58607;

26-JUN-2002 (first entry)

Cress genomic fragment containing microsomal delta-12 desaturase gene.

Cress; microsomal delta-12 desaturase; delta-12 hydroxylase;

delta-12 fatty acid hydroxylase; enzyme; plant; vegetable oil; seed oil;

fat; oil; heart disease; gene; ds.

Arabidopsis thaliana.

Key Location/Qualifiers

FT exon 433..520

FT intron 521..1654

FT misc_signal 1659..1661

FT /note= "this represents the ATG start codon for the delta-12 desaturase gen, the cDNA for which is given in record ABL58599"

US6372965-B1.

16-APR-2002.

14-AUG-1998; 98US-00133962.

17-NOV-1992; 92US-00977339.

15-OCT-1993; 93WO-US009987.

20-JUN-1994; 94US-00262401.

(DUPO) DU PONT DE NEMOURS & CO E. I.

Lightner JE, Okuley JJ, Hitz W, Kinney MJ, Perez-Grau L;

Yadav NS; WPI; 2002-392229/42.

P-PSDB; ABB80027.

XX New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or
 PT delta-12 fatty acid hydroxylase for creating transgenic plants and
 PT producing seed oil with altered levels of unsaturated fatty acids.
 PS Claim 1; Col 99-102; 54pp; English.

CC The invention relates to an isolated nucleic acid fragment encoding or
 CC comprising a sequence encoding a plant enzyme that is a delta-12
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.
 CC Chimeric genes comprising nucleic acids of the invention are used to
 CC create transgenic plants with altered levels of unsaturated fatty acids,
 CC and can modify plant lipid composition. Nucleic acids of the invention
 CC can be used as hybridization probes to isolate or amplify nucleotide
 CC sequences encoding other fatty acid desaturases or fatty acid desaturase-
 CC related enzymes. They can also be used in restriction fragment length
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in
 CC seed oil of oil producing plant species. They can also be used to produce
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic
 CC acids of the invention can combine the high oleate trait of transformed
 CC seeds with mutations for altered fatty acid compositions to obtain new
 CC fatty acid compositions and/or improved agronomy. A vegetable oil low in
 CC total saturates and high in monounsaturates would provide significant
 CC health benefits to consumers (reduced risk of coronary heart disease) as
 CC well as economic benefits to oil processors. The current sequence
 CC represents a cress genomic fragment containing microsomal delta-12
 CC desaturase gene
 CC XX

Sequence 2973 BP; 762 A; 637 C; 569 G; 1005 T; 0 U; 0 Other;

Query Match 35.3%; Score 454; DB 6; Length 2973;

Best Local Similarity 63.8%; Pred. No. 1e-101;

Matches 688; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

QY 109 ATCCACCGTTCACGTTAAGCATGGAAGAGGATTCCTACCATGCTTTGAGCGAT 168
 Db 1741 AACCGCTTCTCGGTGGAGATGGAAGAAAGCAATCCGCGCATTTGTTCAAGCCT 1800
 QY 169 CTGTATCCGCTCATCACTATGTTGTTATGATGATCTATGTTGCTTCTTACT 228
 Db 1801 CAATCCCTCGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860
 QY 229 ACCTTGAACAGCTATATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 288
 Db 1861 ACGTGGCAACATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1920
 QY 289 TTTACGCTTTTGTCAAGCTAGCATCTCAACGCGCTCTGGGTCATGCGTCAAGATGTG 348
 Db 1921 TCTATGGCGCTGTCAAGGCTGTGTCTTAATCTGTTATCTGGGTATGCCAGAAATGCG 1980
 QY 349 GTCAACATGCAATTTAGGCACTACAGTGTATGATGATGATGATGATGATGATGATG 408
 Db 1981 GTCAACATGCAATTTAGGCACTACAGTGTATGATGATGATGATGATGATGATGATG 2040
 QY 409 CGGCTCTCCACCCCGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 468
 Db 2041 CTTCTCTCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2100
 QY 469 CAAATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
 Db 2101 CTGATCTCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2160
 QY 529 ATTCAAACTTTTAACATCAACCCGCGGAGTTCCTCTTGTGTTTCTGTTGACTT 588
 Db 2161 ACGGAAATACCTCAACACCTCTTGGAGCATGATGATGATGATGATGATGATGATGATG 2220
 QY 589 TAGATTTCCGTATACCTCTTAATCTATCTGCGGCAAGAAATACCGGAGTTTGCA 648
 Db 2221 TCGGCTGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 2280
 QY 649 ACGACTTTGATCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708
 Db 2281 GCCATTTCTTCCCAAGCTTCCATCTAATGACCGAAGAGCGCTCCAGATATACCTCT 2340


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Oy 889 ACTGATCAAAAGGCGCCTTATCAACATCGATAGGATTTCGGTTCCTGATCGGGTTT 948
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Db 1015 ACTGGCTCAGGGGAGCTTTGGCTACGCTAGACAGAGACTAGSAACTTGGACAAAGTGT 1074
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Oy 949 TCCACGAGCTTACACACACTCAGCTCTTGCAATCAATTGATCTCATACATTCCACATTATC 1008
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Db 1075 TCCACAACATTACAGACACACCTGGCTCATCACTGTTCTCGACAATGCCGATTATA 1134
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Oy 1009 ATGCAAGGAGGAGGAGGATGCAATCAAGCCAGTGTGGGCGAGTACTATATAATCGACA 1068
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Db 1135 ACGCAATGGAAGCTACAAAGGCGATTAAGCCAAATTTCTGGAGACTATACAGTTGATG 1194
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Oy 1069 GGAATCCAAATTTCAAGCAATGTATAGAGAGGCTAAGGAATGCATCTACATCGAGCCG 1128
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    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Oy 1129 ATGAGATAGCGAGCACAAAGGTGTGTTCTGGTACCAACAAGATTAATCAAAAAGTGT 1186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1255 ACAGGGAGGTGACAAAGAAAGTGTGTACTGTACAACAATAAGTATAGAGATGATG 1312
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OM nucleic - nucleic search, using SW model

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Searched: 682709 seqs, 27747546 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	715.8	55.7	1358	US-09-059-769-1	Sequence 1, Appli
3	705.4	54.9	1312	US-09-059-769-3	Sequence 3, Appli
4	699.8	54.5	1364	US-08-872-302-3	Sequence 3, Appli
5	455.6	35.5	1231	US-08-314-596-44	Sequence 44, Appli
6	455.6	35.5	1231	US-08-320-982-44	Sequence 44, Appli
7	455.6	35.5	1231	US-08-819-037-44	Sequence 44, Appli
8	455.6	35.5	1231	US-09-045-940-44	Sequence 44, Appli
9	455.6	35.5	1372	US-09-133-962A-1	Sequence 1, Appli
10	454.4	35.4	1476	US-08-872-302-1	Sequence 1, Appli
11	454	35.3	2973	US-09-133-962A-15	Sequence 15, Appli
12	432.4	33.6	1222	US-08-314-596-43	Sequence 43, Appli
13	432.4	33.6	1222	US-08-320-982-43	Sequence 43, Appli
14	432.4	33.6	1222	US-08-819-037-43	Sequence 43, Appli
15	432.4	33.6	1222	US-09-045-940-43	Sequence 43, Appli
16	432.4	33.6	1448	US-08-314-596-39	Sequence 39, Appli
17	432.4	33.6	1448	US-08-320-982-39	Sequence 39, Appli
18	432.4	33.6	1448	US-08-819-037-39	Sequence 39, Appli
19	432.4	33.6	1448	US-09-045-940-39	Sequence 39, Appli
20	432	33.6	1426	US-09-133-962A-3	Sequence 3, Appli
21	431	33.5	1155	US-08-675-650B-5	Sequence 5, Appli
22	431	33.5	1155	US-09-354-231B-9	Sequence 9, Appli
23	431	33.5	1155	US-09-128-602B-9	Sequence 9, Appli
24	431	33.5	1155	US-09-995-297-9	Sequence 9, Appli
25	429.4	33.4	1155	US-08-675-650B-1	Sequence 1, Appli
26	429.4	33.4	1155	US-08-675-650B-3	Sequence 3, Appli
27	429.4	33.4	1155	US-09-354-231B-11	Sequence 11, Appli

28	429.4	33.4	1155	US-09-128-602B-11	Sequence 11, Appli
29	429.4	33.4	1155	US-09-995-297-11	Sequence 11, Appli
30	427.8	33.3	1155	US-09-354-231B-13	Sequence 13, Appli
31	427.8	33.3	1155	US-09-128-602B-13	Sequence 13, Appli
32	427.8	33.3	1155	US-09-995-297-13	Sequence 13, Appli
33	426.2	33.2	1155	US-09-354-231B-15	Sequence 15, Appli
34	426.2	33.2	1155	US-09-354-231B-17	Sequence 17, Appli
35	426.2	33.2	1155	US-09-128-602B-15	Sequence 15, Appli
36	426.2	33.2	1155	US-09-128-602B-17	Sequence 17, Appli
37	426.2	33.2	1155	US-09-995-297-15	Sequence 15, Appli
38	426.2	33.2	1155	US-09-995-297-17	Sequence 17, Appli
39	425.2	33.1	1155	US-08-907-608-1	Sequence 1, Appli
40	425.2	33.1	1155	US-09-354-231B-1	Sequence 1, Appli
41	425.2	33.1	1155	US-09-128-602B-1	Sequence 1, Appli
42	425.2	33.1	1155	US-09-482-287-1	Sequence 1, Appli
43	425.2	33.1	1155	US-09-966-888-1	Sequence 1, Appli
44	425.2	33.1	1155	US-09-995-297-1	Sequence 1, Appli
45	424.6	33.0	1155	US-08-907-608-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-161-994A-1
Sequence 1, Application US/09161994A
Patent No. 6333448
GENERAL INFORMATION:

APPLICANT: BAROR, Maureen
APPLICANT: BARAS, Antoni
APPLICANT: DAHLQVIST, Anders
APPLICANT: GUMMELSON, Per-Olov
APPLICANT: LEE, Michael
APPLICANT: SODAL, Steffen
APPLICANT: STYMER, Sten
APPLICANT: LENMAN, Marit
TITLE OF INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
FILE REFERENCE: BAROR-1
CURRENT APPLICATION NUMBER: US/09/161,994A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1

LENGTH: 1128
TYPE: DNA
ORGANISM: Crepis alpina
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1125)
US-09-161-994A-1

Query Match 55.9%; Score 718.6; DB 4; Length 1128;
Best Local Similarity 77.4%; Pred. No. 3.8e-198;
Matches 871; Conservative 0; Mismatches 254; Indels 0; Gaps 0;

QY	51	CGTGGTGGATGCGATTCATCTGAGGGAACATCTTGAACGTGCGCAT	110
DB	4	GTGTGGCGTGGCGCGTGGTGGACTTCGCAAAACCCCTCATGAAAGTGTTCAGT	63
QY	111	CCACCGTTCAGTTTAAAGCATCTGAAGAGCATCTCTACCCATCTTGAGCGAT	170
DB	64	CCACCGTTCAGCGGAGTGTCTCAAGCAAGCATCTCTCCATCTTCAAGCAT	123
QY	171	GTCATCGGTATCATATGTTGTCATGATCTCATTTGCTTATGTTCTTACTAC	230
DB	124	GTAATCGGTCTCTTACTATAGTCCAGATCTATATGCGCTTACTTACTTTC	183
QY	231	CTTGCAACAGTATATCTTATCTTATCTTCAACCTTGCTTACAGATGCGCGT	290
DB	184	CTTGCGCAAAATATCATTCGATTCCTCCGCCCTTACCTTACCTTGGCCCTT	243

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QY 291 TACTGTTTGTCAAGTAGCATCTCCACCGGCTCTGGGTATCGGTCAAGAAATGCGT 350
D 244 TACTGTTTGTCAAGTAGCATCTCCACCGGCTTATGGGTATCGGTCAAGAAATGCGT 303
QY 351 CACATGATTTAGCATCTACAGTGTATGTATGATGATTTGGATTCGGTCCATTCG 410
D 304 CACATGATTTAGCATCTACAGTGTATGTATGATGATTTGGATTCGGTCCATTCG 363
QY 411 GCTCTCCACACCCGATTTCTTGGAAATATAGCCACAGAAATCACACGCAACACA 470
D 364 TTTCTCAGACCCGATTTCTTGGAAATATAGCCACGGAACACACGCAACACA 423
QY 471 AATTCTCCTGATTAAGATGAAGTTTACATTCCTTAACGTAAAGTGAAGTGAAGTTAT 530
D 424 AATTCTCCTGATTAAGATGAAGTTTACATTCCTTAACGTAAAGTGAAGTGAAGTTAT 483
QY 531 TCCAACTCTTAACTCAATCCACCGGGGAGTGTCACTTGGTGTGGTGGTCACTTA 590
D 484 TATTAAGTCTCAACACCCACCTGGCCGACTGTGATTAATGATCACTTCACTCA 543
QY 591 GGATTTCCGTTATACCTCTTAATATATCTCGGCAAGAAATACGGAGGTTTCCAC 650
D 544 GGTCTCCCTATATCTCTTACCAATTTTCCGCAAGAAATGAAGTTTCCAC 603
QY 651 CACTTGAATCCATGATGATCAATTTTCAACGATGTGAACGGCTTCAAGTTTGCATCC 710
D 604 CATTTCGACCCCATGATGATGATTTTCAAGAGCGTGAACGGCTTCAAGTTTGCATCC 663
QY 711 GATTTGGTCTCTCGCTGATTTTATGATCAATCAAGCTTCTTGAAGCAAGAAAGGGCA 770
D 664 GATCTGGCTCTCTCGCTGATTTTATGATCAATCAAGCTTCTTGAAGCAAGAAAGGGCA 723
QY 771 GCTTGGTATCAACATGATGATGATTTCAATTCAGTATGATGATGATGATGATGATG 830
D 724 GCTTGGTATCAACATGATGATGATTTCAATTCAGTATGATGATGATGATGATGATG 783
QY 831 ATCACTATTTTGAACACACACCATCTCTCACTCCCTCATTAATGATCAACGAAATGAC 890
D 784 ATCACTATTTTGAACACACACCATCTCTCACTCCCTCATTAATGATGATGATGATG 843
QY 891 TGGATCAAGGCGCTTATCAACATGATGATGATTTGGGTTCCGATCGGTTTTC 950
D 844 TGGCTCAAGGCGCTTATCAACATGATGATGATTTGGGTTCCGATCGGTTTTC 903
QY 951 CACGAGTTTACACACACTCACTCTTGCATGATTTGATCTCATATTCACATTTATCAT 1010
D 904 CATGATGTTACACACACTCACTCTTGCATGATTTGATCTCATATTCACATTTATCAT 963
QY 1011 GCAAGGAGGAGGAGGATGATCAATGATGATTTGGGCGGATCTATTAATGAATGACAG 1070
D 964 GCGAAGGAGGAGGAGGATGATCAATGATGATTTGGGCGGATCTATTAATGAATGACAG 1023
QY 1071 ACTCAATTTTCAAGCAATGATTAAGAGGATGAAGGATGATCACTATGAGGCGGAT 1130
D 1024 ACTCAATTTTCAAGCAATGATTAAGAGGATGAAGGATGATCACTATGAGGCGGAT 1083
QY 1131 GAGGATAGCGAGCAAAAGTGTGTCTGTGTACCAAGATGTAA 1175
D 1084 AAAAGTAGGAGTCCAAAGGTGTATATTGTATCAATAAATTCTGA 1128

```

RESULT 2

US-09-059-769-1

Sequence 1, Application US/09059769

Patent No. 6329518

GENERAL INFORMATION:

APPLICANT: Green, Allan

APPLICANT: Singh, Surinder

APPLICANT: Lemman, Marc

APPLICANT: Stymne, Sten

TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses

NUMBER OF SEQUENCES: 20

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fieber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1358 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 30..1151
US-09-059-769-1
Query Match 55.7%; Score 715.8; DB 4; Length 1358;
Best Local Similarity 78.2%; Pred. No. 2.7e-197;
Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;
QY 29 ATATATCAACAACATGGGTGCTGTGTGTCGATGTCGATTCATCTGAGGAAAAAATCAT 88
D 17 ATCAATTTATCAACATGGGTGCTGTGTGTCGATGTCGATTCATCTGAGGAAAAAATCGGT 70
QY 89 CTTTGAAGTGTGTCGATGTCGATTC---ACGTTTCACTTGAAGCATCTGAAGAAAGGAT 145
D 71 CATGAAGTGTGTCGATGTCGATTCGATGATCCCTTCACTGATGAATGAAGCAAGCAAT 130
QY 146 TCCATCCATTTCTTTAGAGGATGTCATCCGCTCATCACTATGATGATGATGATGATGAT 205
D 131 CCGTCCCATTTCTTCAAGAGATGTAATCCGCTCATCTATGATGATGATGATGATGATGAT 190
QY 206 CATGTTGCTGATGTCATCTTCTTACTTACTTGAAGAAACAGCATATCCCTTATTTCTTACACC 265
D 191 CATATTTGCTGATGTCATCTTCTTACTTCTTGGCAACATATATCCCTTCTTCTTACTAG 250
QY 266 TCTGCTTACTTACTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 325
D 251 TCTAGCTTACTTACTGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGAT 310
QY 326 CTGGTGTATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCGATGTCG 385
D 311 ATGATCTCTGGCCACCAAGTGTGTACATGCTTGAACATCACTGATGATGATGATGATGAT 370

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Qy 386 CATTGTTGATTCGTGCTCATTCGAGGCTCTCTCCATCCCGATTTCTTGGAAATATAG 445
 Db 371 CACTGTGGGCTTCATTCCTCCACTCATTTCTCTCCACCCCGATTTCTTGGAAATATAG 430
 Qy 446 CCACAGATATACCAACGCAACCAATTCATCTGATATAGATGATGATTTACATTCCTAA 505
 Db 431 TCACCGGATATACCAATTCACCAAGATTCATGATGATGATGATGATGATGATGATGAT 490
 Qy 506 ACGTATGCAAGGCAAGATTTATTCAAACTTCTTAACATCCACCGGCGGAGTGT 565
 Db 491 AAGCAATTCACCACTCCGCGATCTATTAATCTTTAAACCAACCACTGATGCGCTGT 550
 Qy 566 CACTTGTGTTGCTGATTCATTCAGATTTCCGTTATCTTAACTTAACTTAACTTAACTT 625
 Db 551 GCTTTGATTTATTCATTCATCCCTAGATTTCTTTATACCTTTGCAAAATATTTCCGG 610
 Qy 626 CAAGAAATACGAGGATTTGCAACCACTTGAATCCATGATGATGATGATGATGATGATG 685
 Db 611 CAAGAAATACGAGGATTTGCAACCACTTGAATCCATGATGATGATGATGATGATGATG 670
 Qy 686 TGAAGGCTTCAATTTTGTATCGATTTGCTCTTCTGCTGATTTATGCAATCAA 745
 Db 671 TGACCGGTTTACGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 730
 Qy 746 GCTTCTTGTATGACCAAAAGGAGGAGCTTGGGATATCAACATGATGATGATGATGATG 805
 Db 731 AGTTGCTGTATGACCAAAAGGAGGAGCTTGGGATATGATGATGATGATGATGATGATG 790
 Qy 806 AGGTGTAAAGCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 865
 Db 791 AGGCGTATTTTACCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 850
 Qy 866 TCATTATGATTCACCAAGGAGGAGCTTGAATGAAAGGCGCTTATCAAAATGATGATGATG 925
 Db 851 TCATTATGATTCACCAAGGAGGAGCTTGAATGAAAGGCGCTTATCAAAATGATGATGATG 910
 Qy 926 TTTGCGGTTCTGATCGGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 985
 Db 911 CTTTGATTCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 970
 Qy 986 GATCTCATATTCACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 1045
 Db 971 GTTTTCATTCATTCACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1030
 Qy 1046 GGGGAGTACTATTAATTCAGAGATTCCTCAATTTTCAAAACATGATGATGATGATGATG 1105
 Db 1031 GGGGAGTACTATTAATTCAGAGATTCCTCAATTTTCAAAACATGATGATGATGATGATG 1090
 Qy 1106 GGAATGATTCATTCAGAGCCGATGAGATGAGAGCAAAAGGTGTTCTGATGATCA 1165
 Db 1091 GGAATGATTCATTCAGAGCCGATGAGATGAGAGCAAAAGGTGTTCTGATGATCA 1144
 Qy 1166 CAAGATGTATCAAA 1180
 Db 1145 TAAATGTGATCATTA 1159

RESULT 3
 ; US-09-059-769-3
 ; Sequence 3, Application US/09059769
 ; Patent No. 6329518
 ; GENERAL INFORMATION:
 ; APPLICANT: Green, Allan
 ; APPLICANT: Singh, Surinder
 ; APPLICANT: Lemman, Marit
 ; APPLICANT: Styne, Sten
 ; TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses
 ; TITLE OF INVENTION: Therefor
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder
 STATE: Colorado
 COUNTRY: US
 ZIP: 80303
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/059,769
 FILING DATE: April 14, 1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU P06226
 FILING DATE: 15-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: AU P06223
 FILING DATE: 15-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/043706
 FILING DATE: 16-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/050403
 FILING DATE: 20-JUN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ferber, Donna M.
 REGISTRATION NUMBER: 33,878
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 499-8080
 TELEFAX: (303) 499-8089
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1312 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Crepis sp.
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 26..1147
 US-09-059-769-3

Query Match 54.9%; Score 705.4; DB 4; Length 1312;
 Best Local Similarity 78.6%; Pred. No. 2,7e-194;
 Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;

Qy 77 GGAAGAAACATCTGTAAGCTGTGCGATGATC--ACCGTCAAGTTAAGCGATCT 133
 Db 55 GGAAGAAAGCTGTATGAGAGCTGTCTAGTTGATTCAGTAACTTCTCAGATGATTT 114
 Qy 134 GAGAAAGCAATTCCTACCCATGCTTGAAGCATCTGTCAATCCGATCATCATATGT 193
 Db 115 GAGCAAGCAATTCCTACCATGCTTCAAGCATCTGTATGATGATGATGATGATGATG 174
 Qy 194 TGTTCATGATCTCATTTGTGCTATGTTCTTCTTACTTACCTTGAACAACGATATCCCTCT 253
 Db 175 TGTTCAGATCTCATTAATTCCTTACATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 234
 Qy 254 TATTCCTACACCTGCTTACCTGATGATGAGTGGCCGTTTACGTTTGTGAAGTATGAT 313
 Db 235 TCTTCCTCATCTCTTACGCTTACCTTACCTTACCTTACCTTACCTTACCTTACCTTAC 294
 Qy 314 CTTACCGGCTCTGAGTCAATGCTCAAGATGTGTACCATGATGATGATGATGATGATGATG 373
 Db 295 CTTACCGGCTCTGAGTCAATGCTCAAGATGTGTACCATGATGATGATGATGATGATGATG 354
 Qy 374 GTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 433
 Db 355 ATGGGTGAGAGCACTGTGAGCTTTCATCATCATCATCATCATCATCATCATCATCATCAT 414

QY 434 TTGGAATATAGCCACAGGAATTCACAGCCACAAATTCATCTGATTAAGT 493
DB 415 TTGGAATATAGCCACAGGAATTCACAGCCACAAATTCATCTGATTAAGT 474
QY 494 TTACATTCCTAAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 553
DB 475 TTACATTCCTAAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 534
QY 554 CGGCGAGTGTTCATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 613
DB 535 TGTGCGAGT 594
QY 614 TAATATCTCGGCGAAGAAATACGGAGTGTGTGTGTGTGTGTGTGTGTGTGT 673
DB 595 AAATATCTCGGCGAAGAAATACGGAGTGTGTGTGTGTGTGTGTGTGTGTGT 654
QY 674 TTTCACAGT 733
DB 655 TTTCACAGT 714
QY 734 TTATGCAATCAAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 793
DB 715 TTATGCAATCAAGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 774
QY 794 AATTCAGTACTAGT 853
DB 775 AGTTCAGTACTAGT 834
QY 854 TCTCTACT 913
DB 835 TCACT 894
QY 914 AATGATGAGATTTGGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 973
DB 895 AATGATGAGATTTGGGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 954
QY 974 CTTCGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1033
DB 955 CATGATATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1014
QY 1034 CAAGCAGT 1093
DB 1015 CAAGCAGT 1074
QY 1094 TAGAGAGCTTAAGATGATCTTACATGAGCCGAGTGAAGAGAGAGAGAG 1153
DB 1075 TAGAGAGCTTAAGATGATCTTACATGAGCCGAGTGAAGAGAGAGAGAG 1128
QY 1154 GTTCGTACCAACAAGATGATCAAA 1180
DB 1129 TTATGTGATCAATTAATGTGATCA 1155

RESULT 4
US-08-872-302-3
Sequence 3, Application US/08872302
Patent No. 5846784
GENERAL INFORMATION:
APPLICANT: Hitz, William D
TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
TITLE OF INVENTION: Developing Seeds of Vernonia galamensis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. duPont de Nemours and Co.
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,302
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Majorian, William R
REGISTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-1084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1364 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 103..1254
US-08-872-302-3

Query Match 54.5%; Score 699.8; DB 2; Length 1364;
Best Local Similarity 75.8%; Pred. No. 1.1e-192;
Matches 894; Conservative 0; Mismatches 277; Indels 8; Gaps 2;

QY 112 CACGCTTACAGTGAAGCATCTGAAGAAAGCATCTCCATCCATGCTTGAAGCATCTG 171
DB 188 CACATCTCGTTAAGGATTAAGAAAGCAATCCCTCGCATTTGCTTCAAGCATCTG 247
QY 172 TCATCCGCTATCATATGTTGTTGATGATCTATGTTGCTTATGTTCTTACTACC 231
DB 248 CCATCCGCTATCATATGTTGTTGATGATCTATGTTGCTTATGTTCTTACTACC 307
QY 232 TTGAAACAGTATATCTCTTATCTCAACCTGCTGCTTACCTAGCATGCGCTGT 291
DB 308 TCGCAACTCTTACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 367
QY 292 ACTGTTTGTCAAGTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 351
DB 368 ACTGTTTGTCAAGTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 427
QY 352 ACATGATTTAGGAGTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 411
DB 428 ATCATGTTTATGAGTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 487
QY 412 CTCCTCTCAAGGATTTCTGTTGAAATATGACACAGGAATCAACAGCCAAACAA 471
DB 488 TTCTCTCAAGGATTTCTGTTGAAATATGACACAGGAATCAACAGCCAAACAA 547
QY 472 ATTCATCTGATTAAGTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 528
DB 548 ATTCATCTGATTAAGTATGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 607
QY 529 ---ATTCCAACTTTTAAACATCAACCCGCGAGTGTACTTGTGTGTGTGTGA 585
DB 608 CCAATTTCAATTTCTTGACAAACCCCTGTGTCAATCTTATGTTGATCAATGTGA 667
QY 586 CTTAGATTTTCTGTTATCTCTTAACTAATCTGCGGCAAGAAATACAGGAGTTTG 645
DB 668 CTTGCGGTTCTTATTAATCTCTTGAACAATATTTTGAAGCAAAATACAAAGTTTG 727
QY 646 CCAACCACTTGTATCCATGATCTCAATTTTCAACGATCTGAAGCGGTTCAAGTTTGC 705
DB 728 CCAACCACTTGTATCCATGATCTCAATTTTCAACGATCTGAAGCGGTTCAAGTTG 787
QY 706 TATCCGATTTGCTGCTGCTGATTTTATGCAATCAAGCTTCTGTAGACGAAAG 765
DB 788 TATCGATGTTGCTGCTGCTGATTTTATGCAATCAAGCTTCTGTAGACGAAAG 847
QY 766 GGGGAGCTTGGTATTAACAATGATCAAGATTTCAAGTACTAGGTATAGCGTTCTTG 825


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Db      848 GGTTCGGTGGTATGCGATGTAACGAGCCCAAGTGTGGCTGATCCCTTCATTA
Qy      826 TTTTATCATCATTTTGGACACCAACCCATCTCTCACTCCCTCATATTAATGATCAACCGAA
Db      908 TAAATGATCATCTTATCTCCACACACACCCATCTGTCTTCCCTCATATTAATGATCAACCGAA
Qy      886 GAAATCTGATCAAAAGGCGCTTATCAACATGATGAGGATTTGGGTTCTGATCCGG
Db      968 GAACTGGATCAAAAGGACCTTGAATCAATGATGATGATTTGGGTTCTGATCCGG
Qy      946 TTTTCCACGATGATACACACTCACTCTTTCATCATTTTATGATCTCATATTCACATT
Db      1028 TGTTCATGAGTCACTCAACACACGCTGTGATCATTTTGTCCCGTACATTCACACTT
Qy      1006 ATCATGCAAGGAAAGGAGGATGCAATCAAGCCAGTGTGGGGAGTACATTAATAATCG
Db      1088 ATCATGCAAGGAGGAGGAGGATGCAATTAAGCCGGTGTAGGGAGTATCGATGATCG
Qy      1066 ACAGAGACTCCAAATTTTCAAGCAATGATATAGAGAGGCTAAGAAATGATTCATTCAGAC
Db      1148 ATAGAGCTCCGTTTATCAAAACATGATGAGAGAGGAGGAGATGATTCATTCAGATCG
Qy      1126 CCGATGAGATGAGAGACCAAGGCTGTCTGTGATCCACAAAGTGAATCAAAAAGT
Db      1208 CAGATGAAGATGAAGACCAAGGCTGATGATGATGATGATGATGATGATGATGATGATG
Qy      1186 GTATGTCATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      1268 GTACGT--AGTACGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      1246 TTATCATTAAGAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG
Db      1326 ATGAAGATTAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG

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RESULT 5

US-08-314-596-44

Sequence 44, Application US/08314596

Patent No. 5668292

GENERAL INFORMATION:

APPLICANT: SOMERVILLE, CHRIS

APPLICANT: VAN DE LOO, FRANK

TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO

TITLE OF INVENTION: PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: CUSHMAN DARBY & CUSHMAN L.L.P.

STREET: 1100 NEW YORK AVENUE, N.W.

CITY: WASHINGTON

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/314,596

FILING DATE: 26-SEP-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KOKUTIS, PAUL N.

REGISTRATION NUMBER: 16,773

REFERENCE/DOCKET NUMBER: 206905/1220

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-861-3000

TELEFAX: 202-822-0944

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

LENGTH: 1231 base pairs

TYPE: nucleic acid

;

STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-314-596-44

Query Match 35.5%; Score 455.6; DB 1; Length 1231;
Best Local Similarity 63.9%; Pred. No. 5,46-122;
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

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Qy      109 ATCCACGGTTCACGTTAAGCATCTGAAGAAAGGATTCCTACCATGCTTTGAGGCAT
Db      55 AACCGCTTCTCGGTGGAGATCTGAAGAAAGCAATCCCGCATTTGTTCAAGCCT
Qy      169 CTGTATCCGGTCACTCATATGATGTTGATGATGATGATGATGATGATGATGATGATGATG
Db      115 CAATCCCGCTGCTTCTCTCACTTATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      229 ACTTGCACCAAGATATATCTCTTATTTCTTACACTCTGCTTACCTAGATGACCTCG
Db      175 ACCTGCGCACCAATTAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Qy      289 TTTATCTGTTTGTCAAGTATGATCTCTCAACCGGCTCTGGGTGATGGTCAAGATGTG
Db      235 TCTATTTGGGCTGTCAAGCTGTGTCTTAACTGATGATGATGATGATGATGATGATGATGATG
Qy      349 GTCAACATGATTTAGGAGACTACAGATGATGATGATGATGATGATGATGATGATGATGATG
Db      295 GTCAACAGATTTAGGAGACTACAGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      409 CGGCTCTCTCAACCGGTATTTCTTGTGAATATGACAGAGATCAACGCAACA
Db      355 CTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Qy      469 CAATTAATCTGATGAAGATGAAGTATTAATCTTAACGTAATGATGAAGTCAAGATTT
Db      415 CTGATCCCTGTAAGAGATGAAGTATTTGCTCAAGAGAGAAATCAAGATTAAGTGT
Qy      529 ATTCGAATCTTCAATCAACCGGAGAGTTCATCTTGTGTGATGATGATGATGATGATGATG
Db      475 ACGGGAATTAATCAACCGCTTGAAGATCAATGATGATGATGATGATGATGATGATGATG
Qy      589 TAGATTTCCGTATATCTCTTAACTAATATCTGCGGCAAGAAATGAGGAGTTGGCA
Db      535 TCGGATGGCCCTTGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      649 ACGATTTGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      595 GCGATTTCTTCCCAAGCTTCCATCAATGATGATGATGATGATGATGATGATGATGATGATG
Qy      709 CCGATTTCCGTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      655 CTGATGGGGATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      769 CAGCTTGGATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      715 TGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
Qy      829 TGATCAATATTTGACACCAACCATCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Db      775 TGATCACTTACTTGACACCACTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
Qy      889 ACTGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGATGATG
Db      835 ACTGCTCAAGGAGCTTTGGCTACGTAAGAGAGCTAGAGAAATTTGAACAAGGTGT
Qy      949 TCAACAGCTTACACACTACGCTTGTGATCAATTTGATCTCATATTCACATTAATC
Db      895 TCAACACATTAACAGACACAGTGTCTATCACTGTTCTGACAAATGCCGATTAATA
Qy      1009 ATGCAAGGAAGCAAGGATGATCAATCAAGCAGTGTGGGCTACTATTAATTCACA
Db      955 ACGCAATGGAAGCTACAAAGGCGATTAAGCAATTTGAGGAGACTATTAACAGTTGATG

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COUNTRY: U.S.A.
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/819,037
 FILING DATE: 19-MAR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/320,982
 FILING DATE: 11-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/314,596
 FILING DATE: 26-SEP-1994
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1231 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-819-037-44

Query Match 35.5%; Score 455.6; DB 3; Length 1231;
 Best Local Similarity 63.9%; Pred. No. 5.4e-122;
 Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

QY 109 ATCCACCGCTTCACGTTAAGCATGTAAGAAAGCATTCCTAACCCATGCTTTGAGCGAT 168
 DB 55 AACCGCTTTCGCGTGGAGATCTGAAGAAAGCATCCCGCGCATGTTCAAAACGCT 114
 QY 169 CTGTCATCCGCTCATCATCTATGTTGTCATGATCTGATGTTGCTTCTTACT 228
 DB 115 CAATCCCTGCTCTTCTCCATCCTTATCAGTGAATCATATATACCTCATGCTTCTACT 174
 QY 229 ACCTTGAAACAGCATATATCCCTCTTATCTCAGACCTCTGAGCTTACCTAGCATGAGCCG 288
 DB 175 ACGTGGCAACATTAATCTCTCTCTCCCTCAGCCTCTCTCTTACTTGGCTTGGCAC 234
 QY 289 TTATAGTCTTGTCAAGCTAGCATCTCACCGGCTCTGGGTCATCCGTCACGATGTG 348
 DB 235 TCTATGGGCTGTCAAGGCTGTGCTTAATGATCTGGGTATATACCCAGATGCG 294
 QY 349 GTCAACATGATTTAGGCACTTACCATGTTGATGATGATGATGATGATGATGATGATG 408
 DB 295 GTCAACAGCATTAAGGCACTTACCATGTTGATGATGATGATGATGATGATGATGATG 354
 QY 409 CGGCTCTCCCTACCCCGTATTTCTTGGAAATATAGCCACAGAAATGACAGCGCAACA 468
 DB 355 CTTCTCTCTGCTGCTTACTTCTCTGGAAGTATAGTCAATGCGCGTCAACATTCACACA 414
 QY 469 CAATTCATCTGATTAAGATGAAGTTTACATTCCTTAAAGTGAAGTGAAGTGAAGTGA 528
 DB 415 CTGATCCCTCGAAGAGATGAAGTATGTCCTCCAAAGCAAGTATCAAGTCAAGTGT 474
 QY 529 ATTCCAAATCTTAAACATCAACCCGCGAGTGTCACTTGTGTTGTTGTTGATTT 588
 DB 475 ACGGAATATACCTCAACACCTCTTGGACCATCATCATATTAACCTCTCAAGTTTCTC 534
 QY 589 TAGGATTTCCGTTATCTTAACTTAATATCTGGGCAAGAAATAGGAGGATTTGCA 648
 DB 535 TCGGCTGCGCTTGTATCTTAACTTAACTTCTGCGAGACCTGATATACGAGGTTGCTT 594
 QY 649 ACCACTTGTATCCATGATCAATTTTCAAGTGAAGCGGTTCAAGTTTGTCTAT 708
 DB 595 GCCATTTCTTCCCAAGCTCCCATCTAATGAACGGAAGCGCTCAAGTATATACCTCT 654
 QY 709 CCGATTTCCGCTTCTGCTGTATTTTATGCAATCAAGCTTCTGTAGCAGCAAAAGGGG 768
 DB 655 CTGATGGGGATTTCTAGCCGCTGTGTTTGGCTTTTACCGTTACGCTGCTCACAAGGGA 714

QY 769 CAGCTGGGATATCAACATGATGACCAATTCAGTACTAGTGTAAAGCGTCTTCTGTTT 828
 DB 715 TGGCTCGATGATCTGCTCTACAGGATACCGCTTCTGATGTGAATGCGTTCCGCTCT 774
 QY 829 TGATCATATTTTGAACCAACCATCTTCTCACTCTCTCATTTATGATTTCAACCGATGA 888
 DB 775 TGATCATCTTACTTACAGACACTCATCCCTGTTGCTTCTCATCATCATCATCAGAGTGG 834
 QY 889 ACTGATCAAGGGCGCTTATCAACATCATGATGATGATGATGATGATGATGATGATGATG 948
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 QY 949 TCCAGACGTTACACACTCAGCTCTTGCATCTTATGATCTCATATTCACATTTATC 1008
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 QY 1009 ATGCAAGAGAGCAAGGATCAATCAAGCATGTTGGCGAGTACTATTAATGACA 1068
 DB 955 ACGCAATGAGATCAAAAGCGATTAAGCCAAATTTGGAGACTATTAACAGATTGATG 1014
 QY 1069 GACTCCATTTTCAAGCAATGATGAGAGGCTAAGGATGATCATCATTCAGGCCG 1128
 DB 1015 GAACACGCTGTATGTAGCGATGTATAGGAGGCAAGAGAGTGTATCTATGTAGAACGG 1074
 QY 1129 ATGAGATAGGAGACACAAAGTGTCTGTGATACCAAGATGTATCAAAAGGTG 1186
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RESULT 8
 US-09-045-940-44
 Sequence 44, Application US/09045940
 Patent No. 6433250

GENERAL INFORMATION:
 APPLICANT: SOMERVILLE, CHRIS
 TITLE OF INVENTION: USE OF PLANT FATTY ACYL HYDROXYLASES TO
 PRODUCE HYDROXYLATED FATTY ACIDS AND DERIVATIVES IN PLANTS
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: PILLSBURY MADISON & SUTRO L.L.P.
 STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.

COUNTRY: U.S.A.
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Microsoft Word
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/045,940
 FILING DATE: 23-MAR-1998
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/320,982
 FILING DATE: 11-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/314,596
 FILING DATE: 26-SEP-1994
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1231 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-045-940-44

Query Match 35.5%; Score 455.6; DB 4; Length 1231;
 Best Local Similarity 63.9%; Pred. No. 5.4e-122;

Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

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109 ATCCACGGTTCACGTTAAGCATGGAAGAAAGCATTCCTACCATTCCTTGGAGCAT 168
55 AACGGCTTTCTCGGTGGAGATCTGAAGAAAGCAATCCCGCATGTTTCAAGCCT 114
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229 ACCTTGAAACAGATATCCCTTATCTTACACCTCTGGCTTACCTACGAGCCCG 288
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235 TCTATGGGCTGTCAAGGCTGTGTCTTATCTGATCTGGGTCACTTACCCAGATCG 294
349 GTCAACATGATTTAGGACATCAAGATGATGATGATGATGATGATGATGATGAT 408
295 GTCAACAGCATTCAGCATCAACATGCTGATGACACAGTTGGTCTTATCTTCAAT 354
409 CGGCTCTCTCAACCCGATTTCTCTTGGAAATATAGCAGAGAAATGACAGCCACA 468
355 CTTCTCTCTGCTCTTACTTCTCTGAAATATGATGATGATGATGATGATGATGAT 414
469 CAATTCATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
415 CTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 474
529 ATTCCAACCTTCTTAAATCAACCCGAGATGATGATGATGATGATGATGATGAT 588
475 ACGGAAATATCTCAACACCTCTTGGAGCATGATGATGATGATGATGATGATGAT 534
589 TAGATTTCCGTTATATCTTATATCTTCCGGAAGAAATACGGAGATTTGCA 648
535 TCGGTGCGCTTGTACTTACCTTAAAGTCTTGGGACACCGATATACGGGTTCGCT 594
649 ACCATTTGATCCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
595 GCATTTCTTCCCAAGCCTCCCATCTAATGATGATGATGATGATGATGATGATGAT 654
709 CCGATTTGCTTCTGCTGATTTATGATGATGATGATGATGATGATGATGATGATGAT 768
655 CTGATGCGGTATCTTACCGCTGTTTGGTCTTACCGTTCACGCTCTCACAAGGGA 714
769 CAGTTGGGTATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
715 TGGCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774
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775 TGATCATTTACTGACACACATCTATCCCTGCTCTCATGATGATGATGATGATGAT 834
889 ACTGATCAAAAGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGAT 948
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955 ACGCATGAGAGCTTCAAAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014
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1129 ATGAGATGAGAGACAAAGGTGTTCTGTGATCAACAAGATGATGATGATGATGATGAT 1186
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RESULT 9
US-09-133-962A-1
Sequence 1, Application US/09133962A
Patent No. 6372865
GENERAL INFORMATION:
APPLICANT: JONATHAN EDWARD LIGHTNER
JOHN JOSEPH OKULEY
TITLE OF INVENTION: GENES FOR MICROSOMAL FATY ACID
DELTA-12 DESATURASES AND RELATED
ENZYMES FROM PLANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/133,962A
FILING DATE: 14-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNIE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1043-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302)992-5481
TELEFAX: (302)773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1372 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULAR TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: p92103
FEATURE:
NAME/KEY: CDS
LOCATION: 93..1244
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-133-962A-1

Query Match 35.5%; Score 455.6; DB 4; Length 1372;
Best Local Similarity 63.9%; Freq. No. 5.7e-122;
Matches 689; Conservative 0; Mismatches 389; Indels 0; Gaps 0;

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109 ATCCACGGTTCACGTTAAGCATGGAAGAAAGCATTCCTACCATTCCTTGGAGCAT 168
175 AACGGCTTTCTCGGTGGAGATCTGAAGAAAGCAATCCCGCATGTTTCAAGCCT 234
169 CTGTATCCGGTCACTATGATGTTGTCATGATCTCATTTGTCCTTACT 228
115 CAATCCCGCTCTTCTCTACCTTATCAGTACATATTAAGCTTCAATGCTTACT 294
229 ACCTTGAAACAGATATCCCTTATCTTACACCTCTGGCTTACCTACGAGCCCG 288

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OY 649  ACACCTTGGATCCCATGAGTCGAATTTTCAACGATCGTGAACGCGTTCAAGTTTGGTAT 708
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Db 753  GCCATTTTCTCTTACAGCCTTATATACAAAGACGTGAGCGTCTCCAAATATBTGGCTT 812
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OY 709  CCGATTCGGCTTCTCGCTGATTTTATATGCAATCAAGCTTCTTGTAGCAGCAAAAGGGG 768
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Db 813  CGGATTTAGGGATGATGATCAATGTCGTTCAATCCTTTATTCGTGTCTGTAGCAAAAGGG 872
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OY 769  CAGCTTGGGTATCAACATGTACGCAATTCAGTACTAGGTGTAGAGCTGTCTTCTGTT 828
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Db 873  TGGCTTGGGTATATGATGATGATGGATCCCGCTACTGATGTGTGAACGGAATTCGTGTGA 932
    |||||
OY 829  TGATCAGATTTTGGACACACCCATCTCTCACTCCCTCATATGATTTCAACCGAATGGA 888
    |||||
Db 933  CGATACGTAACCTTAAACACTCACTCACTTCACTTATGCCCCATATATAGCTAGAGTGG 992
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OY 949  TCCAGAGCTTACACACACTCACTGCTTGCATTTGATGTCAATTCACATTCACATATC 1008
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Db 1053  TCCATAAATCAACATATCAACACGCTGACACATTTGTCTCGACGATGCTCATATATA 1112
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OY 1009  ATGCAAGGAAGCAAGGATGCAATCAAGCCAGTGTGGGCGAGTACTATAAATATGACA 1068
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Db 1113  ACGCATATGAGGACCAAGCAAGAGTGAAGCTTGTCTGGAGATATATACATTTGAGAG 1172
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OY 1069  GCACTCCAATTTTCAAGCAATGTATAGAGGCTTAAAGATGATCTTACATCGAGCCCG 1128
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Db 1173  GGACTCCCTTTTACGTACCAATATGAGAGGCAAGGAGAGTGTGTGTCGTGATCGAG 1232
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OY 1129  ATGAGGATAGCGAGCAAGAGTGTGTTCTGTATCAACAAGATG 1172
    |||||
Db 1233  ATGAGGGGAGGCTCAGGAGGTGTGTTTGTATCAAGATAG 1276
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RESULT 11
US-09-133-962A-15
Sequence 15, Application US/09133962A
Patent No. 6372965
GENERAL INFORMATION:
APPLICANT: JONATHAN EDWARD LIGHTNER
JOHN JOSEPH OKULEY
TITLE OF INVENTION: GENES FOR MICROSOFT PATTY ACID
DELT-12 DESATURASES AND RELATED
ENZYMES FROM PLANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/133,962A
FILING DATE: 14-Aug-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 07/977,339
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNN M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: BB-1043-D
TELECOMMUNICATION INFORMATION

```

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TELEPHONE: (302) 992-5481
TELEFAX: (302) 773-0164
TELEX: 835420
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 2973 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: pAF2-6
FEATURE:
NAME/KEY: exon
LOCATION: 433..520
FEATURE:
NAME/KEY: intron
LOCATION: 521..1654
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-133-962A-15

Query Match      35.3%; Score 4541; DB 4; Length 2973;
Best Local Similarity 63.8%; Pred. No. 2.5e-121;
Matches 688; Conservative 0; Mismatches 390; Indels 0; Gaps 0;

109  ATCCACGGTTCACGTTAAGCATGTGAAGAACGATTCCTACCCATTGCTTTGAGCAT 168
Db  1741 AACCGCCTTTCGCGTGGAGATTTGAAGAACGATTCGCCGCATGTTTCAAGCT 1800
Qy  169 CTGTCAATCCGGTCATCACTACTAGTTGTATCATGATCTCATTTGTCCTATCTTACT 228
Db  1801 CAATCCCGCTCTTCTCTCACTTACAGTGCATCATATATAGCTCATAGCTTCTACT 1868
Qy  229 ACCTTGCACACGATATATCCCTCTTATCTCTAACCCTTGGCTTACTTAGAGGCCG 288
Db  1861 ACGTCGCACCAATATCTCTCTCTCCCTCAGCCTCTCTCTACTTGGCTTGGCCAC 1920
Qy  289 TTTACGTGTTTGTTCAGAGCTAGCATTCCTCAACCGGCTCTGGGTCATCGGTACAGATGTG 348
Db  1921 TCTATGGGCTGTCAAGGCTGTCTTCTTACTGTGATCTGGGTATAGCCACGAAATGG 1980
Qy  349 GTCAACCATGCAATTAGGCACTACCAAGTTGATGATGACATTTGATTTGTTGCTCAT 408
Db  1981 GTCAACCATGCAATTAGGCACTACCAATGGCTGATGACACAGTTGGTCTTATCTTTCAT 2040
Qy  409 CGGCTCTCTCAACCCGTAATTTCTCTTGGAAATATAGCCACAGAAATCACTACGCCAACA 468
Db  2041 CCTTCTCTCTCGTCCCTTACTCTCTCTGGAATGATGATCGCCGTACCATTTCAACA 2100
Qy  469 CAATTCACCTGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
Db  2101 CTGATATCCCTGAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2160
Qy  529 ATTCCAAACTTCTTAAACATCCACCGGCGAGTGTTCATTTGGTGTGTTGGTGA 588
Db  2161 ACGGGAATACCTCAACACCTCTTGGAGCATCATGATGATTAACGTCAGTTTGCC 2220
Qy  589 TAGATTTCCGTTATACCTCTTAACTTAATATCTTGGGCAAGAAATATAGGGAAGTTTGCA 648
Db  2221 TCGGATGGCCCTTGTACTTATAGCTTTTAAAGTCTCTGACAGACCGTATGACGGGTGCGTT 2280
Qy  649 ACCGCTTGAATCCCATAGTCATTTTCAACGATGATGATGATGATGATGATGATGATGAT 708
Db  2281 GCCATTTCTTCCCAACGCTCCCATCTACATGATGATGATGATGATGATGATGATGATGAT 2340
Qy  709 CCGATTTCCGCTCTCTGCTGATTTTATGATGATGATGATGATGATGATGATGATGATGATGAT 768
Db  2341 CTGATGGGGGATTTCTAGCCGTCTGTTTGTCTTTACCGTTTACGCTGCTGCAACAAGGA 2400

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/320,982
FILING DATE: 11-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/314,596
FILING DATE: 26-SEP-1994
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 1222 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-045-940-43

Query Match 33.6%; Score 432.4; DB 4; Length 1222;
Best Local Similarity 61.3%; Pred. No. 2.8e-115;
Matches 716; Conservative 0; Mismatches 446; Indels 6; Gaps 1;

QY 109 ATCCACCGTTACGTTAAGCATCTGAAAGAAAGCATTCCTACCATTCCTTTGAGCAT 168
DB 55 AGCCCTCTTACACTTGCTGACCTCAAGAGAGCATCCACCCATTCCTTGAACGCT 114
QY 169 CTGTCATCCGGTCACTCATCTATGTTGTTCAAGATCTGATTCGCTATGCTTCTACT 228
DB 115 CTTTTGCGCTCATCTCTCATGTTGCTTAAGATGCTCTTAAGTTTCTTTTCTACT 174
QY 229 ACCTTGCAACACGATATATCCCTTATTCCTAACCTCTGCTTACCTAGCATGGCCG 288
DB 175 CGATGGCACCAACTCTTCCCTTACATCTCTTCCGCTCTCGATGTCGCTGGCTGG 234
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DB 355 CTGACACTTCTGCTTCATATTTTTCATATGAAATATAGCCATCGCCGACCATTTTACA 414
QY 469 CAATTCATCTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
DB 415 TAGGATCTCTGAGGAGACGAGATGCTGCCGAAATCAAGTCGAAATTTTCATGT 474
QY 529 ATTCAAACTTCTTAACATCAACCCGGGAGATGTTCACTTGGTGTTCGTTGACTT 588
DB 475 ATTCTAAGTACTCAAAACACCCGAGGTCAAGTTTTCACACTTGTCTGCAAGCTCTCC 534
QY 589 TAGGATTTCCGTTATACCTCTTAATAATCTCGGGCAAGAAATACGGAGGTTTGGCA 648
DB 535 TTGGCTGGCTTTTATCTTAGCTTCAATGCTCTGTAGACCTTACGATCGCTTGTCTT 594
QY 649 ACCACTTTGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
DB 595 GCCATTTATGATCCCTATGCCCCCAATTTTCGAAAGAAAGGCTTCAATTTACATYG 654
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DB 715 TGGCTTGGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 774
QY 829 TGATCAATATTTGACACACACCATCTCTCACTCTCATATGATTAACCCGATGGA 888
DB 775 TGATCAATATTTGACACACACCATCTCTCACTCTCATATGATGATGATGATGATGAT 834
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QY 1069 GCACTCCAAATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
DB 1015 GTACCCATTTTACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1074
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DB 1075 ATGAGAGAGCTCTTACACAAAGGCTTTTCTGTGTGTCACCAAGTATATTAAGTGA 1134
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DB 1135 TGTAGCTGTTTCTTTAAGAGAGTAAATTAAGACAAAGAGATGTGTGTATGTAT 1194
QY 1243 AAATTAATTAAG 1270
DB 1195 GTGTTTAATAAG 1222

Search completed: June 23, 2004, 14:45:08
Job time : 93 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 14:00:28 ; Search time 454 Seconds
(without alignments)
12966.299 Million cell updates/sec

Title: US-10-069-772-1

Perfect score: 1285
Sequence: 1 aaaagctcactctctctga.....aaaaaaaaaaaaaaaa 1285

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3017426 seqs, 2290544650 residues

Total number of hits satisfying chosen parameters: 6034852

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCTR_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	715.8	55.7	1358	9 US-09-981-124-1	Sequence 1, Appl1
2	705.4	54.9	1309	9 US-09-981-124-3	Sequence 3, Appl1
3	681	53.0	1199	9 US-09-981-124-19	Sequence 19, Appl1
4	484.4	37.7	1566	13 US-10-425-114-14778	Sequence 14778, A
5	484.4	37.7	2931	13 US-10-424-599-123945	Sequence 123945, A
6	484.4	37.7	6220	15 US-10-465-800-3	Sequence 3, Appl1
7	484.4	37.7	6220	15 US-10-176-149-3	Sequence 3, Appl1
8	481.2	34.7	1457	13 US-10-425-114-12782	Sequence 12782, A
9	445.8	34.7	1422	9 US-09-837-751-5	Sequence 5, Appl1
10	444.8	34.6	1411	9 US-09-852-399-3	Sequence 3, Appl1
11	436.8	34.0	1411	9 US-09-837-751-3	Sequence 3, Appl1
12	434.2	33.8	1155	16 US-10-330-775-5	Sequence 5, Appl1
13	431	33.5	1155	9 US-09-995-297-9	Sequence 9, Appl1
14	431	33.5	1155	10 US-09-771-904-9	Sequence 9, Appl1

15	431	33.5	1155	17 US-10-715-100-9	Sequence 9, Appl1
16	429.4	33.4	1155	9 US-09-995-297-11	Sequence 11, Appl1
17	429.4	33.4	1155	10 US-09-771-904-11	Sequence 11, Appl1
18	429.4	33.4	1155	17 US-10-715-100-11	Sequence 11, Appl1
19	427.8	33.3	1155	9 US-09-995-297-13	Sequence 13, Appl1
20	427.8	33.3	1155	10 US-09-771-904-13	Sequence 13, Appl1
21	427.8	33.3	1155	17 US-10-715-100-13	Sequence 13, Appl1
22	426.8	33.2	1164	15 US-10-185-578-1	Sequence 15, Appl1
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37	424.6	33.0	1155	16 US-10-330-775-3	Sequence 3, Appl1
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41	423	32.9	1155	17 US-10-715-100-7	Sequence 7, Appl1
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43	422	32.8	1155	10 US-09-771-904-3	Sequence 3, Appl1
44	422	32.8	1155	17 US-10-715-100-3	Sequence 3, Appl1
45	411	32.0	1357	17 US-10-419-865-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-981-124-1
Sequence 1, Application US/09981124
Patent No. US20020166144A1
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lemhan, Marit
APPLICANT: Skymne, Sten
TITLE OR INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
FILE REFERENCE: 26-98A
CURRENT APPLICATION NUMBER: US/09/981.124
CURRENT FILING DATE: 2001-10-17
PRIOR APPLICATION NUMBER: US 09/059769
PRIOR FILING DATE: 1998-04-14
PRIOR APPLICATION NUMBER: US 60/043706
PRIOR FILING DATE: 1997-04-16
PRIOR APPLICATION NUMBER: AU P06223
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: AU P06226
PRIOR FILING DATE: 1997-04-15
PRIOR APPLICATION NUMBER: US 60/050403
PRIOR FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1358
TYPE: DNA
ORGANISM: Crepis palaestina
FEATURES:
NAME/KEY: CDS
LOCATION: (30)..(1151)
OTHER INFORMATION:
US-09-981-124-1
Query Match 55.7%; Score 715.8; DB 9; Length 1358;

Best Local Similarity 78.2%; Pred. No. 2,5e-184; Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;

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Qy 326 CTGGGTATCGGTACGAAATGTGTCAACAGATGTCAGTACGATCCAGTGAATGATGA 385
Db 311 ATGATCTCTGCGCCAGATGTGTGACACATGCTTTAGCAACTACATGTTTGAACGA 370
Qy 386 CATTTGATGATTCGTGCTCAATTCGCGCTCTCTCAACCCCGATTTCTTGGAAATATAG 445
Db 371 CACTGTGGCTTCAATCTCTCACTATTTCTCTCAACCCCGATTTCTTGGAAATATAG 430
Qy 446 CCAAGAAATACCAACGCAACCAAAATCACTGATAGATGAATTTCAATCTCTAA 505
Db 431 TCACCGGAATACCAATTCACACAAAGTTGATGATGAATGAATTTCAATCTCTAA 490
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RESULT 2
US-09-981-124-3
; Sequence 3, Application US/09981124
; Patent No. US2002016144A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lemman, Marit
; APPLICANT: Styenne, Sten
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
; FILE REFERENCE: 26-98A
; CURRENT APPLICATION NUMBER: US/09/981.124
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/043706
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: AU P06223
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 60/050403
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1309
; TYPE: DNA
; ORGANISM: Crepis sp.
; FEATURES:
; NAME/KEY: misc.feature
; LOCATION: (937)..(937)
; OTHER INFORMATION: N is any nucleotide residue
; NAME/KEY: CDS
; LOCATION: (126)..(1147)
; OTHER INFORMATION:
; NAME/KEY: misc.feature
; LOCATION: (901)..(901)
; OTHER INFORMATION: N is any nucleotide residue
US-09-981-124-3

Query Match 54.9%; Score 705.4; DB 9; Length 1309;
Best Local Similarity 78.6%; Pred. No. 1.7e-181;
Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;

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Db 112 GAAGCAAGCAATTCCTTCAACCATGCTTTGAGCGATCTGTCAATCGGTCATATATGT 171
Qy 194 TGTTCATGATCTATGTTGTGCTATGCTTCTTACTTCTTGGCAACATATATCCCTCT 253
Db 172 TGTTCAGATCTCAATATGCTTATCATCTTCTTCTTGGCAACATATATCCCTCTAA 231
Qy 254 TATTCCTACACCTGTGCTTACCTAGATGAGCCGTTTACTGTGTTTGTCAAGTATGAT 313
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 ; Sequence 19, Application US/09981124
 ; Patent No. US2002016144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Green, Allan
 ; APPLICANT: Singh, Surinder
 ; APPLICANT: Lemman, Maric
 ; APPLICANT: Skymne, Sten
 ; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MO
 ; TITLE OF INVENTION: FATTY ACID METABOLISM
 ; FILE REFERENCE: 26-98A

; CURRENT APPLICATION NUMBER: US/09/981.124
 ; CURRENT FILING DATE: 2001-10-17
 ; PRIOR APPLICATION NUMBER: US 09/059769
 ; PRIOR FILING DATE: 1998-04-14
 ; PRIOR APPLICATION NUMBER: US 60/043706
 ; PRIOR FILING DATE: 1997-04-16
 ; PRIOR APPLICATION NUMBER: AU P06223
 ; PRIOR FILING DATE: 1997-04-15
 ; PRIOR APPLICATION NUMBER: AU P06226
 ; PRIOR FILING DATE: 1997-04-15
 ; PRIOR APPLICATION NUMBER: US 60/050403
 ; PRIOR FILING DATE: 1997-06-20
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 19
 ; LENGTH: 1199
 ; TYPE: DNA
 ; ORGANISM: Vernonia galamensis
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (44)-(1195)
 ; OTHER INFORMATION:
 ; US-09-981-124-19
 Query Match 53.0%; Score 681; DB %; Length 1199;
 Best Local Similarity 78.3%; Pred. No. 7.2e-15;
 Matches 839; Conservative 0; Mismatches 229; Indels 4; Gaps 2;
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 QY 167 ATCTGATCGGCTCATCATCTATGTTGTTGATGCTGCTGCTGCTGCTGCTGCTGCT 226
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 QY 284 GCCCGTTACTGTTTGTCAAGCTAGCATCTCAACGCGCTGCGGCTCATGCTGACGA 343
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Qy 1004 TTATCATCAAAAGGAGGAGATGCAATCAAGCGATGTTGGCGGAGTCTAATAAT 1063
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Db 1134 GGCTGATGAGATGACCGACCAAAAGGCAATATGATCTGATCAACAAGTTGTA 1185

RESULT 4

US-10-425-114-14778
; Sequence 14778, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 14778
; LENGTH: 1586
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3028-001-B9_FLI
US-10-425-114-14778

Query Match 37.7%; Score 484.4; DB 13; Length 1586;
Best Local Similarity 65.8%; Pred. No. 3.6e-121;
Matches 704; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

Qy 109 ATCCACGCTTACGTTAGCGATCGTAGAAGGAGTCCATCCATTCGTTGAGCAT 168
Db 156 AACCTCCATTTAGTTCAGCCAAATCAAGAGGTATTCACCTTACGTTTCCAGGCTT 215
Qy 169 CTGTCATCCGCTCATCATATATGTTTCATGATCTCATTTGTCCTATGCTTCACT 228
Db 216 CTGTTTCCGCTCATCTCTCATATGTTTACGACTCACCATACCTTTCGCTCTAT 275
Qy 229 ACCTTGCAAAACGATATTCCTTATTTCTCAACCTCTGCTTACCTAGATGCGCG 288
Db 276 ATGTGCCACCATATCTTCCACCTCTCTCCAGCCCTCTCTTCTTGGAGGCGCA 335
Qy 289 TTTACTGTTTGTGAAGCTACCTCACCGGCTCGGGTCACTGATCAAGATG 348
Db 336 TCTACTGGGCTGTCCAAAGGTGATCTTACTGAGTTGGGTCTATGCCATGAGTGTG 395

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Db 396 GCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 455
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Db 456 CGGCTCTCTCAACCCGATATTTCTTTGAAATATATAGCCACAGAAATACACCGCAACA 515
Qy 469 CAATTCATCTGATACGATGAAATTTATCATTTCTTAAACGTAAGTCGAAGTCAATTT 528
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Db 576 ACTCTAAATACCTTAAACATCTTCAGCAAGTCTCAGTCTGTCATCCTCAGCCTCAC 635
Qy 589 TAGGATTTCCGTTATACCTCTTAACTAATATCTGCGGCAAGAAATACCGGAGTTTGCA 648
Db 636 TTGGTTGGCCTTTGATCTGCTTTAAATGTTTGTGAAGGCTTATGATGATTTGCTT 695
Qy 649 ACCACTTTGATCCGATGAGTCAATTTTCAAGATCGTGAACGCGTTCAAGTTTGTCTAT 708
Db 696 GCACTATGACCCATATGATGCTCCATTTACTGATCGTGAACGCTTCAAAATATATATAT 755
Qy 709 CCGATTCGCTCTCTGCTGATATTTATGCAATCAAGCTTCTGTAGACCAAAAGGG 768
Db 756 CAGATGACGAGATCTTGCAGATATGATATGAGCCCTTTCCGCTTCCATGCAAAAGGAC 815
Qy 769 CAGCTGGGTAATCAACATGACCAATTCAGTACTAGTATGATGATGATGATGATGATGAT 828
Db 816 TTGCTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 875
Qy 829 TGATCAATATTTGACACCAACCATCTCTGCTCTCATATGATTCGAACGATGGA 888
Db 876 TGATCAATATTTGACACCAACCATCTCTGCTCTCATATGATTCGAACGATGGA 935
Qy 889 ACTGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGAT 948
Db 936 ACTGATCAAAAGGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGAT 995
Qy 949 TCCAGAGCTTATCAACACCTGCTGATCATTTGATTCATATTCATTCATTCATTCATTCAT 1008
Db 996 TCCATATATTTACAGACCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1055
Qy 1009 ATGCAAGAGGAGGAGGATGATCAAGGAGTGTGGGCGAGTACTATTAATTCGACA 1068
Db 1056 ATGCAATGAGGAGGATGATCAAGGAGTGTGGGCGAGTACTATTAATTCGACA 1115
Qy 1069 GGACTCCATTTTCAAGCAATGATATAGAGGCTAAGAAATGATCTACATTCGAGCGCG 1128
Db 1116 AGACTCCATTTTCAAGCAATGATATAGAGGAGGAGGAGGAGTGTATTTATGATGAGCGAG 1175
Qy 1129 ATGAGATGAGGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1178
Db 1176 ATCAAGTACGAGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1225

RESULT 5

US-10-424-599-123945/C
; Sequence 123945, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 123945

LENGTH: 2931
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_8292C.1
US-10-424-599-123945

Query Match 37.7%; Score 484.4; DB 13; Length 2931;
Best Local Similarity 65.8%; Pred. No. 5.2e-121;
Matches 704; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

QY 109 ATCCACCGTTACGTTAGCGATCTGAGAAAGCAATTCACCCATTGCGTGAAGCAT 168
DB 1631 AACCTCCATTATGCTCAGCCAAATCAAGAAAGTCAATCCACTCACTGTTCCAGCGTT 1572
QY 169 CCGTATCCGGGATCATATATATGTTGTTCAATGATCTCATTTTGGCTATGCTTCTACT 228
DB 1571 CCGTTTCCGCTCATCTTCTCTATGTTGTTAGCACTCAACAGCCCTTCTCTTAT 1512
QY 229 ACCCTGCAAAACAGTATATCCCTTATCTTACACCTGCGCTTACCTAGCATGGCCCG 288
DB 1511 ATGTTGCCACCATTAATCTCAACCTCTTCCAGCCCTCTCTTCTTGGCATGGCCAA 1452
QY 289 TTTACTGTTTGTCAAGCTAGCATCTTCAACGCGCTCTGGGTCAATCGGTCAAGATGTG 348
DB 1451 TCTACTGGGCTGTCCAAAGGTTGCATCTTACGAGTTGGGTCAATGGCCATGAGTGTG 1392
QY 349 GTACACATGCAATTTAGCGATCAAGCTGATGATGATGATGATGATGATGATGATGAT 408
DB 1391 GCGACATGCAATTCAGTACATCAAGTGTGATGATGATGATGATGATGATGATGATGAT 1332
QY 409 CGGCTCTCTCAACCCCGTATTTCTCTGGAATATATAGCAAGATCAACAGCCCAACA 468
DB 1331 CCGGCTCTCTCAACCCCGTATTTCTCTGGAATATATAGCAAGATCAACAGCCCAACA 1272
QY 469 CAATTCATCTGATTAACGATGAAGTTTACATCTCTAAACGTAAGTGAAGTGAAGTTT 528
DB 1271 CTGGTCTCTGAGCGGATGAAGTATGTTGTCAAAGAGAACTGATCAAGTGGT 1212
QY 529 ATTCCAACCTCTTAAACATCAACCGGCGAGGTGTCACTTGGTGTTCGGTGTGACTT 588
DB 1211 ACTCTAAATACCTTAAACATCTCTCAAGGAGGTCTCACTCTCTGTCACCCCTCAAC 1152
QY 589 TAGGATTTCCGTTATACCTCTTAATATCTCGGCGCAAGAAATACGGAGAGTTGGCA 648
DB 1151 TTGGTGGCCCTTGATCTGCTTTAAATGTTCTGGAAGCCCTTAATGATTTGCTT 1092
QY 649 ACCACTTTGATCCATGATGATCAATTTTCAACGATCTGGAAGCCGTTCAAGTTTGTAT 708
DB 1091 GCGACTATGACCCATATGATGATCCCATTTTACTGATCTGGAAGCATTCATAATATATAT 1032
QY 709 CCGATTTGGGTCTTCTGCTGATTTTATGCAATCAAGTTTGTAGACGAAAGGG 768
DB 1031 CAGATGAGAGGATCTTCAAGATATGATGACCTTTTCCGTTCCCATGGAAGAAAGAC 972
QY 769 CAGTTGGGTATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
DB 971 TTGGCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 912
QY 829 TGATCAATTTTGGACACACACCATCTCTCACTCTCTCATTTGATTTCAACCGAATGGA 888
DB 911 TGATTAACATTTCTTGACGATATCTCACCCGATGCTCCACATTAACCTCTCTGATGGG 852
QY 889 ACTGATGAAAGGCGCTTATCAACAATCGATGATGATGATGATGATGATGATGATGATGAT 948
DB 851 ACTGATGAAAGGCGCTTATCAACAATCGATGATGATGATGATGATGATGATGATGATGAT 792
QY 949 TCACGAGGTTACACACTCACTGCTTGATCATTTTGTATCTCATATTCACATTAATC 1008
DB 791 TCACATTAATTAACACACTCACTGATGATGATGATGATGATGATGATGATGATGATGAT 732
QY 1009 ATGCAAGGAAGCAAGGATGATCAAGCAAGTGTGGCGAGTACTATTAATTCACA 1068

DB 731 ATGCAATGAGGCTCAAAAGGCAATMAAACCATTTTGGAGATTAATCGTTGATG 672
QY 1069 GGACTCCATTTTAAAGCAATGTATAGAGAGGTAGGAATGATCTACATCGAGCCG 1128
DB 671 AGACTCCATTTTGTCAAGGCAATGTGAGAGAGGCAAGAGTATTTATGTGGAGCAG 612
QY 1129 ATGAGATAGGAGCAAAAGGTGTCTGTGATACCAAGATGTATATCA 1178
DB 611 ATCAAGATACGAGAGCAAGAGTGTATTTTGTGATCAACATTAATGATGGA 562

RESULT 6
US-10-465-800-3
Sequence 3, Application US/10465800
Publication No. US20040029283A1
GENERAL INFORMATION:
APPLICANT: Filialti, Joanne
TITLE OF INVENTION: Intron Double Stranded RNA Constructs and Uses thereof
FILE REFERENCE: 16517.266
CURRENT APPLICATION NUMBER: US/10/465,800
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 60/390,186
PRIOR FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 6220
TYPE: DNA
ORGANISM: Glycine max
US-10-465-800-3

Query Match 37.7%; Score 484.4; DB 13; Length 6220;
Best Local Similarity 65.8%; Pred. No. 8.1e-121;
Matches 704; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

QY 109 ATCCACCGTTACGTTAGCGATCTGAGAAAGCAATTCACCCATTGCGTGAAGCAT 168
DB 4816 AACCTCCATTATGCTCAGCCAAATCAAGAAAGTCAATCCACTCACTGTTCCAGCGTT 4875
QY 169 CCGTATCCGGGATCATATATATGTTGTTCAATGATCTCATTTTGGCTATGCTTCTACT 228
DB 4876 CCGTTTCCGCTCATCTTCTCTATGTTGTTAGCACTCAACAGCCCTTCTCTTAT 4935
QY 229 ACCCTGCAAAACAGTATATCCCTTATCTTACACCTGCGCTTACCTAGCATGGCCCG 288
DB 4936 ATGTTGCCACCATTAATCTTCAACCTCTTCCAGCCCTCTCTTCTTGGCATGGCCAA 4995
QY 289 TTTACTGTTTGTCAAGCTAGCATCTTCAACGCGCTCTGGGTCAATCGGTCAAGATGTG 348
DB 4996 TCTACTGGGCTGTCAAGGTTGATGATCTTGAAGTTGGGTCAATGGCCATGAGTGTG 5055
QY 349 GTACACATGCAATTTAGCGATCAACGATGATGATGATGATGATGATGATGATGATGAT 408
DB 5056 GCGACATGCAATTCAGTACATCAAGTGTGATGATGATGATGATGATGATGATGATGAT 5115
QY 409 CGGCTCTCTCAACCCCGTATTTCTCTGGAATATATAGCAAGAAATCAACAGCCCAACA 468
DB 5116 CCGGCTCTCTCAACCCCGTATTTCTCTGGAATATATAGCAAGAAATCAACAGCCCAACA 5175
QY 469 CAATTCATCTGATTAACGATGAAGTTTATCAATCTCTTAAACGTAAGTGAAGTCAAGATT 528
DB 5176 CTGGTCTCTTGAAGGAGATTAAGTATTTGCGCAAGACAAAGTCCGTATCAAGTGGT 5235
QY 529 ATTCCAACCTTTTAAACATCAACCCGGGCGAGGTGTCACTTTGGTGTGTTGCGTTGACTT 588
DB 5236 ACTCTAAATACCTTAAACATCTCTCAGGCAAGATGCTCACTTGTCTGTCAACCTCAAC 5295
QY 589 TAGGATTTCCGTTATACCTCTTAATATATCTGCGGCAAGAAATACGGAGGTTGGCA 648
DB 5296 TTGGTGGCCCTTGATCTGCTTTAAATGTTCTGGAAGCCCTTAATGATGATTTGCTT 5355
QY 649 ACCACTTTGATCCATGATGATCAATTTTCAACGATCTGGAAGCCGTTCAAGTTTGTAT 708

Db 5356 GCCACTATGACCCATATGATGCTCCATTTACTCTGATCTGAAAGCACTTCAATATATATAT 5415
 Qy 709 CCGATTTGCGTCTTCTGCTGATTTTATGCAATCAAGCTTCTTGTAGACAGAAAGGGG 768
 Db 5416 CAGATGCAAGGAGTACTTGCAGATGATGCTTTTCCGCTTTCGATGCGAAAGAGAC 5475
 Qy 769 CAGCTTGGGTAATCAACATGACGAAATTCAGTACTGAGTGTAAAGCTGTCTTCGTTT 828
 Db 5476 TTGCTGGGTGGTGTGTGTTATGAGAGTTCATGCTGATGTCATGATGATTTTGGTGT 5535
 Qy 829 TGATACATATTTTGGACACACACCCATCTCTGCACTCCCTCATATGATTTCAACCGAATGSA 888
 Db 5536 TGATTAATTTCTTTCAGCATCTACTCCCTGCACTTCCACATTTACCTTCTGATGAGG 5595
 Qy 889 ACTGATCAAAAGCGCCCTTATCAACATGATGAGGATTTGGGCTTCTGATTCGGGTTT 948
 Db 5596 ACTGTTAGAGAGACTTTTACAGACAGTGTATGATGATTTAGATTCCTGAAGAGTCT 5655
 Qy 949 TCCAGACGTTACACACTCACTGCTTTCATCATTTGATCTCATACATTCACATTTATC 1008
 Db 5656 TCCAAATATTAACAGACACTCATGTAGCACTGCTTCTTCCCAATGCGACATTTATC 5715
 Qy 1009 ATGCAAGGAAGCAAGGAGTATGCAATCAAGCCAGTGTGGCGAGTACTATAAATCGACA 1068
 Db 5716 ATGCAATGAGGCTACAAAGGCAATTAACCCATTTGGAGAGTATTTAGCGTTGATG 5775
 Qy 1069 GGAATCCAAATTTTCAAGCAATGATATAGAGGCTTAAGAAATGATCTACATCGAGCCG 1128
 Db 5776 AGACTCCATTTGTCAAGGCAATGTGAGAGGAGCAAGAGTGTATTTATGTGAGCGAG 5835
 Qy 1129 ATGAGATAGGAGACAAAGGTGTCTGTGTACCAACAAGTGTATCA 1178
 Db 5836 ATCAAGTACGAGAGCAAAAGGTGTATTTGTGTACCAACAATTAAGTTGGA 5885

RESULT 7

US-10-176-149-3
 ; Sequence 3, Application US/10176149
 ; Publication No. US20030172399A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fillat, Joanne, J.
 ; TITLE OF INVENTION: Nucleic Acid Sequences and Methods of Use for the Production of F
 ; FILE REFERENCE: 16518.056
 ; CURRENT APPLICATION NUMBER: US/10/176.149
 ; PRIOR FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US 60/151.224
 ; PRIOR FILING DATE: 1999-08-26
 ; PRIOR APPLICATION NUMBER: US 60/172.128
 ; PRIOR FILING DATE: 1999-12-17
 ; PRIOR APPLICATION NUMBER: US 09/638.508
 ; PRIOR FILING DATE: 2000-08-11
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 6220
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 US-10-176-149-3

Query Match 37.7%; Score 484.4; DB 15; Length 6220;
 Best Local Similarity 65.8%; Pred. No. 8.1e-121;
 Matches 704; Conservative 0; Mismatches 366; Indels 0; Gaps 0;

Qy 109 ATCCACCGTTCAGTTAAGCGATCTGAGAAAGCAATTCCTTACCCATTCCTTGTAGAGCAT 168
 Db 4816 AACCTCCATTTAGTCTACGCAATCAAGAGGTATTCACCTACTGTTTCCAGCGTT 4875
 Qy 169 CTGTGATCCGCTCATATAGTATGTTGTATGATCTCATTTGTTCCATATGCTTTTACT 228
 Db 4876 CTGTTTCCGCTCATTTCTATATGTTGTATGAGACTCAACATACCTTTCGCTCTAT 4935
 Qy 229 ACCTTGCAAAACGATATCCCTTATTTCTTACACCTTGTGCTTACCTAGACATGCCCCG 288

Db 4936 ATGTGCCACCATTACTTCCACCTCTTCCAGCCCTCTCTTTCTTGGACATGCCCCA 4995
 Qy 289 TTTACTGTTTGTCAAGCTATGACATCCGACCGGCTCTGAGTATCGGTACAGATATG 348
 Db 4996 TCTACTGGCTGTGCAAGGTGTGATTCCTTACTGAGATTTGGGTATTTGCCATGATGTG 5055
 Qy 349 GTCAACATGATTTTACGACATCAAGATGATGATGATGATGATGATGATGATGATGATG 408
 Db 5056 GCCACATGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5115
 Qy 409 CGGCTTCCTCAACCCGATTTCTTGGAAATATGACCAAGATATGACCAAGCAACA 468
 Db 5116 CCGGCTCTCTGATCCATCTTTTCAATGAAATACGCAATGCGGCTACCACTTCAACA 5175
 Qy 469 CAATTCACGTGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
 Db 5176 CTGGTTCCTTGAAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5235
 Qy 529 ATTCGAACTTTTATCAATTCACCCGCGAGGTTCATCTTGTGTGTTGATGAT 588
 Db 5236 ACTCTAAATACCTTAAACATCTCCAGGCAAGTCTCATCTTGTCTGATCACCCTCAC 5295
 Qy 589 TAGGATTTCCGTTAATCCTTAACTAATATCTGCGGCAAGAAATPACGGAGTTGGCA 648
 Db 5296 TTGGTGGCCCTTGTACTTGGCTTTAAATGTTTCTGAAAGCCCTTATGATGATTTGCTT 5355
 Qy 649 ACCACTTGTATCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708
 Db 5356 GCCACTATGACCCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5415
 Qy 709 CCGATTTGCGTCTTCTGCTGTATTTATGCAATCAAGCTTCTTGTAGACAGAAAGGGG 768
 Db 5416 CAGATGCAAGGAGTCTGCAATGATGATGATGATGATGATGATGATGATGATGATGATG 5475
 Qy 769 CAGCTTGGGTAATCAACATGACGAAATTCAGTACTGAGTGTAAAGCTGTCTTCGTTT 828
 Db 5476 TTGCTGGGTGGTGTGTGTTATGAGAGTTCATGCTGATGTCATGATGATTTTGGTGT 5535
 Qy 829 TGATACATATTTTGCACACACCCATCTGATCTCCCTCATATGATTTCAACCGAATGSA 888
 Db 5536 TGATTAATTTCTTGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5595
 Qy 889 ACTGATCAAAAGCGCCCTTATCAACATGATGATGATGATGATGATGATGATGATGATGAT 948
 Db 5596 ACTGTTAGAGAGGCTTTAGCAACAGTATGATGATGATGATGATGATGATGATGATGATGAT 5655
 Qy 949 TCCAGACGTTACACACTCACTGCTTTCATCATTTGATCTCATACATTCACATTTATC 1008
 Db 5656 TCCAAATATTAACAGACACTCATGTAGCACTGCTTCTTCCCAATGCGACATTTATC 5715
 Qy 1009 ATGCAAGGAAGCAAGGAGTATGCAATCAAGCCAGTGTGGCGAGTACTATAAATCGACA 1068
 Db 5716 ATGCAATGAGGCTACAAAGGCAATTAACCCATTTGGAGAGTATTTAGCGTTGATG 5775
 Qy 1069 GGAATCCAAATTTTCAAGCAATGATATAGAGGCTTAAGAAATGATCTACATCGAGCCG 1128
 Db 5776 AGACTCCATTTGTCAAGGCAATGTGAGAGGAGCAAGAGTGTATTTATGTGAGCGAG 5835
 Qy 1129 ATGAGATAGGAGACAAAGGTGTCTGTGTACCAACAAGTGTATCA 1178
 Db 5836 ATCAAGTACGAGAGCAAAAGGTGTATTTGTGTACCAACAATTAAGTTGGA 5885

RESULT 8

US-10-425-114-12782
 ; Sequence 12782, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Jiongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12782
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701211444_FLI
US-10-425-114-12782

Query Match 37.4%; Score 481.2; DB 13; Length 1457;
Best Local Similarity 65.6%; Pred. No. 2,66-120; Indels 0; Gaps 0;
Matches 702; Conservative 0; Mismatches 368; Indels 0; Gaps 0;

109 ATCCACCGTTACCGTTAAGCATGTAAGAAAGCGATCTACCCATGCTTGAAGCAT 168
112 AACCCCATTTAGTCTGACGCAAAATCAAGAGTATCCACCTGCTTCCAGCGT 171
169 CTGTCATCCGTCATCATCTATGTTGTTCAATGATCTCATGTTGCTTCTTACT 228
172 CTGTTTCCGCTCATCTCTATGTTGTTCAAGCTCACAATAGCTTGGCTCTACT 231
229 ACCTTGAAACGATATCCCTTATCTCTACCTCTGCTTACCTAGACAGCCCG 288
232 ATGTTGCCACCATTAATCTTCAACCTCTCCAGCCCTCTCTTCTTGGCATGCGAA 291
289 TTATCGTTTGTCAAGCTAGCATCTCACCGGCTCTGGGTCATCGGTCAAGATG 348
292 TCTACTGGCTGTCAAGGATGATCTTACCTGAGATTTGGGTCTATGCTCAGATG 351
349 GTCAACATGATTTAGCAGTACCAAGTTGATGATGATGATGATGATGATGATG 408
352 GCCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 411
409 CGGCTCTCTCAACCCGCTATTTCTTTGGAAATATAGCAAGAAATACCAAGCA 468
412 CGGCTCTCTCAACCCGCTATTTCTTTGGAAATATAGCAAGAAATACCAAGCA 471
469 CAATTCATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 528
472 CTGCTCTCTCAACCCGCTATTTCTTTGGAAATATAGCAAGAAATACCAAGCA 531
529 ATTCCTAACTTTTAAATCAATCAACCCGCTATTTCTTTGGAAATATAGCAAG 588
532 ACTCTAAATCTTAAATCAATCAACCCGCTATTTCTTTGGAAATATAGCAAG 591
589 TAGATTTCTGTTTACTCTTTAAATATCTGCGGCAAGAAATACCGGAGTTT 648
592 TTGCTTGGCTCTGTTTACTCTTTAAATATCTGCGGCAAGAAATATAGCAAG 651
649 ACCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 708
652 GCACTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 711
709 CGATTTCTGCTCTCTGCTGTTTATGCAATCAAGCTTCTTTAGCAAGAAAGGG 768
712 CAGATGAGGAGTCTTGAATATGCTATGAGCTTTTCTGCTTCCATGCAAGAA 771
769 CAGCTGGGATCAATCAATGATGATGATGATGATGATGATGATGATGATGATG 828
772 TTGCTTGGCTCTGTTTACTCTTTAAATATCTGCGGCAAGAAATATAGCAAG 831
829 TGATCAATATTTTGAAGCAACATCTCTGCTCTCTGCTCTCTGCTCTCTGCT 888
832 TGATCAATATTTTGAAGCAACATCTCTGCTCTCTGCTCTCTGCTCTCTGCT 891
889 ACTGATCAAGAGGCTTATCAATCAATGATGATGATGATGATGATGATGATGATG 948

992 ACTGATGAGGAGCTTTAGCAACATGATGATGATGATGATGATGATGATGATG 951
949 TCCAGACGTTACACACATGATGATGATGATGATGATGATGATGATGATGATG 1008
952 TCCATATATATACAGACTATGATGATGATGATGATGATGATGATGATGATGAT 1011
1009 ATGCAAGAGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1068
1012 ATGCAAGAGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1071
1069 GATCTCCAAATTTTGAAGCAATGATGATGATGATGATGATGATGATGATGATG 1128
1072 AGATCTCATTTGTGAAGCAATGATGATGATGATGATGATGATGATGATGATG 1131
1129 ATGAGATGAGAGCAACAAAGTGTCTGATGATGATGATGATGATGATGATG 1178
1132 ATCAAGATGAGAGCAACAAAGTGTCTGATGATGATGATGATGATGATGATG 1181

RESULT 9
US-09-837-751-5
; Sequence 5, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: Gossypium sp.
; NAME/KEY: CDS
; LOCATION: (98) .. (1246)
US-09-837-751-5

Query Match 34.7%; Score 445.8; DB 9; Length 1422;
Best Local Similarity 63.5%; Pred. No. 1,1e-110; Indels 0; Gaps 0;
Matches 681; Conservative 0; Mismatches 392; Indels 0; Gaps 0;

109 ATCCACGTTACCGTTAAGCATGTAAGAAAGCGATCTACCCATGCTTGAAGCAT 168
180 AGCCACCTTACCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 239
169 CTGTCATCCGTCATCATCTATGTTGTTCAATGATCTATGTTGCTTACTTACT 228
240 CGGTTTAAAGCTATCTCATATCTCTTTAAGATTTAATGAGCTCTCTTTTAA 299
229 ACCTTGAAACGATATCTCTTATTTCTTAACTCTGCTTACCTAGATGAGCCG 288
300 ATGAGGCAACCAATTAATCTCTCTCAAGCTCTCTCTCAAGCTGCTTGGCT 359
289 TTATCGGTTTGTCAAGCTAGATGATGATGATGATGATGATGATGATGATGATG 348
360 TTATTTGGCCATGCAAGGTTGATTTTGAAGCGGCTTTGGGCTATAGCCATGAT 419
349 GTCAACATGATTTAGGACATCAAGTGTGATGATGATGATGATGATGATGATG 408
420 GCACTATGCTTCAAGATATGATGATGATGATGATGATGATGATGATGATGATG 479
409 CGGCTCTCTCAACCCGCTATTTCTTTGGAAATATAGCAAGAAATACCAAGCA 468
480 CTCTCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 539

QY 469 CAATTCCTGATACGATGAAGTTTACCTTCTTAAACGTACGTAAGTCAAGATT 528
Db 540 CCGGTTCCCTCGAAGGATGATGATGTTCTGTTCCCAAAAATCTGTTAAGATGAT 599
QY 529 ATTCGAATCTTAAACATCAACCGGCGAGTGTCACTTGTGTTGGTGTGACTT 588
Db 600 GGGCCAAACATTCACACATCCAGGATCGGTTCTGTCTCAATCACTTCACTTACC 659
QY 589 TAGATTTCCGTTATACCTCTTAACTAAATCTCGGCGAAGAAATACGAGGTTTCCA 648
Db 660 TTGGTTGCGGCTTAACTTAACTTCAAGTTGCGGCGGCTTACAGACAGGTTGCTT 719
QY 649 ACCACTTGAATCCATGATGATCAATTTCAAGATCGTAAGCGGTTCAAGTTTCTAT 708
Db 720 GCCACTATGACCTTACCGCCCAATATTTTCCGACCGGGAACGACTCCAAATCTATATCT 779
QY 709 CGGATTTGGTCTTCTGCTGATTTTATGCAATCAAGCTTCTGTACAGCAAAAGGG 768
Db 780 CTGAGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 839
QY 769 CAGCTTGGGTAATCAACATGTAAGCAATTCAGTACTAGTGTAGCGTGTCTTCTT 828
Db 840 TAGGTTGGGTAATGATGTTTATGAGGATGATGATGATGATGATGATGATGATGAT 899
QY 829 TGATCAATATTTGCAACACACCATCTCTCACTCCCTCATATGATTTCAACCGAATGA 888
Db 900 TGATCAATATTTGCAACACCATCTCTCACTCCCTCATATGATTTCTCGAGTGGG 959
QY 889 ACTGATCAAGAGGCGCTTATCAACATGTAAGGATTTGGGTTCCGTAAGCGGTTT 948
Db 960 ACTGATCAAGAGGCGCTTATCAACATGTAAGGATTTGGGTTTAAACAGGTTT 1019
QY 949 TCCAGACGTTTACACACACTCACTCTTGCATCATTTGATCTCATACATTCACATTTATC 1008
Db 1020 TCCATATATATACCACTCACTGATGATGATGATGATGATGATGATGATGATGAT 1079
QY 1009 ATGCAAGAGCAAGGATGATCAACAGGATTTGGGCGAGTACTATTAATTCGACA 1068
Db 1080 ATGCAAGAGGCGCTTATCAACATGTAAGGATTTGGGTTTAAACAGGTTT 1139
QY 1069 GAGCTCCATTTTCAACATGTAAGGATTTGGGCGAGTACTATTAATTCGACA 1128
Db 1140 GAGCTCCATTTTCAACATGTAAGGATTTGGGCGAGTACTATTAATTCGACA 1199
QY 1129 ATGAGATAGGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1181
Db 1200 ATGAGATAGGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1252

RESULT 10
US-09-852-399-3

; Sequence 3, Application us/09852399
; Patent No. US20020045232A1

; GENERAL INFORMATION:

; APPLICANT: Qiu, Xiao

; TITLE OF INVENTION: PRODUCTION OF CONJUGATED LINOLEIC AND

; FILE REFERENCE: BNZ-002

; CURRENT APPLICATION NUMBER: US/09/852,399

; PRIOR FILING DATE: 2001-05-09

; PRIOR APPLICATION NUMBER: USSN 60/203,027

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO: 3

; LENGTH: 1411

; TYPE: DNA

; ORGANISM: Calendula officinalis

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (89)...(1237)

; US-09-852-399-3

Query Match 34.6%; Score 444.8; DB 9; Length 1411;
Best Local Similarity 63.4%; Pred. No. 2.1e-110;
Matches 680; Conservative 0; Mismatches 392; Indels 0; Gaps 0;
QY 109 ATCCACCGTTCACCTTAAAGCATCTGAAGAAAGGATTCCTTACCATTTCTTGAAGCAT 168
Db 174 AACCCCATTTACAGTTGAGACATCAAGAAAGGATTCCTTACCATTTCTTGAAGCAT 233
QY 169 CTGTATCCGCTCATCACTATGATGATGATGATGATGATGATGATGATGATGAT 228
Db 234 CGTATATGTTTCAATTTTCAATGATGATGATGATGATGATGATGATGATGATGAT 293
QY 229 ACCTTGCAAGAGATATCTCTTATCTTATCACTCTGCTTACCTTACCTGAGCCG 288
Db 294 ACATGCGCAAAATTAATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 353
QY 289 TTATCTGTTTGTCAAGCTAGCATCTTACCTGAGCTCTGAGTATGATGATGATGAT 348
Db 354 TTATCTGAGCGCTGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 349 GTCAACATGCAATTTAGGAGTATGATGATGATGATGATGATGATGATGATGAT 408
Db 414 GCATATGATTTTATGAGACCAACCAATGATGATGATGATGATGATGATGATGAT 473
QY 409 CGGCTCTCTCAACCCGATTTCTTGTGAATATGAGCAAGATATCAACCGCAACA 468
Db 474 CGTTCTTATCTGCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 533
QY 469 CAATTCATCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
Db 534 CGGCTCTGATGAGCATATGATGATGATGATGATGATGATGATGATGATGATGAT 593
QY 529 ATTCGAATCTTATCAACATCAACCGGAGGATTTCACTTGTGTTGGTGTGACTT 588
Db 594 CCGGCGGATCTTAAACCAACCAACCGGAGGATTTCACTTGTGTTGGTGTGACTT 653
QY 589 TAGATTTCCGTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 648
Db 654 TCGGTTGCGCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTAT 713
QY 649 ACCACTTATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
Db 714 GCATTTGAGCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773
QY 709 CCGATTTGCGCTTCTGCTGATTTTATGCAATCAAGCTTCTTGTAGCAGCAAAAGGG 768
Db 774 CCGAGCGGAGATCTTACCGTATGCTTGTATCTTCCGATCGCAATGACCAAGGGC 833
QY 769 CAGCTTGGGTAATCAACATGTAAGCAATTCAGTACTAGTGTAGCGTGTCTTCTT 828
Db 834 TCAGTGGGCTTAACTATGATGATGATGATGATGATGATGATGATGATGATGAT 893
QY 829 TGATCAATATTTGACACACACCATCTCTCACTCCCTCATATGATTTCAACCGAATGA 888
Db 894 TGATCAATATTTGACACACACCATCTCTCACTCCCTCATATGATTTCAACCGAATGA 953
QY 889 ACTGATCAAGAGGCGCTTATCAACATGTAAGGATTTGGGTTCTGTAAGCGGTTT 948
Db 954 ATGTTTACGAGGCGCTTCAACATGTAAGGATTTGGGTTCTGTAAGCGGTTT 1013
QY 949 TCCAGACGTTTACACACTCAAGTCTTGCATCTTATGATTTCACTTCACTTATTC 1008
Db 1014 TCCATATATATACCACTCACTGATGATGATGATGATGATGATGATGATGATGAT 1073
QY 1009 ATGCAAGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
Db 1074 ATGCAAGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1133
QY 1069 GAGCTCCATTTTCAACATGTAAGGATTTGGGCGAGTACTATTAATTCGACA 1128
Db 1134 GAGCTCCATTTTCAACATGTAAGGATTTGGGCGAGTACTATTAATTCGACA 1193
QY 1129 ATGAGATAGGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGAT 1180

Db 1194 ATGAGAGGTGAGAGATGCTGTTATGCTATGCTAATTAAGATTGAAGAA 1245

RESULT 11
US-09-837-751-3

; Sequence 3, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Gossypium sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (79) ..(1233)
US-09-837-751-3

Query Match 34.0%; Score 436.8; DB 9; Length 1411;
Best Local Similarity 64.0%; Pred. No. 3.2e-108;
Matches 660; Conservative 0; Mismatches 372; Indels 0; Gaps 0;

Qy 109 ATCCACCGTTCACCTTACGATCGAAGAAAGCATTCCTACCCATGCTTGAAGCAT 168
Db 158 AGCCCTCGTTACGCTCGCTGATCAAGCAAGCATTCGCCCATGTTTCCGCGCT 217
Qy 169 CTGTCATCCGCTCATCATATATGTTGTCATGATCTCATTTGCTATGCTTCTACT 228
Db 218 CCGCTCTTCGATCTCTCTCTCAAGTGCATGATGCTTACCTCTTCTTCTTACT 277
Qy 229 ACCTTGCAAGACGTAATCCCTTATCTTACACCTCTGCGTTACCTAGCATGCGCG 288
Db 278 ACATTGCAACATCATATTTTCACTTCTCCCAACACCTTCTTCAATGCTTGCGCTG 337
Qy 289 TTTACTGCTTTTGTCAAGTACATCTCTCAACCGGCTCTGGGTCTATCGGTACCAATGTG 348
Db 338 TCTATGGGTTCTCCAAAGTTCATCTCCACCGGTGTTGGTCAATCCACACGATGGG 397
Qy 349 GTCAACATGATTAAGCATACGATGATGATGATGATGATGATGATGATGATGATGAT 408
Db 398 GTCAACAGCTTTCAAGACATCAATGATGATGATGATGATGATGATGATGATGATGAT 457
Qy 409 CGGCTCTCTCAACCCCGATTTCTTGTGAATAATAGCAGCAAGATCAACGCGCAACA 468
Db 458 CCGGCTCTTATAGTCCCGATCTTCTGTGAATAATAGCAGCAACCGGCTGATCTTCAAT 517
Qy 469 CAATTTCACTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
Db 518 CCGGCTCTTATAGTCCCGATTTCTTGTGAATAATAGCAGCAACCGGCTGATCTTCAAT 577
Qy 529 ATTCAAACTTCTTAACATCAACCGGCGATGATGATGATGATGATGATGATGATGATGAT 588
Db 578 TTGGGAATATCTTAACATCAACCGGCGATGATGATGATGATGATGATGATGATGATGAT 637
Qy 589 TAGAATTCCTGTTATCTTAACTAATATCTGGGAGAGAAATACGGAAGTTTGGCA 648
Db 638 TTGGTGGCTATATCTTAACTAATATCTGGGAGAGAAATACGGAAGTTTGGCA 697
Qy 649 ACCACTTGAATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
Db 698 CCGCACTAATACCTTATGAGCGCCCATTTATCTCCGATGCGAAGGCTACAAATTTACATCT 757

Qy 709 CCGATTCGGTCTCTCTGCTGATTTTATGCAATCAAGCTTCTTGACGACAAAGGG 768
Db 758 CCGATTCGGTCTCTCTGCTGATTTTATGCAATCAAGCTTCTTGACGACAAAGGG 817
Qy 769 CAGCTTGGGTAATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
Db 818 TGGCTTGGCTTTTATGCACTTATGAGGGCTCTTCAATATGATGATGATGATGATGATGAT 877
Qy 829 TGATCAATATTTTGAACAGCAACCCATCTCTGATCCCTCATTTATGATGATGATGATGATGAT 888
Db 878 TGATCACTTCTTGAACATCTCTGATCCCTCATTTATGATGATGATGATGATGATGATGAT 937
Qy 889 ACTGATCAAAAGGCGCTTATCAACAATGATGATGATGATGATGATGATGATGATGATGAT 948
Db 938 ATTGGTTCCGAGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 997
Qy 949 TCCAGACGTTACACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
Db 998 TCCATATCATCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1057
Qy 1009 ATGCAAGAGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1068
Db 1058 ATGCAATGAGAGCACTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1117
Qy 1069 GCACTCCATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1128
Db 1118 GCACTCCATTTTCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1177
Qy 1129 ATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1178 ACCTGTTGGTGTG 1189

RESULT 12
US-10-330-775-5
; Sequence 5, Application US/10330775
; Publication No. US20030221217A1
; GENERAL INFORMATION:
; APPLICANT: Saskatchewen Wheat Pool
; TITLE OF INVENTION: PLANT PBD2 CODING SEQUENCE BALANCING FOR FATTY ACID PROFILING IN
; FILE REFERENCE: 4810-64260
; CURRENT APPLICATION NUMBER: US/10/330,775
; CURRENT FILING DATE: 2002-12-26
; PRIOR APPLICATION NUMBER: CA 2,382,767
; PRIOR FILING DATE: 2002-05-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica juncea
US-10-330-775-5

Query Match 33.8%; Score 434.2; DB 16; Length 1155;
Best Local Similarity 63.5%; Pred. No. 1.5e-107;
Matches 680; Conservative 0; Mismatches 388; Indels 3; Gaps 1;

Qy 111 CCACCGTTACGTTAAGCATCTGAAGAAAGCATTCCTACCCATGCTTGAAGCATCT 170
Db 85 CCGCTCTTCAAGATGAGAGCTCAAGAAAGCATTCACCGCATGCTTCAAGAGCTCC 144
Qy 171 GTCAATCCGCTCATATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 230
Db 145 ATCCCTGCTCTCTCTCTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 204
Qy 231 CTGCAAAAGATATCCCTTATCTTATCTTACACCTGCTGCTTACATGATGATGATGATGATGAT 290
Db 205 GTGCGACACATCTTCT 264
Qy 291 TACTGTTTGTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 350
Db 265 TACTGCGCTGCGCAAGGCTGCTCTTACCGGCGTCTGGGTGATGATGATGATGATGATGATGAT 324


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Db      925 TTCCAAATATACGACGACGCGCGCATCTCTTCTCGACCATGCCGATTAT 984
Qy      1008 CATGCAAGAGAGCAAGGAGATGATCAAGCAAGTGTGGGAGATCTATTAATTCAGC 1067
Db      985 CATGCAAGAGAGCAAGGAGATGATCAAGCAAGTGTGGGAGATCTATTAATTCAGC 1044
Qy      1068 AGCACTCCAAATTTTCAAGCAATGTATAGAGGCTAAGAGATGATCTATTCAGGCC 1127
Db      1045 GGGAGCGCGGTGTTAAGCGCATGTGAGGGAGCGGAGAGTGTATCTATGTGGAACG 1104
Qy      1128 GATGAGATACGAGCACAAAAGGTGTCTGTCTGCTCCCAAGATTAATCA 1178
Db      1105 GACAGGCAAGGTGAGAAAGAGTGTGTGTGTGTAACAATAAAGTTATGA 1155

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RESULT 14
US-09-771-904-9
; Sequence 9, Application US/09771904
; Publication No. US20030131379A1
; GENERAL INFORMATION:
; APPLICANT: Debonte, Lorin R.
; APPLICANT: Fan, Zhegong
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063003
; CURRENT APPLICATION NUMBER: US/09/771,904
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 08/874,109
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-09-771-904-9

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Query Match      33.5%; Score 431; DB 10; Length 1155;
Best Local Similarity 63.3%; Pred. No. 1.1e-106;
Matches 678; Conservative 0; Mismatches 390; Indels 3; Gaps 1;

Qy      111 CCACGCTTACGATTAAGGATCTGAAAGAGATTTCTACCATCTGCTTGAAGGATCT 170
Db      85 CCGCCCTTACCTGCGGAACTCAAGAAAGCAATCCACGCACTGTTTCAAGCGTCG 144
Qy      171 GTCAATCCGATCATATATATGTTGATGATCTATCTATGCTTCTACTAC 230
Db      145 ATCCCTGGCTTTCTCTACCTCATCTGGGACATCATAGCCTCTGCTTCTACTAC 204
Qy      231 CTTCGAACAGTATCTCTTATCTTCTTCTACCTCTGCTTACCTAGAGCCGCTT 290
Db      205 GTCCGACACGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 264
Qy      291 TACTGTTTCTCAAGTAGCATCTCTCAAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCT 350
Db      265 TACTGCGGCTTCCAGGCGTGTGCTCTTACCGGCGCTTGGGCTATGACCGAGTGGCG 324
Qy      351 CACCATGATTTAGCGATCACTACAGTTGATGATGATGATGATGATGATGATGATGAT 410
Db      325 CACCAAGGCTTCAAGGATCACTACAGTTGATGATGATGATGATGATGATGATGATGAT 384
Qy      411 GCTTCTCTCAAGGCTTCTCTTCTGAAATATGACCAAGAAATCACCGCAACACA 470
Db      385 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 444
Qy      471 AATTCAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 530
Db      445 GGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 504
Qy      531 TCCAACTTCTTAACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 590

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Db      505 GGCAAGTACTCAACACCTTTGGAGCAGCCGATGATTAACGGTTCAGTCACTCTC 564
Qy      591 GGATTTCCGTTATATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTT 647
Db      565 GGTGCGCTTGTGTACTTATAGCTTCAACGCTCTGGGGAACCTTACAGAGGGCGCTTCT 624
Qy      648 AACCATTTGATCCCATGATGATCAATTTTCAAGCATGTAAGCGGCTTCAAGTTTGTCTA 707
Db      625 TGCCATTTCAACCCCAAGCTTCCATCTTCAACAGAGCTGAGGCTTCAAGATATATCATC 684
Qy      708 TCCGATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 767
Db      685 TCCGAGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 744
Qy      768 GCAGCTTGGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 827
Db      745 GTTGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 804
Qy      828 TTGATCACTATTTTCAACCAACCATCTCTCACTCCCTCATTTATGATTTCAACCGAATG 887
Db      805 TTGATCACTATCTTCAACCAACCATCTCTCACTCCCTCATTTATGATTTCAACCGAATG 864
Qy      888 AACTGATCAAGGCGCTTATCAACAATGATGATGATGATGATGATGATGATGATGATGAT 947
Db      865 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 924
Qy      948 TTCCAGCACTTATCAACCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1007
Db      925 TTCCAGCACTTATCAACCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 984
Qy      1008 CATGCAAGAGAGCAAGGAGATGATCAAGCAAGTGTGGGAGATCTATTAATTCAGC 1067
Db      985 CATGCAAGAGAGCAAGGAGATGATCAAGCAAGTGTGGGAGATCTATTAATTCAGC 1044
Qy      1068 AGCACTCCAAATTTTCAAGCAATGTATAGAGGCTAAGAGATGATCTATTCAGGCC 1127
Db      1045 GGGAGCGCGGTGTTAAGCGCATGTGAGGGAGCGGAGAGTGTATCTATGTGGAACG 1104
Qy      1128 GATGAGATACGAGCACAAAAGGTGTCTGTCTGCTCCCAAGATTAATCA 1178
Db      1105 GACAGGCAAGGTGAGAAAGAGTGTGTGTGTGTAACAATAAAGTTATGA 1155

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RESULT 15
US-10-715-100-9
; Sequence 9, Application US/10715100
; Publication No. US20040083503A1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharna
; APPLICANT: Fan, Zhegong
; APPLICANT: Debonte, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; FILE REFERENCE: 07148-072002
; CURRENT APPLICATION NUMBER: US/10/715,100
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/995,297
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURES:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-10-715-100-9
Query Match      33.5%; Score 431; DB 17; Length 1155;

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Best Local Similarity 63.3%; Pred. No. 1.1e-106; Matches 678; Conservative 0; Mismatches 390; Indels 3; Gaps 1;

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OY 111 CCACGGTTCAGGTTAAGGATCTGAAGAAGGATTCCTACCATTCCTTGAGGAGTCT 170
DB 85 CCGCCCTTCACTGTCGGAAGACTCAAGAAAGCAATCCACCGCATCTTTCAAGGCTCG 144
OY 171 GTCATCGGTCATCACTAATGTTGTTCATGATCTCAATGTTGCTTACTTACTAC 230
DB 145 ATCCCTCGCTCTTCTTCTTACTCATCTGAGCATATCATATAGCTCCCTCTTACTAC 204
OY 231 CTGGAACAGGTATATCCCTTATTCCTTACCTGAGTACCTAGCAATGCGGCTT 290
DB 205 GTGCGACACCTTACTTCCCTCTCTCCCTCAACCTCTCTCTTACTTGGCCCTCTC 264
OY 291 TACTGTTTGTTCAGTACGATCCTCAACCGGCTCTGAGTCATCGTCAAGATGTGT 350
DB 265 TACTGGGCTGCGAGGCTGCGCTCTTAACCGGCTCTGAGTCATAGCCACGAGTGGC 324
OY 351 CACCATGATTTAGGACTACCACTTGAATGATGATGATGATGATGATGATGATGATG 410
DB 325 CACCAAGCTTCAGGACTACCACTGAGGCTGAGACACCGTGGCTCATCTTCCACTCC 384
OY 411 GCTCCCTCACCCGCTATTTCTTGAATATAGCAAGGAATCACCAAGCAACACA 470
DB 385 TTCTCTCTGCTCTTCTTCTCTGAAATGATCATGACGACACCATTCACACT 444
OY 471 AATTCATCGATTAACGATGAATTTACATTCCTTAACGTAAGTCGAAGTCAGATTTAT 530
DB 445 GGCCTCCCTGAGAGAGAGAGAGTGTTCCTCCAGAAAGAGTCAAGATCAAGTGTAC 504
OY 531 TCCAACTTCTTAACATTCACCGGCGAGTGTTCATTTGAGTGTTCGTTGACTTTA 590
DB 505 GGCAGATCTCAACACCTTTGGAGCGCACCGTGAATGTTAACGTTCACTCTC 564
OY 591 GGAATTCGTTATACCTTAACTAATCTCGGCA---AGAAATACGGAGGTTTGC 647
DB 565 GGCCTGCTTTGATTTAGCTTCAAGCTTCGAGGAGACCTTACGACGCGGCTTCGT 624
OY 648 AACCACTTGAATCCCATGATGTCATTTTCAACGATCGTAACGCTTCAAGTTTGTCTA 707
DB 625 TGGCATTTCAACCCCAAGGCTCCATCTCAACGACGCGTGTCCAGATATATATC 684
OY 708 TCCGATTTGCTTCTGCTGTATTTATGCAATCAAGCTTCTTGAACGACAAAGGG 767
DB 685 TCCGAGCTGAGCATCTCGCCGTCTGCTACGCTCTACCGCTGCTGTCCAAAGA 744
OY 768 GCAGCTTGGATATCAATGATGAGCAATTCAGTACTAGTGAAGGCTTCTTCTGT 827
DB 745 GTTGCTCGATGCTGTCTTCAAGAGTTCCTTCTGATTTGTCAACGGGTTCTTAGT 804
OY 828 TTGATCAGATTTTGCACACACCCATCTCTCACTCCCTATATATATCAACGATGG 887
DB 805 TTGATCAGTACTTACAGACAGCGATCTTCCCTGCTCACTATGACTCGTGTAGTGG 864
OY 888 AACTGATCAAAAGCGCTTATCAACAATCGATGAGGATTTGGGTTCTGTGATCGGTT 947
DB 865 GATTGTTGAGGGGAGCTTTGGCCACCGTGAAGAGACTACGGAATCTTTGAACAGGTC 924
OY 948 TTCCAGAGCTTACACACCTGAGCTTGTGATCTTGTATCATATTCACATTTAT 1007
DB 925 TTCCAAATATACGAGACGAGCTGGGCACTCTGTTTTCGACCAATGCGCATTTAT 984
OY 1008 CATGCAAGAGCAAGGATGATCAAGCCAGTGTGGCGAGTACTATAAATGCAC 1067
DB 985 CATGAGATGAGAGCTACGAGAGCGATTAAGCCGATACCTAGGAGAGTATATCAATTGAT 1044
OY 1068 AGGATCCAAATTTCAAGCAATGATATAGAGGCTTAAGAAATGATCTACATGAGCCC 1127
DB 1045 GGGAGCGCGGTGTAAAGCGATGAGGAGGAGGAGAGTGTATCTATGTGAACCG 1104
OY 1128 GATGAGATGAGGACCAAAAGGTGTCTGTGTACCAAGATGTAATCA 1178
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DB 1105 GACAGCGAAGTGAGAGAAAGTGTGTCTGTGTAACAATAGTTATGA 1155

Search completed: June 23, 2004, 15:51:15
Job time : 457 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 11:52:13 ; Search time 3580 Seconds

(without alignments)
15557,486 Million cell updates/sec

Title: US-10-069-772-1

Perfect score: 1285
Sequence: 1 aaagctcactctctcgtga.....aaaaaaaaaaaaaaaaaaaa 1285Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vl.*
30: em_hcg_hum.*
31: em_hcg_inv.*
32: em_hcg_mus.*
33: em_hcg_other.*
34: em_hcg_pln.*
35: em_hcg_rod.*
36: em_hcg_mam.*
37: em_hcg_vir.*
38: em_sy.*
39: em_hcgo_hum.*
40: em_hcgo_mus.*
41: em_hcgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1285	100.0	1285	6 AX089471	AX089471 Sequence
2	1152	89.6	1152	8 COF245938	AR245938 Calendula
3	871	67.8	1419	8 AY166773	AY166773 Helianthu
4	750.4	58.4	979	8 AY166776	AY166776 Rubbeckia
5	738	57.4	979	8 AY166777	AY166777 Dimorphot
6	728.6	56.7	1435	8 CAY16285	Y16285 Crepis alpi
7	715.8	55.7	1358	6 CAY167437	AR367437 Sequence
8	715.8	55.7	1358	6 AX031160	AX031160 Sequence
9	715.8	55.7	1358	6 BD061164	BD061164 Plant fat
10	715.8	55.7	1358	6 CAY16283	AY16283 Crepis pala
11	705.4	54.9	1312	6 AR367438	AR367438 Sequence
12	705.4	54.9	1312	6 AX031162	AX031162 Sequence
13	705.4	54.9	1312	6 BD061165	BD061165 Plant fat
14	699.8	54.5	1364	6 AR064128	AR064128 Sequence
15	694.8	54.1	979	8 AY166778	AY166778 Helichrys
16	673	52.4	1406	8 AY462108	AY462108 Stokesia
17	496.4	38.6	110900	8 AP006377	AP006377 Lotus cor
18	495.4	38.6	1291	8 AF074324	AF074324 Borago of
19	487.6	37.9	1259	8 AF525534	AF525534 Vernicia
20	486.6	37.9	1259	8 AP251844	AP251844 Helianthu
21	481.6	37.5	1507	8 AF188264	AF188264 Vernonia
22	478.8	37.3	1452	8 AF083163	AF083163 Olea euro
23	478.4	37.2	1475	8 AF188263	AF188263 Vernonia
24	476.4	37.1	1556	8 SOYMO6DA	L43921 Glycine max
25	474.4	36.9	1466	8 AF192486	AF192486 Sesamum i
26	473.8	36.9	1219	8 AF071892	AF071892 Prunus ar
27	467.4	36.4	1344	8 HAN292275	AR292275 Helianthu
28	467.4	36.4	1345	8 AF251843	AF251843 Helianthu
29	465.6	36.2	1447	8 PCU86072	U86072 Petroselinu
30	462	36.0	1356	8 CPY16284	Y16284 Crepis pala
31	461.8	35.9	1472	8 SCY120LDS	X92847 S. commerson
32	455.6	35.5	1231	6 AR037150	AR037150 Sequence
33	455.6	35.5	1231	6 T65761	T65761 Sequence 44
34	455.6	35.5	1372	6 AR207486	AR207486 Sequence
35	455.6	35.5	1372	6 ATHD12A2A	L26296 Arabidopsis
36	455.6	35.5	1451	8 AY039572	AY039572 Arabidops
37	455.6	35.5	1451	8 AP002063	AP002063 Arabidops
38	455.6	35.5	85657	8 AC069473	AC069473 Arabidops
39	454.4	35.4	1476	6 AR064127	AR064127 Sequence
40	454	35.3	1152	8 AY142057	AY142057 Arabidops
41	454	35.3	2973	6 AR207494	AR207494 Sequence
42	453.6	35.3	1451	8 AY084545	AY084545 Arabidops
43	453.4	35.3	1580	6 BD171810	BD171810 Gene part
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45	449	34.9	1300	8 AY178445	AY178445 Trichosan

ALIGNMENTS

RESULT 1
AX089471
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AX089471 1285 bp DNA linear PAT 21-MAR-2001
Sequence 1 from Patent WO0116362.
AX089471 GI:13443732
AX089471.1 GI:13443732
Calendula officinalis
Calendula officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Calenduleae; Calendula.
Feussner,I., Hornung,B., Fritzsche,K., Peltzsch,N. and Renz,A.

TITLE Fatty acid desaturase gene from plants
JOURNAL Patent: WO 0116362-A 1 08-MAR-2001;
BASF AKTIENGESELLSCHAFT (DE)
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KIYKLNLPGRVPTLVPLTGLPRLYLNISGKYGRANHPDPSPIFENDERY
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ORIGIN

Query Match 100.0%; Score 1285; DB 6; Length 1285;
Beech Local Similarity 100.0%; Pred. No. 0;
Matches 1285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AAAAGCTACTTCTCTGTGAGGGTAATTATATCAACAACATGGGTGTCGGA 60
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DB 61 TGTGGATTCATCTGAGGAAAAAATCATCTTGAACGTGTGCACTGCATCCGTTCA 120
QY 121 CGTTAAGGATCTGAAGAAAGGATTCCTACCCATGCTTGAAGGATCTGCATCCGGT 180
DB 121 CGTTAAGGATCTGAAGAAAGGATTCCTACCCATGCTTGAAGGATCTGCATCCGGT 180
QY 181 CATCATATCTATGTTGTCATGATCTCATGTTGCTATGCTTCTACTACCTTGCAACA 240
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QY 241 CGTATATCTCTTATTCCTACACCTCTGCGCTTACCTACGATGCGCGTTTACTGCTTT 300
DB 241 CGTATATCTCTTATTCCTACACCTCTGCGCTTACCTACGATGCGCGTTTACTGCTTT 300
QY 301 GTCAAGTACGATCTCAACCGGCTCTGCGTCAATGCGTCAAGTGTGTCACCATGTCAT 360
DB 301 GTCAAGTACGATCTCAACCGGCTCTGCGTCAATGCGTCAAGTGTGTCACCATGTCAT 360
QY 361 TTAGGACTACAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
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DB 1201 TGTATGCTTAATTAAGTTGTTAACTTCTATTCGTTGTAATTAATTAATTAAGAGAA 1260
QY 1261 AAAAAAAAAAAAAAAAAAAAAA 1285
DB 1261 AAAAAAAAAAAAAAAAAAAAAA 1285

RESULT 2
COP245938 1152 bp mRNA linear PLN 22-DEC-1999
LOCUS Calendula officinalis partial mRNA for (8.11)-linoleoyl desaturase
DEFINITION (des8.11 gene).
ACCESSION AJ245938
VERSION AJ245938.1 GI:6634079
KEYWORDS (8.11)-linoleoyl desaturase; des8.11 gene.
SOURCE Calendula officinalis
ORGANISM Calendula officinalis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Calenduleae; Calendula.
REFERENCE
1 Fritsche, K., Hornung, E., Peitzsch, N., Renz, A. and Feussner, I.
Isolation and characterization of a calendic acid producing
(8.11)-linoleoyl desaturase
FEBS Lett. 462 (3), 249-253 (1999)
JOURNAL MEDLINE
PUBMED 20086417
10622705
REFERENCE 2 (bases 1 to 1152)
AUTHORS Feussner, I.
TITLE Direct Submission
JOURNAL Submitted (02-SEP-1999) Feussner I., Hormonforschung, Institut fuer
Pflanzenbiochemie, Weinberg 3, D-06120 Halle/Saale, GERMANY
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ORIGIN

Query Match 89.6%; Score 1152; DB 8; Length 1152;
 Best Local Similarity 100.0%; Pred. No. 4.6e-292;
 Matches 1152; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGGGTCTGGTGGTGGATGCGATTCATCTGAGGAGAAAAACATCTGTAACGTGTG 60
QY 102 CCACTGCATCCACCGTTCAAGGATCTGAAGAAAGGATTCCTACCATTCCTT 161
DB 61 CCACTGCATCCACCGTTCAAGGATCTGAAGAAAGGATTCCTACCATTCCTT 120
QY 162 GAGGATCTGTCATCCGTCATCATCTATGTTGTCATGATTCATTCCTATGTC 221
DB 121 GAGGATCTGTCATCCGTCATCATCTATGTTGTCATGATTCATTCCTATGTC 180
QY 222 TTCTACTACTCTGCAACACGTATATCCCTTTATCTTCAACCTCTGCTTACCTAGCA 281
DB 181 TTCTACTACTCTGCAACACGTATATCCCTTTATCTTCAACCTCTGCTTACCTAGCA 240
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DB 541 TTGACTTTAGGATTCGCTTATACCTCTTAACTAATCTTGGGCAAGAAATACGGAGG 600
QY 642 TTGGCCAAACATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCG 701
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QY 702 TTGCTATCCGATTCGGCTCTCTGCTGATTTTATAGCAATTCAGCTTCTTGACAGCA 761
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QY 942 CGGCTTTTCCACGAGCTTACACACACACATCTCTGATTCATTCATTCATTCATTC 1001
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QY 1122 GAGCCGATGAGATTCACGACCAAGGCTGTCTGATCCACAGATGATTCATTA 1181
DB 1081 GAGCCGATGAGATTCACGACCAAGGCTGTCTGATCCACAGATGATTCATTA 1140
QY 1182 AGGTATATGCA 1193
DB 1141 AGGTATATGCA 1152

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RESULT 3
 AY166773
 LOCUS
 DEFINITION
 Helianthus annuus delta12-fatty acid acetylase mRNA, complete cds.
 ACCESSION
 AY166773
 VERSION
 AY166773.1 GI:31322134
 KEYWORDS
 ORGANISM
 Helianthus annuus (common sunflower)
 Helianthus annuus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.
 REFERENCE
 1 (bases 1 to 1419)
 Cahoon, E.B., Schnurr, J.A., Huffman, E.A. and Minto, R.E.
 Fungal responsive fatty acid acetylases occur widely in
 evolutionarily distant plant families
 Plant J. 34 (5), 671-683 (2003)
 2 (bases 1 to 1419)
 Cahoon, E.B.
 Direct Submission
 Submitted (18-OCT-2002) Crop Genetics, DuPont, Bldg. 402
 Experimental Station, Wilmington, DE 19880-0402, USA
 JOURNAL
 TITLE
 AUTHORS
 REFERENCE
 JOURNAL
 FEATURES
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ORIGIN

GHHAYSDYQIDIDIVGVLSALTYPPFSWKYSHRNHNANTSLDNDVYIPEKAKAY
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 Best Local Similarity 82.1%; Pred. No. 4.3e-218;
 Matches 1015; Conservative 0; Mismatches 220; Indels 2; Gaps 1;

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 97 CATCTGAGGAGAAAACATCCTTGAACGTGTGCCAGTGCATCCACCTTCAAGTAAAGC 156
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 157 ATCTGAAGAAAGCATTCCTACCCATTGCTTGAAGCGATCTGTCAATCGGTCATCACT 216
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 217 ATCTGATTCATGATCTCATTTGCTTATGCTTCTTACTACTTGCAGAAACGATATACC 276
 250 CTCTTATTCCTACACCTCTGGCTTACCTAGACAGGCGGTTTACTGCTTGTGTAAGTA 309
 277 CTCTTATTCCTACACCTCTGGCTTACCTAGACAGGCGGTTTACTGCTTGTGTAAGTA 336
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 910 CAACATTCGATATAGTATGTAAGCGGCTTCTGTTTATGATCAATTTTGAACGACCTC 969

Db 937 CGACAATGATAGGAGATTTTGGATTCCTCGAATAGGAGTTTTCATGATGTCACCCACATC 996
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 Db 1177 GCATATATTTGGTATCATTAATATGTAATC--AGTATACATGAAACATGAGTATGCTT 1234
 Qy 1210 AATTAAGTGTTAACCTTTCATTCGCTGTAATTAAT 1246
 Db 1235 AAGTATTTGTAATTCCTATTAATTAAGGATTAATGAT 1271

RESULT 4
 AY166776
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Rudbeckia hirta
 Rudbeckia hirta
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Rudbeckia.
 1 (bases 1 to 979)
 Cahoorn, E.B., Schurr, J.A., Huffman, E.A. and Minto, R.B.
 Fungal responsive fatty acid acetyltransferases occur widely in
 evolutionarily distant plant families
 Plant J. 34 (5): 671-683 (2003)
 2 (bases 1 to 979)
 Cahoorn, E.B.
 Direct Submission
 Submitted (19-OCT-2002) Crop Genetics, Dupont, Bldg. 402
 Experimental Station, Wilmington, DE 19880-0402, USA

REFERENCE
 JOURNAL
 TITLE
 AUTHORS
 JOURNAL
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ORIGIN

Query Match 58.4%; Score 750.4; DB 8; Length 979;
 Best Local Similarity 85.3%; Pred. No. 2.3e-186;
 Matches 835; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
 Qy 138 AAGGCATTCGCCCCCATGTCTTGAAGCATTCGTCATCGTACTATGTTGTT 197
 Db 1 AAGGCATTCGCCCCCATGTCTTGAAGCATTCGTCATCGTACTATGTTGTT 60

QY 615 AATATCTGGGGCAAGAAATACGGAGGTTTGCCAAACCACTTGTGATCCATGATGCCAATT 674
 Db 481 AATGTTCTTGGCAAGAAATATGAAAGTTTGGCAACCACTTGTGATCCATGATGCCAATT 540
 QY 675 TTCAACGATCGTGAACGGCTTCAAGTTTGTGATCCGATTTCCGCTTCTCGCTGATATT 734
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 QY 795 ATTCAGATCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 854
 Db 661 GTTCCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
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 Db 841 TTGATCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
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 Db 901 ATACCAATTTTGGGCGAGTACTATTAATTCGATGATGATGATGATGATGATGATGATGAT 960
 QY 1095 AGAGAGGCTAAGGAATGC 1112
 Db 961 AGAGAGGCTAAGGAATGC 978

RESULT 6
 CAY16285 1435 bp mRNA linear PLN 23-DEC-2000
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 DEFINITION Y16285
 ACCESSION Y16285
 VERSION Y16285.2 GI:11991459
 KEYWORDS delta 12 fatty acid acetylase.
 SOURCE Crepis alpina
 ORGANISM Crepis alpina
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae; Crepis.
 REFERENCE 1
 Lee, M., Leeman, M., Banas, A., Bafor, M., Singh, S., Schweizer, M., Nilsson, R., Liljenberg, C., Dahlqvist, A., Gummesson, P., Sjöedahl, S., Green, A. and Stymer, S.
 Identification of non-heme diiron proteins that catalyze triple bond and epoxy group formation
 Science 280 (5365), 915-918 (1998)
 JOURNAL MEDLINE 98239771
 PUBMED 9572738
 REFERENCE 2
 Lee, M.A.
 Direct Submission
 Submitted (21-JAN-1998) M.A. Lee, Nilsson Ehle Laboratory, Sualof Weibull Ab, S-26881, Svalov, SWEDEN
 Revised by [4]
 3 (bases 1 to 1435)
 REMARK Lee, M.A.
 Direct Submission
 Submitted (22-DEC-2000) M.A. Lee, Nilsson Ehle Laboratory, Sualof Weibull Ab, S-26881, Svalov, SWEDEN
 COMMENT On Dec 24, 2000 this sequence version replaced gi:3341397.
 FEATURES
 location/Qualifiers
 1..1435
 source

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 ORIGIN
 Query Match 56.7%; Score 728.6; DB 8; Length 1435;
 Best Local Similarity 77.5%; Pred. No. 1,36-180;
 Matches 897; Conservative 0; Mismatches 254; Indels 6; Gaps 1;
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QY 1164 CACAAGATGATCAAA 1180
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RESULT 7
AR367437 1358 bp DNA linear PAT 12-SEP-2003
LOCUS AR367437
DEFINITION Sequence 1 from patent US 6329518.
ACCESSION AR367437
VERSION AR367437.1 GI:34600636
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1358)
AUTHORS Green, A., Singh, S., Lenman, M. and Strymne, S.
TITLE Plant fatty acid epoxigenase genes and uses therefor
JOURNAL Patent: US 6329518-A 11-DEC-2001,
FEATURES
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ORIGIN
Query Match 55.7%; Score 715.8; DB 6; Length 1358;
Best Local Similarity 78.2%; Pred. No. 3e-177;
Matches 903; Conservative 0; Mismatches 237; Indels 15; Gaps 3;
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RESULT 8
AX031160 1358 bp DNA linear PAT 20-SEP-2000
LOCUS AX031160
DEFINITION Sequence 1 from Patent W09846762.
ACCESSION AX031160
VERSION AX031160.1 GI:10278513
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 ACCESSION AR367438
 VERSION AR367438.1 GI:34600637
 KEYWORDS
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 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1312)
 AUTHORS Green, A., Singh, S., Ienman, M. and Styne, S.
 TITLE Plant fatty acid epoxigenase genes and uses therefor
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 Best Local Similarity 78.6%; Pred.No. 1.6e-174;
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RESULT 12
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LOCUS Sequence 3 from Patent WO9846762.
DEFINITION AX031162
ACCESSION AX031162
VERSION AX031162.1 GI:10278515
KEYWORDS
SOURCE
ORGANISM
Crepis sp.
Crepis sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Crepis.
1
REFERENCE
AUTHORS Green, A., Singh, S., Stymer, S. and Lemman, M.
TITLE Plant fatty acid epoxidase genes and uses therefor
JOURNAL Patent: WO 9846762-A 3 22-OCT-1998;
GREEN ALLAN (AU) ; SINGH SURINDER (AU) ; COMM SCIENT IND RES ORG
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ORIGIN

Query Match 54.9%; Score 705.4; DB 6; Length 1312;
Best Local Similarity 78.6%; Pred. No. 1,66-174;
Matches 870; Conservative 0; Mismatches 228; Indels 9; Gaps 2;
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Qy	529	--ATTCCAAATCTTAAACATCCACCCGGGCGAGTGTCACTTGGTGTTCGGTGA	585
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Qy	586	CTTTAGATTTCCGTTAATCCTCTTAATTAATATCTCGGCGCAAGAAATCGGAGGTTTG	645
Db	668	CTTTGGGCTTTCCTTAACTCTTGAACCAATATTTCAAGGCAAGAAATCAAAAGTTTG	727
Qy	646	CCAACCACTTGTATCCCATAGTGCATATTTCAACGATCGTGAAGCGCTTCAAGTTTGC	705
Db	728	CCAACCACTTGTATCCCATAGTGAAGCCCATCTTCAAGTACGTGAAGCAATCCAGTCTGTC	787
Qy	706	TATCCGATTTGGTCTCTGCTGTATTTATGCAATCAAGCTTCTTGTAGCAGCAAAAG	765
Db	788	TATCGGATGTGGTCTCATTTCTGTGTTTTACGGGCTTAAGTTTCTTGTACGAAAAAG	847
Qy	766	GGGCAAGTTGGGTAAACAAGATGAACGAATTCAGATCTAGGTGAAGGTGTTCTTG	825
Db	848	GGTTCGGTGGGTAAAGCATGAATGAACGAGCCCAAGTGTGGGCTGATATCCTTCATTA	907
Qy	826	TTTTGATCAATATTTGGACACACACCCATCTCTCACTCCTCATTTATGTTCAACCGAAT	885
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Qy	886	GGAATGATCAAAAGCGGCTTATCAACAAATGATAGGAATTTGGGTTCTGTAATGGG	945
Db	968	GGAATGATCAAAAGGAGCTTGAATCAATCGATAGGATTTGGGTTCTCTGAATAGGG	1027
Qy	946	TTTTCCAGAGTTAACACACTACGCTTGCATATTTGATCTCATATTCATTCACATTT	1005
Db	1028	TGTTTCATGAGTCACTTCAACACACGTTGTCACTATTTGTCCCGTACATTCACATTT	1087
Qy	1006	ATCATGCAAGGAAGCAAGGATCAATCAACGAGTGTGGGCGAGTACATATAAAATCG	1065
Db	1088	ATCATGCAAGGAAGCGAGCGAACCAATTAAGCCGGTGTTAAGGGAGATAGGATGATCG	1147
Qy	1066	ACAGGATCTCCATTTTCAAAGCATGTTATAGAGGCTTAAGAAATGCATTAATCGAGC	1125
Db	1148	ATAGGATCTCGTTTAAACAAACATGTGGAAGGCGCAAGAAATGCAATCAATCGAGC	1207

Qy 135 AAGAAAGCATTCCTTACCCATGCTTGAGAGCATCTGTCATCCGGTCATCATACTATGTT 194

Db 1 AAGAAAGCATTCCTTACCCATGCTTGAGAGCATCTGTCATCCGGTCATCATACTATGTT 60

Qy 195 GTTCATGATCTCATCTGTCGCTATGTCCTTCTACTACCTTGCAACACAGTATATCCCTTT 254

Db 61 TTTCATGATCTTCATCTGTCGCTATGTCCTTCTACTACCTTGCAACACAGTATATCCCTTT 120

Qy 255 ATTCTTACACTCTGGCTTACCTACAGCATGGCCGGCTTACTGCTGTTTGTCAAGCTAGCATC 314

Db 121 CTCCRCCTCATCTCGCTTACTTATCCGTGCGCGGTTATGCTTTGTCAAGCTAGCATTT 180

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2004, 12:44:38 ; Search time 2555 Seconds
(without alignments)
15018.748 Million cell updates/sec

Title: US-10-069-772-1
Perfect score: 1285
Sequence: .1 aaagctcactctctctgta.....aaaaaaaaaaaaaaaa 1285

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST.*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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19: em_gss_pln:*
20: em_gss_vtc:*
21: em_gss_fun:*
22: em_gss_mam:*
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24: em_gss_pro:*
25: em_gss_rdg:*
26: em_gss_phg:*
27: em_gss_vtl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	505.6	39.3	691 13	BQ994479 QGF7F12.Y
2	495.4	38.6	725 13	BQ866257 QGC7H15.Y
3	437	34.0	613 14	CF098768 QHN8F08.Y
4	406.4	31.6	624 14	CF096571 QHN23019.

5	358.6	27.9	530	14	CF091557
6	358.2	27.9	989	11	CK269848
7	352	27.4	1856	11	AY104050
8	350.6	27.3	1080	13	BQ238570
9	349	27.2	973	14	CK262936
10	342	26.6	918	14	CK269030
11	336.6	26.2	963	14	CK270183
12	332.2	25.9	764	10	AM201738
13	330.4	25.7	948	14	CK278983
14	330	25.7	616	13	BQ973950
15	329.8	25.7	811	14	CF511517
16	327.6	25.5	756	13	BQ836275
17	323.4	25.2	911	14	CF215372
18	322.4	25.1	784	12	B1925058
19	321.8	25.0	763	13	BQ853589
20	320.4	24.9	1807	12	B1683572
21	318.2	24.8	809	10	BE988745
22	311.6	24.2	753	13	BQ857435
23	304.6	23.7	891	14	CK250323
24	302.6	23.5	714	9	AM100780
25	302	23.5	870	14	CF212392
26	300.8	23.4	798	13	BQ858101
27	300.8	23.4	901	14	CK263172
28	300.4	23.4	772	12	B1933814
29	294.6	22.9	876	14	CD760583
30	294	22.9	676	14	CD715491
31	294	22.9	676	14	CD715677
32	294	22.9	676	14	CD719893
33	293.6	22.8	823	14	CF511848
34	293	22.8	676	14	CD717551
35	292.4	22.8	705	13	BQ939824
36	291.8	22.7	755	12	BM109924
37	291.2	22.7	901	14	CB978093
38	290.2	22.6	905	14	CB349164
39	290	22.6	558	13	BQ981901
40	289.8	22.6	667	14	CD717827
41	289.8	22.6	757	14	CA801285
42	288.2	22.5	696	13	BU010610
43	288.2	22.4	707	14	CA782495
44	287.8	22.4	704	14	CF809003
45	286.8	22.3	665	14	CD717639

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION OGF7F12.YF.ab1 OG EFGHU lettuce serritola lactuca sativa cDNA clone
ACCESSION BQ994479
VERSION BQ994479.1 GI:22414014
KEYWORDS
ORGANISM
SOURCE
Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichoriaceae; Lactuca.
1 (bases 1 to 691)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,
Ellison,P., Kolkmann,J., Stabaugh,M.S., Livingston,K., Zhou,Y.,
Lai,Z., Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenome.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Agriculture Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742

Db	102	AGATCCTGGAAGTGTCCCAAGT-GATTCACCGTTTTCAATTAAGTATTAAAGAAAGCA	160
Qy	145	TTCCATACCCATTGCTTTAGAGGATGTGTATCTCCGGTCATCATCTATGTGTTCAATGATC	204
Db	161	TCCCTGCCCATATGCTTCAAGGAGTCCGGTATCCGTTCACTTACATATGTGTTCAAGATTC	220
Qy	205	TCATGTGTCCTATGTCTTCTATCTACTCTTGCAAAACAGTAATACCTCTTATTCCTAAC	264
Db	221	TGATTTGTGCTACGTTTTCTTACTCTCTTGCAAAATACATATATTCCTTTCTTCCAGCTC	280
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Db	281	CTTTGGCCTACTTACTCTTGCCGGTTTTATGTGTTCTGTCAAGCAAGCATCTCAGAGGCT	340
Qy	325	TCTGGGTCAATCGGTACGAAATGTGTTCACCAATGCAATTAGACATACCAAGTTGATTGAG	384
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Qy	385	ACATGTGTGATTCGTGCTCCATTCATTTGGGCTCTCTCACCCCGATTTCTTTGGAAATATA	444
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Qy	445	GCCACAGAAATCACACGCGCAACACAAATTCACTGATTAAGATGAAGTTTACATTCTTA	504
Db	461	GCCATCGAAATCACCATGCAACAAATAATTCCTGATTAATGATGAAGTTTACATTCTTA	520
Qy	505	AACGTAATCTCAAGGTCAAGATTTATTCCAACTTTTAAACAATCAACCCGGGCGAGTGT	564
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Db	581	TCACTTGTGTGTTTAAAGTTCACTCTAGGATTTCTTTAATCTTTAATATAATTTCTG	640
Qy	625	GCAAGAAATACGGAGGTTTGCCAACAACCTTGTATCCATGAGTCCAAATTTTCAACGATC	684
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Qy	685	GTGAACGCGTTCAAGTTTTGTATC 709	
Db	701	GCGAGCGAATTCAGGTTCTGTATTC 725	

REFERENCE
AUTHORS
1 (bases 1 to 613)
Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Riesberg, L.,
Lih, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolman, J., Slabaugh, M. S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
TITLE
Lettuce and Sunflower ESTs from the Composite Genome Project
URL
<http://compgenomics.ucdavis.edu/>

JOURNAL COMMENT

Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Aasmundson Hall, UCD, Davis, CA 95616, USA
Tel.: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdyc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig OH CA Contig156400, see <http://cgpdb.ucdavis.edu/>

```

for details.
Plate: QHN8 row: F column: 08.
Location/Qualifiers
1. .613
/organism="Helianthus argophyllus"
/mol_type="mrna"
/db_xref="taxon:73275"
/clone="QHN8F08"
/lab_host="E. coli"
/clone_lib="OH N sunflower H. argophyllus (drought stress)"
/vector="pGEM-T; The library was constructed from
three different sources (seeding, root and leaf) of RNA
from a single genotype. cDNAs were pooled and cloned into
a high-copy vector pGEM-T. Details of library construction
can be obtained at http://cgpbp.ucdavis.edu/"

```

Query Match	Similarity	Score	ID	Length
Best Local	85.8%	437	DB 14	613
Matches	485	Conservative	0	Mismatches 80; Indels 0; Gaps 0;
QY	37	ACAACATGGGTGCTGTGGTGGTGGATGTGGATTCGATCTGAGGAGAAAAACATCCTTGAAC	96	
DB	565	AAACATGGGTGAGGTGGCCGGATGTCAAGCCCATCTGAGGGGCAAAAACATCCTCGAAC	506	
QY	97	GTTGGCCAGTCGATCCACCGTTACCGTTAAGGCATCTGAAAGAAAGCGATTCTTACCATY	156	
DB	505	GTTGCCCATTTGATCCACATTCATCTTAAGCGATCTAAAGAAAGCAATCCCTGCTCACT	446	
QY	157	GCTTTGAGCGATCTGTATCCGGGCATCATCTATCTGTTGATCATCTCATTTGTCCT	216	
DB	445	GCTTGAAGCATCTGTATCCGTTCACTTAATGTTGTTCACTAGACTCATTTGGGCT	386	
QY	217	ATGTTCTTCTACTACCTTTGCAAAACGATATCCCTTATTTCTTACACCTCTGCTTACC	276	
DB	385	ATGCTTTTACTTCTCTTGCAACACATACATCCCTCTTCTTCAACCCATGGGCTTACC	326	
QY	277	TAGATAGGCCCGTTTACTGCTTTGTGAAGTAGACATCCCAACGGGCTCGGGTCATCG	336	
DB	325	TAGATAGCCGGTTTACTGCTTTGTGAAGTAGACATCCCACTGAGGCTATGGTCAATCG	266	
QY	337	GTCAAGATGTGTCAACCATGATTTTGAAGCTACAGCTAGTTGATGACATTTGGTAT	396	
DB	265	GTCAAGATGGGTGACCAATGCTATAGTAGCTACCAATGATGATGACATTTGGGCT	206	
QY	397	TCTGTCTTCATTCGGGCTCTCTCAACCCCGTATTTCTCTTGAAGTATAGCCACAGAAATC	456	
DB	205	TCTGTCTTCATTCAGCTCTCTTATACCCCTTATTTCTTGGAAATTAAGCCATGGAAAC	146	
QY	457	ACCAAGCCCAACAAATTCCTGATTAAGATGAAGTTTACATTCCTTAAAGTAAAGTGA	516	
DB	145	ACCAAGCCCAACAGAAATTCGCTTGAATTAAGATGAAGTTTACATTCCTTAAAGCAAGGCA	86	
QY	517	AGGTCAAGATTTATTCGAAATCTTAAACAATCCAGGCGAGGTTCATCTTTGGTGT	576	
DB	85	AAAGTTGAGTTTACTCAAGACTTCTTAAACAATCCCGTGGCGAGGTTCATCTTTGGTGT	26	
QY	577	TTGGGTGACTTTAGATTTCCGTT 601		
DB	25	TTAGATTACTTAAGGATTTCCCTT 1		

RESULT	4
CF096571	
LOCUS	
DEFINITION	624 bp mRNA linear EST 22-JUL-2003
ACCESSION	CFO96571
VERSION	OHN23J19.yg.ab1 OH N sunflower H argophyllus (drought stress)
KEYWORDS	Helianthus argophyllus cDNA clone OHN23J19, mRNA sequence.
SOURCE	CF096571.1 GI:33135638
ORGANISM	.EST. Helianthus argophyllus Helianthus argophyllus Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 624)
Kozlik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, J., Kolman, J., Slabagden, M. S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Brédiford, K.
lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>
Unpublished (2002)

Contact: Alexander Kozik [R.W.Michmore]
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Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michmore@vegmail.ucdavis.edu]
belongs to contig GH_CA_Config3889, see <http://gsnpd.ucdavis.edu/>
for details
Plate: GH23 row: J column: 19.

FEATURES	source
Location/Qualifiers	1. .624

ORIGIN

Query Match	31.6%;	Score 406.4;	DB 14;	Length 624;
Best Local Similarity	84.2%;	Pred. No. 2e-49;		
Matches 458;	Conservative 0;	Mismatches 86;	Indels 0;	Gaps 0;

QY	CTCTTAATCTATATCTCGGCGAAGAAATACGGAGGTTGCAACCACTTGAATCCCAAG	665
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Db	1 CTCTTGACTACATTTCTGCGAAGAAATACGGAGGTTGCAACCACTTGAATCCACTA	60
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Db	61 AGTCCGATTTTCAACCGAGCGTGAAGAAATTCAGGTGTGTATATCGAATATGGTATCTCT	120
QY	726 GCTGTATTTTATGCAATCAAGCTCTTGTATGAGCAAAAGGGGCGCTTGGGTATTCAC	785
Db	121 GCGGTTTTGTATGCACTTACACTTGTATGAGCAAGGGGGTAACTTGGGTGCAAGC	180
QY	786 ATGTACGCAATTTCCAGTACTAGGTGTAAAGCGTGTCTTTCGTTTGTATCAATATTTGCAC	845
Db	181 ATGTATTTAAATCCGAGTGTAGGTGTGCAATGTTTTTCGTTTGTATCAATATTTGCAC	240
QY	846 CAGCCCATCTCTCACTCCCTCAATTATGATTCACACCGAATGGAATCGAATCAAAGGGGCC	905
Db	241 CATACCCATCTCTCACTCACTATATATATTCACACCGAATGGAATCGAATTTGAAGGGGCA	300
QY	906 TTATCAACAATCGATAGGGAATTCGGGTTCTCGATTCGGGTTTTTCCAAGCGTTACAC	965
Db	301 TTATCGACAATTGATAGGGAATTTGGGAATTCCTAAATAGGGTTTTTCAATGATGTCAACCA	360
QY	966 ACTACAGTCTTGCAATCATTTGATCTCATACATTTCCACATTTATCATGCAAGGAAGCAAG	1022
Db	361 ACTACAGTCTTGCAATCATTTGATCTCGTACATTTCCACATTTATCAAGCAAGGAAGCAAG	420
QY	1026 GATCAATCAAGCAGAGTGTGGGCGAGTACTATAAATTCGACAGGACTCAATTTTCAAA	1085
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QY	1086 GCAATGTATAGAGAGGCTTAAGGAATGATCTTACATCGAGCCCGATGAGGATAGCGAGAC	1145

Db 481 GCATGTGAGAGAGCCCAAGCAATGCATCTACATCGAACCGATTGAAGATAGGAACAC 540

Qy 1146 AAG 1149
|||

Db 541 AAG 544

Accession	Definition	LOCUS	Result 5
CP091557	QHM8J13.yg.ab1 QH_M sunflower H. argophyllus Helianthus argophyllus CDNA clone QHM8J13, mRNA sequence.	530 bp mRNA linear	EST 22-JUL-2003

REFERENCE	1 (bases 1 to 530)
AUTHORS	Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., St. Laurent, J., and Tanksley, A.R.

JOURNAL
Unpublished (2002)
COMMENT
Contact: Alexander Kozik [R.W.Michelmore]
Contact: Alexander Kozik [R.W.Michelmore]

FEATURES	Location/Qualifiers
source	1. .530

Query Match	27.9%	Score 358.6;	DB 14;	Length 530;
Best Local Similarity	-84.7%;	Pred. No. 1.7e-42;		
Matches 414;	Conservative 0;	Mismatches 74;	Indels 1;	Gaps 1

Qy	10	CTTCTCTGAGGGTAATTATATACAAACAATGGGCTGCGGTGCGATGCGGATC	69
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Qy	70	CATCTGAGGGAAAAACATCCTTGAACGTGAGCCAGTGCATCCACCGTTCACGTTAAACG	129
Db	102	CATCTGAGGGCAAAAACATCTCTCGAAGGTGTCGCCATTGATTCACCATCTTAAGTG	161
Qy	130	ATCTGAGAAAGCGATTCTTACCCATTGCTTTGAGCGATCTGTATCGGTCATCACTACT	189
Db	162	ATCTAAGAAAGCAATCCCTGCTCACTGCTTGGAACGATCTGTATCCGTTCACTTAACT	222
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Db 222 ATGTGTTACAGACCTCATTGTGGCTATGATTTACTTCTTCCCAACATCATCACC 281
 Oy 250 CTTTATTCCTACACCTGCGTTACATGAGATGCGCGTTTACGTTTGTCAAGCTA 309
 Db 282 CTTTCTTCTTCTTACCCCGGCGCTTACTTACGATGCGCGTTTGTGCAAGCTA 341
 Oy 310 GCATCTTACCGCGCTCTGGGTTCATCGGTCAAGATGTGTCAACCATCATTTAGCGACT 369
 Db 342 GCATCTTACCGCGCTCTGGGTTCATCGGTCAAGATGTGTCAACCATCATTTAGCGACT 401
 Oy 370 ACCAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
 Db 402 ACCAATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 461
 Oy 429 TTTCTTGAATATATGACAGACAGATGATGATGATGATGATGATGATGATGATGAT 488
 Db 462 TTTCTTGAATATATGACAGACAGATGATGATGATGATGATGATGATGATGATGAT 521
 Oy 489 GAAGTTTAC 497
 Db 522 GAAGTTTAC 530

RESULT 6
 CK269848 989 bp mRNA linear EST 12-DEC-2003
 LOCUS CK269848
 DEFINITION EST15926 potato abiotic stress cDNA library Solanum tuberosum cDNA
 clone POACP38 5' end, mRNA sequence.

ACCESSION CK269848
 VERSION CK269848.1 GI:39826826
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Solanales; Solanaceae; Solanum.
 Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A. and Baker, B.
 1 (bases 1 to 989)
 Generation of ESTs from abiotic stressed potato tissue
 Unpublished (2003)
 COMMENT Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potaco-array@tigr.org
 Clones can be requested from TIGR via potaco@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.
 Location/Qualifiers

FEATURES
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 /organism="Solanum tuberosum"
 /mol_type="mRNA"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POACP38"
 /tissue_type="abiotic stress treated leaf and root tissue"
 /lab_host="DH10B-Tona"
 /clove_lib="potato abiotic stress cDNA library"
 /note="vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
 supplier: Solanum tuberosum var. Kennebec plants were
 grown from cuttings on a 16hr light/8 hr dark cycle at 25
 C for 3-4 weeks. Abiotic stress conditions were applied to
 four separate sets of plants. Set 1 involved saturation of
 the soil with 150 mM NaCl and tissues were harvested at
 following application of the salt stress (leaves: 2hr,
 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
 Set 2 were grown under the standard conditions and then
 were water stressed by withdrawal of further watering
 applications. Drought stressed plants were harvested after
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
 and 5d). Set 3 were grown under the standard conditions
 and then were cold stressed by placement at 4 C. Cold
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,

2d. Set 4 were grown under the standard conditions and
 then were heat stressed by placement at 35 C. Heat
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d and 4d and heat-stressed roots were harvested at 6 hr,
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and
 equal RNA from each tissue and stress was pooled to
 construct the cDNA library. RNA sample."

ORIGIN
 Query Match 27.9%; Score 358.2; DB 14; Length 989;
 Best Local Similarity 62.9%; Pred. No. 1.3e-42;
 Matches 555; Conservative 0; Mismatches 328; Indels 0; Gaps 0;

Oy 109 ATCCACGGTTCACCTTAAGCATCTGAAGAAAGGATTCCTACCATTCCTTGGAGCAT 168
 Db 107 AGCCCCCTTTACAGTTGGTATATCAAGAAAGCTATCCCACTCACTGCTTCAAGGT 166
 Oy 169 CTGTATCCGGTTCATCTATGTTGTTCAATGATCTCATTTGTTGCTTATGTTTACT 228
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 Oy 229 ACCTTGAAACAGTATATCCCTTATTCCTTACACCTTGGCTTACCTACATGCGCCG 288
 Db 227 ACCTTGAACACCTTATCTTCCACCTCTTCATCCCATATGCTTACATTCGCGCTA 286
 Oy 289 TTTACTGGTTTGTCAAGCTAGCATCCCTCACCGGCTCTGGGTTCATCGTCAAGATGTG 348
 Db 287 TTTACTGATTTGCGAGGTTGTGTTGCACTGATGTTGGTTATATGCCAAGATGTG 346
 Oy 349 GTCAACATGATTTAGGACATACAGTTGATGATGATGATGATGATGATGATGATGAT 408
 Db 347 GCCATACAGCTTTCAGTATATCAATGAGGTTGATGATGATGATGATGATGATGATGAT 406
 Oy 409 CGGCTCTCTACCCCGTATTTCTTGGAAATATAGCAACAGAAATCAACAGCCCA 468
 Db 407 CTGCTCTGTTGTCGGTATCTTCTTGAATATATGATGATGATGATGATGATGATGATGAT 466
 Oy 469 CAATTCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 528
 Db 467 CTGCTCTCTGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 526
 Oy 529 ATTCCAACTCTTAAACATACACCGCGGAGTTCATCTTGGTGGTTCAT 588
 Db 527 ATTCCAACTCTTAAACATACACCGCGGAGTTCATCTTGGTGGTTCAT 586
 Oy 589 TAGATTTCCGTTTATCTTAACTATATCTGCGGCAAGAAATAGGAGGTTTGCA 648
 Db 587 TTGCTGCGCGTGTACTTGGCTTCAATGTTCTGCGAGACCATPAGACCGATTTGCA 646
 Oy 649 ACCACTTGTATCCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 708
 Db 647 GTCACTATGACCTTATAGCCCAATCTAACAACCGGAGGCTTCAAGATCTTCGTTT 706
 Oy 709 CCGATTTCCGTTCTCTGCTGATTTTATGCAATCAAGCTTCTGTAGCAAAAGGG 768
 Db 707 CTGATGCGAGGTTCTGAGGTTGTATCTGATACCGGTTCCTTATGTAAGGTC 766
 Oy 769 CAGTTGGGTTATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 828
 Db 767 TAGCTTGGCTAGTGTGATCTACGATGATGATGATGATGATGATGATGATGATGATGAT 826
 Oy 829 TGATCATTTTTCACACACCATGCTCACTCCCTCAATTATGATTTCAACGGAATGA 888
 Db 827 TGATCATTTTTCACACACCATGCTCACTCCCTCAATTATGATTTCAACGGAATGA 886
 Oy 889 ACTGATCAAAAGCGCTTATCAACATGATGATGATGATGATGATGATGATGATGATGATGAT 948
 Db 887 ATTGCTTAAAGGAGCTTTGGGACACGTGAGAGAGCTATGGGCTTTCTTAAACAGGCT 946
 Oy 949 TCCACGATTTACACATCACTCACTCTTTCATCTTGAATCTC 991
 Db 947 TCCACGATTTACACATCACTCACTCTTTCATCTTGAATCTC 989

RESULT 7
AY104050 1856 bp mRNA linear HTC 16-OCT-2002
LOCUS Zea mays PC0088038 mRNA sequence.
DEFINITION AY104050
ACCESSION AY104050.1 GI:21207128
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1856)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
TITLE Unpublished (2002)
JOURNAL 2 (bases 1 to 1856)
REFERENCE Coe,E.H.
AUTHORS Direct Submission
JOURNAL Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
FEATURES
Source location/Qualifiers
1..1856
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="MaizeDB:634972"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/DuPont Consensus library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN
Query Match 27.4%; Score 352; DB 11; Length 1856;
Best Local Similarity 59.6%; Pred. No. 7,1e-42;
Matches 636; Conservative 0; Mismatches 420; Indels 12; Gaps 2;

109 ATCCACCGTTCAGCTTAAGCGATCTGAAGAAAGCATTCACCCATTGCTTTAGCGAT 168
DB AGCCCTCCGTTCACTGGGTGATGATCAAGAGCCATCCCGCACAGCTTCGAGCGCT 324
169 CTGTATCCGGTTCATCACTATGTTGTTGATGATCTATTTGCTTCTTCTACT 228
DB CGGTCTCAAGTCTTCTCTGATGAGTGTCCAGACTGTGTATCCCGGGGCTCTCT 384
229 ACCTTGAACAAGCGATATCCCTTTATTCCTACACTCTGGCTTACCTAGAGGCGCG 288
DB ACTTGCGGTGGCCATCATACCGGGCTCCCAAGCCCGTCCGCTACGCGCGCTGCGC 444
289 TTTACTGTTTGTGCAAGTACATCTCACCGGCTCTGGGTCTATCGGTCAAGATGTG 348
DB TGTACTGATGCGGAGGGGTGCGGTGACCGGGTGTGAGTCAATCGGACGAGTGG 504
349 GTCAACATGATTTAGCACTACAGATTGATGATGATGATTTGGATTGCTCTCAAT 408
DB GCGACCAAGCGCTTCTCGAGTACTGCTCTCTGAGACGATGCTCGCGCTGCTGCACT 564
409 CGGCTCTCTCAACCGGATTTCTCTGGAATATATAGCAGGAATACCAACGCAACA 468

DB 565 CGTGCATCATGATGTCCTTCTCTGAGAGTACAGCAACGCGGCCACCACTTCACACA 624
QY 469 CAAATTCACTGATTAAGTAAAGTTTACATTCTTAAACGTAAGTCAAGATTT 528
DB 625 CGGGTCTCTGAGCGGACGACGAGGTGTTCGCGCCAAAGAAAGAGCGCTGCGCGT 684
QY 529 ATTGCC---AACTTCTTAACAATCAACCGGGGAGTGTTCATTGGTGTTCGATTGA 585
DB 685 ACACCCGTACGTGTACACACACCGGTGCGCGGGTGTCAATCGTGTGTGACGTCA 744
QY 586 CTTTAGAATTTCCGTTATACCTTTAACTAAATATCTCGGGGAGAAATACGGAGTTTG 645
DB 745 CCTCGGGTGGCCGCTGTAACCTGGAGACCAACGCGTGGCGGCGGACCGGCTTCG 804
QY 646 CCAACCACTTGAATCCCATGAGTCCATTTTCAACGATCGTGAACGCGTTCAAGTTTC 705
DB 805 CTTGCACTTGTGACCCCTTACCGCCCATCTTCAACGACCGGGAGCGCCCAAGTCTTCG 864
QY 706 TATCGAATTTGGTCTTCTGCTGATTTTATGCAATCAAGCTTCTTGAAGCAAAAG 765
DB 865 TCTGGAGCGCGGCGTGTGCGCGGCTGCGGCTGTACAGCTTGGCGGCGCTTCG 924
QY 766 GGGCAGCTTGGTATCAACATGTAAGCAATTCAGTACTAGTGAACGTTCTTCG 825
DB 925 GGGTCTGGTGGGTGGTGGCGGTGATCGCGCGCTGTATGTGAACGCGGCTTCG 984
QY 826 TTTGATCATCATTTTGAACAACAACCCATCTCTCATCTCTCATTTATTTCAACCGAT 885
DB 985 TGCTCATCATCTTACCTGAGACACCCACCGGTCTCTCCCATCACTGAGCGAGT 1044
QY 886 GGAATCTGATCAAGAGCGCTTATCAACATGATGATGAGATTTGGGTTCTGATCGGG 945
DB 1045 GGGATGCTGCGCGCGCGCGCTGCGCACATGAGACCGGACTAGGCACTCTCAACCGCG 1104
QY 946 TTTTCCAGAGCTTATCAACACATCACTACGCTTGTGATCATTTGATCTCATATTCACAT 1005
DB 1105 TGTTCACAAATCATACGAGACACGACGTCGCGGACCACTCTTCTCCACATGCGCACT 1164
QY 1006 ATCATGCAAGAAAGCAAGGATGATCAACGCACTGTTGGGCGAGTACTATTAATTCG 1065
DB 1165 ACCACGCGCATGAGGCGCCACCAAGGAGTCAAGCCCATCTCTGGGGATCATCAACACTTCG 1224
QY 1066 ACAGATCCCAATTTTCAAGCAATGTAAGAGGCTTAAGAAATGATCTTACATCGAGC 1125
DB 1225 ACCGACCCCTGTGTCACAGGCGACCTGCGCGAGGCGAGGAGTGTACTTACGTCGAGC 1284
QY 1126 CCGATGAGATGAGCGACCAAGGTGTGTTCTGTGACCAAGATGT 1173
DB 1285 CGGA-----GGACCGCAAGGCGCTCTGTGTACACAGAAAT 1323

RESULT 8
BU238570 1080 bp mRNA linear EST 06-SEP-2002
LOCUS Ds01_13f05 A Ds01_AAPC_ECORC cold stressed Flkweed seedlings
DEFINITION Ds01_13f05 a sophia cDNA clone Ds01_13f05, mRNA sequence.
ACCESSION BU238570
VERSION BU238570.1 GI:22750395
KEYWORDS EST.
SOURCE Descurainia sophia
ORGANISM Descurainia sophia
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Descurainia.
REFERENCE 1 (bases 1 to 1080)
Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Descurainia sophia Seedlings
TITLE Unpublished (2001)
JOURNAL Contact: Singh,J.A.
COMMENT Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada

KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
066, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
Location/Qualifiers

FEATURES

SOURCE

1. 1080
/organism="Descurainia sophia"
/mol_type="mRNA"
/db_xref="taxon:89411"
/clone="D801.13f05"
/tissue_type="leaf, stem"
/dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
/clone_11b="D801_AAFc_ECORC_cold_stressed_fixweed_seedlin
gs"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI;
Site 2: Xho I; Plants were grown for 1 month at 20°C/16
hrs light/day (average 8 leaves, 1 cm tall, weight
0.02g/plant). Then they were exposed to 20°C, 12 hrs
light/day, for 1 week. Library prepared by C. Piche using
Stratagene kit."

ORIGIN

Query Match 27.3%; Score 350.6; DB 13; Length 1080;
Best Local Similarity 62.8%; Pred. No. 1.6e-41;
Matches 542; Conservative 1; Mismatches 320; Indels 0; Gaps 0;

358 CATTACGAGCTACAGTGTATGATGACATTTGATTTGCTGCTCATTTGGCTCTCC 417
Db 150 CTTTACAGGACTACAGTGTATGATGACAGTGTGCTTATCTTCCATTTCTCTCC 209
Qy 418 TCAACCCGATTTCTTGTGAATATAGCCAGAAATACACGCCAACAATTTAC 477
Db 210 TCGTCCCTTACTTCTTGAATATAGCTATCGCCGACCATTTCCACAGGGTTCC 269
Qy 478 TCGATTAAGATGAATTTAATCTTAACCTTAAGTCAAGTCAAGTTATTCCAAC 537
Db 270 TCGAAGAGATGAATTTGTTGTCCCAAGAAATCTGCAATCAAGTGAAGGCAAT 329
Qy 538 TTCTTAACATCCACCCGGGAGATGTTCACTTTGGTGTGGTTGACTTATAGATTTC 597
Db 330 ACCTCACAAATCTGTGGGAGATGATGATGTGATGTCACCTCGGATGGC 389
Qy 598 CGTATACCTCTTAATATATCTCGGGCAAGAAATACGGAGGTTGCCAACCACTTTC 657
Db 390 CTTTGTACTTACCTTCAAGTATCTGGCAGACCGTATAGCGGTTTGATCCATTTCT 449
Qy 658 ATCCATGAGTCAATTTTCAACGATGTAACCGGTTCAAGTTTGTATCCGATTTTC 717
Db 450 TCCGGAAGGCCCCATCTAAGATGACGTAACGTTCAAAATATACATTTGGATGCCG 509
Qy 718 GTCTTCTCGCTATTTTATGCAATCAAGCTTTTGAAGCAGCAAAAGGGGAGTTGGG 777
Db 510 GTATTTCTGCTGTCTGATGATGTTTACCTTATGCTGTCGACCAAGAAATGCTCGA 569
Qy 778 TAATCAACATGTATGCAATTCAGTACAGGTTAAGGTTTCTGTTTGAATCAT 837
Db 570 TGAATCTCTTACGAGATACCGCTTCTGATATGAAAGGAGGTTCTGCTTGAATATT 629
Qy 838 ATTGACACACACCATCTCTCACTCCCTCAATTAATGATTAACGAAATGAAATGATCA 897
Db 630 ACTTGACGACACATCATCCCTGTTGCTCACTGATTAATCTGAGTGGGATTTGTTAA 689
Qy 898 AAGGCGCTTATCAACAATGATAGGATTTGGGTTCTGTAATCGGTTTTCAGAGAG 957
Db 690 GGGAGGATATAGGCTATACGATGACAGATGATGAAATCTGAAACAAGTGTTCACACA 749
Qy 958 TTACACACATCAAGTGTGATGATTTGATCTATCATTTCAATTAATGATGAAAG 1017
Db 750 TCACGACACACAGTGTGATATCTGTTCTGCAATGCCGATTTATACCGCATGG 809
Qy 1018 AAGCAAGGATGCAATCAAGCAAGTGTGGCGAGTACTATTAATGACAGAGCTCAA 1077

Db 810 AAGCTACAAAGGCGATTAAGCCAACTACTCGAGACTATTTACAGTTCAGTGAACCCCGT 869
Qy 1078 TTTTCAAGCAATGTATAGAGGCTTAGGAAATCATCTATCATGAGCCCGATGAGATA 1137
Db 870 GGTATTAAGGCGATTTATAGGAGGCAAGAGTTATCTATGTATGAACCTGACAGGAG 929
Qy 1138 GCGAGACAAAGGTGTGTTCTGTATCAACAAGATGTAATCAAAAGGTATGTCAATGC 1197
Db 930 GTGAGAAAGAAAGGTGTACTGCTATGATCAATATGATGATGATGATGATGATGATG 989
Qy 1198 AATTGTATGCTTATTAATGATTGT 1220
Db 990 GACCTTACATCTGTTGAATTTGT 1012

RESULT 9
LOCUS CK262936 973 bp mRNA linear EST 12-DEC-2003
DEFINITION CK262936
ACCESSION CK262936
VERSION CK262936.1 GI:39819914
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 973)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A. and Baker, B.
TITLE Generation of ESTs from abiotic stressed potato tissue
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST709015
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

SOURCE

1. 973
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cullivar="Kennebec"
/db_xref="taxon:4113"
/clone="POABJ33"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN

Db 321 GCCATCAGCTTTCAGTATTAACCAATGGGTGATGACACCGTTGACTTATCCCTCACT 380
Oy 409 CGGCTCTCCTCAACCCCGTATTTCTTGGAAATATAGCAAGAAATCAACCAAGCCCA 468
Db 381 CTGCTCTTGTGGTGGCGTACTTCTTGGAAATATAGTATGTGCGCAACCACTCAACA 440
Oy 469 CAATTCACCTGATACGATGAAAGTTTACCTTCAACGTAAGTCGAAGGTCAAGATT 528
Db 441 CTGGCTCCCTGAGGGTATGAGTCTTGTGCGCAAGCAAAATCTCAGCTCGATGGT 500
Oy 529 ATTCCAACCTCTTAACATCAACCCGGGCGAGTTCATCTTGGTGTTCGCTGACTT 588
Db 501 ATTCCAAGTACTGAAACATCAACGAGGCTCTCTCACTTCAATCAACCTCACACTC 560
Oy 589 TAGAGTTCCGTTATACCTTAACTAATATCTGGGGCAAGAAATACGAGGTTTGCA 648
Db 561 TTGGCTGGCCGTTGTACTTGGCTTCAATGATCTGGGACACATACGACGATTTGAT 620
Oy 649 ACCACTTGTATCCCATGAGTCCAAATTTTCAACGATCGTGAACGCGTCAAGTTTGTAT 708
Db 621 GTCACTATGACCTTACAGGCGCAATCTAACAAACGTAAGAGGCTACAGATCTTCTT 680
Oy 709 CCGATTGGTCTTCTGCTGTATTTATGCAATCAAGCTTCTTGTACGACCAAGGCG 768
Db 681 CTGATGCTGAGATCTCGAAGTTGTATCTGCTATACCGTATCTTACGTAAGAAAGTC 740
Oy 769 CAGTGGGTATCAACATGATGCAATTCAGTACTAGGTAGCGTGTCTTCTTCTT 828
Db 741 TAGCTTGGCTAGTGTGATCACTACGATGATACCCCTCTGCTGTGAACGCTTCTTCT 800
Oy 829 TGATCAATATTTGGACCAACCCATCTCTCACTCCCTCATATGATTTCAACCGAATG 888
Db 801 TGATCACTACTTGAAGCACTACCCATCTATCTCCACATCACTACGATTCACCGAGT 860
Oy 889 ACTGATCAAAAGCGCTTATCAACATGATGAGGATTTGGGTTCTGAAATCGGCT 946
Db 861 ATGGCTTGAAGGAGCTTGGCAACCTGTGACAGAGATGAGGGGTTCAACAAGAT 918

RESULT 11
CK270183 963 bp mRNA linear EST 12-DEC-2003
LOCUS EST716261 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION CK270183
ACCESSION CK270183.1 GI:39827161
VERSION 1
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterids; Lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 963)
Buell, C.R., Hart, A., Ziemann, V., Kazmychewa, S.A. and Baker, B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST716262
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potatocarr@tigr.org
Clones can be requested from TIGR via potatocarr@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..963
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POACR59"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"

/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN
Query Match 26.2%; Score 336.6; DB 14; Length 963;
Best Local Similarity 61.4%; Pred. No. 1.7e-39;
Matches 540; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
Oy 375 TTGATGATGACATGTTGGATGCTGCTCCATTCGCTCTCCACCCGATTTCTTCT 434
Db 3 TGGGTGATGACACCGTTGACCTTATCTTCACTCTGCTGTGGTCCGACTTCTCT 62
Oy 435 TGGAAATATGACACGAGAAATCAACCCCAACAAATTAATCTGATGATGATGATG 494
Db 63 TGGAAATATGATGATGCTGCGCACCACTGAGCTCTCCAGCGATGATGATGCTC 122
Oy 495 TACATTCCTTAACGTAAGTGAAGTGAAGTTATTCGAACCTTCAACATTCACCC 554
Db 123 TTGTGCGCAAGCCAAATCTCAGCTCGAGTATTCAGTACTTAAACATTCACCA 182
Oy 555 GGGGAGTGTCTACCTTGGTGTTCGTTGATCTTGAAGATTTCCGTTATACCTCTTA 614
Db 183 GGGAGGTCCTCTCACTTAACATCAACCTCACTTGGCTGGCGTGTACTGCGCTTC 242
Oy 615 AATATCTGGGCAAGAAATACGAGGAGTTTGCACCACTTGTATCCATGATGCAATT 674
Db 243 AATGATCTGGCAGACCATACGACCGATTTGATGATGATGATGATGATGATGAT 302
Oy 675 TTCAACGATGAGGAGGTTCAAGTTTGTATTCGATTTCCGCTCTGCGTGTATTT 734
Db 303 TACAACAAACGATGAGGCTTCAAGTCTTCTTGTGATGATGATGATGATGATGAT 362
Oy 735 TATGCAATCAAGCTTCTTGTAGCAGCAAAAGGCGAGCTTGGTATCAACATGATGCA 794
Db 363 TATGCTATACCGATTTGCTTATGTAAGATGATGATGATGATGATGATGATGAT 422
Oy 795 ATTCAGTACTAGGTGTAAGGCTGTTCTTGTGATGATGATGATGATGATGATGAT 854
Db 423 GTACCCCTCTGCTGTGTAAGGCTTCTTGTGATGATGATGATGATGATGATGAT 482
Oy 855 CTTCACCTCTCATTTATGATTAACGGAATGGAATGGAATGGAATGGAATGGAATG 914
Db 483 CCATCATTCGACATGATGATTAACGAGGATGAGGATGAGGATGAGGATGAGGAT 542
Oy 915 ATTCATGAGGATTTCCGCTTCTGATGAGGATTTTCCAGAGTTACACACTCACTGCT 974
Db 543 TGTGACAGAGACTATGAGGCTTAAACAGGCTTTCACACATCAACGACACTACGTC 602
Oy 975 TTGATCATTTGATCTCATCACTTCAACATTAATGCAAGAGCAAGAGATGCAATC 1034
Db 603 GTGACACATCTGTTCTCAACATGACCACTAACAGGATGAGGCAACCAAGCAGTC 662

REFERENCE	TITLE	JOURNAL	COMMENT
1035	AAGCAGGTTGGGCGAGTACTATATAAAATCGACAGACTCCAAATTTTCAAGCAATGTAT		
663	AAGCCACTACTCGAGACTACTACCAATTCGATGMAACCCGATTTTCAGGCAATGTGG		
1095	AGAGAGGCTAAGAAATGCATCTACATCGAGCCCGANTAGATAGCAAGCAAAAGTGTG		
723	AGGGAACCTAAAGAGTGTCTCTACGTGAGAAAGACGATCATCTCAAGGCAAAAGTGTG		
1155	TTCTGTATACCAAGATGTATATCAAAAAGGTATATGTCATGCAATGTATGCTTAAATA		
783	TTCTGTATACCAAAACAGCTCTGAAATCTAGAACAGAACTCAGCTTGCTTGAATTTGG		
1215	AGTTGTAACCTTCTCTATTCGGTGTAAATTAATTAATTCAT		
843	TCCTTTGGTATATGTTTGTCTAGCTGTCTTGAGTAATGTAAT		
RESULT 12			
AM201738			
LOCUS			
DEFINITION	AM201738 764 bp mRNA linear EST 02-DEC-2001		
LOCUS	g6f6f08.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: 1253		
DEFINITION	Gm-c1027-1504 5' similar to SW:FB62.SOBIN P48631 OMEGA-6 FATTY ACID		
DEFINITION	DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2 ;, mRNA sequence.		
DEFINITION	AM201738		
DEFINITION	AM201738.1 GI:6482481		
DEFINITION	EST.		
DEFINITION	Glycine max (soybean)		
DEFINITION	Glycine max		
DEFINITION	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.		
DEFINITION	1 (bases 1 to 764)		
DEFINITION	Shoemaker, R., Keim, P., Vodkin, L., Erpelidg, J., Coryell, V., Kama, A., Bolla, B., Maria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, C., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Pape, D., Harey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McMan, R., Waterston, R. and Wilson, R.		
DEFINITION	Public Soybean EST Project		
DEFINITION	Unpublished (1999)		
DEFINITION	Contact: Shoemaker R/ Public Soybean EST Project		
DEFINITION	Public Soybean EST Project		
DEFINITION	Washington University School of Medicine		
DEFINITION	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA		
DEFINITION	Tel: 314 286 1800		
DEFINITION	Fax: 314 286 1810		
DEFINITION	Email: est@wustl.edu		
DEFINITION	This clone is available through: Reegen, Invitrogen Corp. 2130		
DEFINITION	South Memorial Parkway Hunttsville, AL 35801 For further information		
DEFINITION	call: (800)-533-4363 or contact via email: cst@reegen.com		
DEFINITION	Insert Length: 1297 Std Error: 0.00		
DEFINITION	High quality sequence stop: 421.		
DEFINITION	Location/Qualifiers		
DEFINITION	1..764		
DEFINITION	/organism="Glycine max"		
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DEFINITION	/tissue_type="cotyledons of 3- and 7-day-old Williams		
DEFINITION	seedlings"		
DEFINITION	/lab_host="DH10B"		
DEFINITION	/clone_id="Gm-c1027"		
DEFINITION	/note="Vector: pBlueScript II SK+, Site_1: EcoRI, Site_2: XhoI; This cDNA library was constructed from mRNA isolated from cotyledons of 3- and 7-day-old Williams seedlings which were propagated on paper towels with distilled water. The cotyledons were flash-frozen in liquid nitrogen, then lyophilized for 72 hours. Unequal amounts of mRNA was used for cDNA synthesis. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First- stranded synthesis was		

performed with 5'-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An anchor nucleotide (Vea, C, or G) was added to the 3' end of the primer (GAAGAGAGAGAGAGAGAACTAGCTTCGAA(T)18) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500 bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBlue-script (cm) II XR Pre-digested vector (pBlue-script II SK(+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). 97% of the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=30). This library was constructed by Dr. Paul Keim and Dr. Virginia Corryell."

ORIGIN

	Query Match	25.9%	Score 332.2	DB 10	Length 764	
	Best Local Similarity	64.9%	Pred. No. 8,66-39			
	Matches 484	Conservative 0	Mismatches 262	Indels 0	Gaps 0	
Qy	294	TGGTTTGTCAAGCTAGCATCTCCACGGCCCTCGGGTCACTGGTCAAGAAATGTGTGCAC	353			
Db	18	TGGGCTGTGCCAAGGTTCGATCTTACTAGGAATTTGGGTCAATGGCCCATGATGTGGCCAC	77			
Qy	354	CATGCATTTTAGCGACTACCACTTGAATTGATGACATTGTGGATTCTGGTCTCATTTGGCT	413			
Db	78	CATGCATTCAGTGCCTACCACTTGCATGATATTTGTGGCCCTTGTCTTCCACTCCGGT	137			
Qy	414	CTCTGCAACCCGGTATTTCTTTGGAATAATPAGCACAAGAAATTCACACGCCAACACAAT	473			
Db	138	CTCTTAGTCCCATCTTTTCAATGAAATACAGCCATGCCGTACACACTCCAACTGGT	197			
Qy	474	TCACTGCATACGATGAAATTTACATTTCTTAAAGTAAAGTGAAGGTCAAGATTATATTC	533			
Db	198	TCTCTTAGGGGGATGAAAGTATTTGTGCCAAAGCAAGATCTGTATCAATGGTACTCT	257			
Qy	534	AAACTTTTAAACAATCCACCCGGGCGAGTGTTCATTGTGTTTCGTTGACTTTAGGA	593			
Db	258	AAATACCTTAAACAATCTCCAGGAGAGTCTCTCACTCTGTGTGCACCCCTCACACTTGGT	317			
Qy	594	TTTCCGTTAATACCTTAACTAATATCTCCGGGCAAGAAATACGGGAGGTTTGCCAAACAC	653			
Db	318	TGGCCCTTGATCTGGCTTAAATAGTTTCTGGAAGCCCTTATGATAGATTTGCTTGCAC	377			
Qy	654	TTTGATCCCATGATGCCAATTTTCAAGATCGTAAAGCGCTTCAAGTTTGTCTATCCGAT	713			
Db	378	TATGACCCATATGTTCCCATTTTACTCTGATGTGTAAAGCACTTCAAAATATATATCAAGT	437			
Qy	714	TTCCGTCCTTCGCTGATTTTATGCAATCAATCAAGCTTCTTTGAGACGAAAGGGCAGCT	773			
Db	438	GCAGAGTACTTGCAGATGTCTATGAGCCCTTTCCGTCCTGCACATGGCAAAAGGACTTGGC	497			
Qy	774	TGGGTATTCACAATGTACGAAATCTCCAGTACTAGGTGTAACGGTCTTGGTTTGTATC	833			
Db	498	TGATGTGTGTGTGTTATGAGATTCATGTCTATGTGCATTAATGATTTTGGTGTGAT	557			
Qy	834	ACATATTTGACACACACCATCTTCACTCCCTCATTTATGATTAATCAACCGAATGAACTGG	893			
Db	558	ACATTTCTTGACGACTACTCACCCCTGCAATGTGACACTTACACTTCTCTGAGTGGGACTGG	617			
Qy	894	ATCAAAAGCGCTTATCAACATCGATAGAGGATTTCCGGTTCCTGAATCCGGTATTTCAC	953			
Db	618	TTGAGAGAGACTTAGCAACAGTGGATAGAGATTTATGGAGATNCTGAACAGGCTTNNCA	677			
Qy	954	GAGCTTACACACTCACTACGCTTTCGATCATTTGATCTCATACATTTCCACATTTATATGCA	1011			

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; asterids, campanulids; Asterales; Asteraceae; Asteroideae; Heliantheae; Helianthus.

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	(bases 1 to 616)			
1	Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison, P., Kolman, J., Stabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L., and Bradford, K.	Letuce and Sunflower ESTs from the Composite Genome Project	http://compgenomics.ucdavis.edu/	
1	Unpublished (2002)			
1	Contact: Alexander Kozik [R.W.Michelmore]			
1	Department of Vegetable Crops, R.W.Michelmore Lab			
1	University of California at Davis (UCD)			
1	Asmundson Hall, UCD, Davis, CA 95616, USA			
1	Tel: 1-(530)-742-1742			
1	Fax: 1-(530)-752-9659			
1	Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]			
1	belongs to contig OH_Ca_Confl31889, see http://cgpdb.ucdavis.edu/			
1	for details.			
1	Plate: QH14 row: E column: 14.			
1	Location/Qualifiers			
1	1. 616			
1	/organism="Helianthus annuus"			
1	/mol_type="rRNA"			
1	/culivar="RHA801"			
1	/db_xref="taxon:4232"			
1	/clone="QH14B14"			
1	/lab_host="E.coli"			
1	/clone_lib="QH ABCDI sunflower RHA801"			
1	/note="Vector: pBRCDNA5f1AB; The library was constructed			
1	from 11 different sources of RNA from a single genotype.			
1	Separate cDNAs were generated using primers that			
1	incorporated unique 5' and 3' tags to distinguish each			
1	source of RNA. cDNAs were then pooled, size-fractionated,			
1	directionally cloned into a custom medium-copy vector and			
1	transformations made with four size classes to minimize			
1	size bias. Details of each source of RNA and library			
1	construction can be obtained at http://cgpdb.ucdavis.edu/			
1	TAG_SEQ=Not found"			
1	ORIGIN			
1	Query Match	25.7%; Score 330; DB 13; Length 616;		
1	Best Local Similarity	83.5%; Pred. No. 2e-38;		
1	Matches	386; Conservative 0; Mismatches 75; Indels 1; Gaps 1		
1	718	GTCCTCGCTGATTTTATGCAATCAAGCTCTTGAGACAAAGGCGAGCTGGG	777	
1	616	GTTTCTCGTAAAGTTTACGACATCAAGCTTCTTGAGCATCAAAAGGGTTGCTGGG	557	
1	778	TAAATCAATGTAACCAATTCAGACTAGTAGTAAAGCGTGTCTTGTTGATCAAT	837	
1	556	TAAATCAATGTAATGAGAGTTCCTCGTAAAGGTAAGTGTCTTGTTGATCAAT	497	
1	838	ATTTCACACACCACTCTCTCACTCCCTCATTTAGATTCAACCGAATGGAAC-TGATC	896	
1	496	ATTTCACACCCCCCATCTCTCGTTACCTATTAGATTCAACCGAATGGAATCTGGATC	437	
1	897	AAAGCGCGCTTATCAACATCGATGAGGGATTCGGGTTCTGAAATCGGGTTTCCACGAC	956	
1	436	AAAGGGGCTTATTGACATTCATGAGACTTCGGGTTCTTAAACAGGGTTTAACTGAC	377	
1	957	GTTACACACACTCAAGCTCTTGATCATTTGATCTGATACATTTCAACATTTATGCAAG	1014	
1	376	GTTACACATTAACGACGTCCTGATCATTTGATTTGATTCATTCACATTTATGCAAG	317	
1	1017	GAAAGCAAGGATGCAATCAAGCAAGTGTGGGCGAGTACTATAAATGCAAGAGTCCA	1074	
1	316	GAGGCAAGAGAGCAATCAAGCAAGCTGTGGGTGAGTATTATAAGTGCATGAGACCCG	257	
1	1077	ATTTTCAAGCAATATATAGAGGCTAAGAGATCATCTGATCGAGCCCATGAGAT	1133	
1	256	ATTTTCAAGCGATGTGAGAGAGGCGAAGAGATGATTTTCAATTTGAGCCGATGAGAT	197	
1	1137	AGCGAGCAAAAGGTGTGTTCTGGTACCAAGATGTAATCA	1178	

RESULT 15	CF511517	831 bp	mRNA	linear	EST 09-SEP-2003
LOCUS	CF511517				
DEFINITION	Cabud0002.11R.E01 Vitis vinifera cv. cabernet sauvignon (Clone 8)				
ACCESSION	CF511517				
VERSION	CF511517.1	GI:34543265			
KEYWORDS	EST.				
SOURCE	Vitis vinifera				
ORGANISM	Vitis vinifera				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.				
AUTHORS	1 (bases 1 to 831)				
TITLE	Goed da Silva, P., Jandolino, A., Lim, H., Baek, J., Jones, K. and Cook, D.				
JOURNAL	Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages				
COMMENT	Unpublished (2003)				
CONTACT	Contact: Douglas Cook, PhD				
CAES	CAES Genome Facility				
UC Davis	UC Davis, Plant Pathology				
One Shields Ave, Davis, CA 95616, USA					
Tel: 530 754 6561					
Fax: 530 754 6617					
Email: drcoc@ucdavis.edu					
Seq primer: GCCAACGATGCTCTAG.					
FEATURES	Location/Qualifiers				
source	1..831				
	/organism="Vitis vinifera"				
	/mol type="mRNA"				
	/cultivar="Cabernet Sauvignon (Clone 8)"				
	/db xref="taxon:29760"				
	/clone="Cabud0002.11R_E01"				
	/sex="Hermaphrodite"				
	/dev stage="Pre-bloom (10-11 days before bloom)"				
	/lab host="DH5alpha"				
	/clone_id="Vitis vinifera cv. cabernet sauvignon (Clone 8) Bud - CABUD"				
	/note="Organ: Bud; Vector: pDR; Site 1: SfiI; Site 2: SfiI; CABUD is a cDNA library of Vitis vinifera cv. cabernet sauvignon. Clone 8 dissected buds. Samples were collected May 13, 2002 from pre-bloom plants (10-11 days before bloom), pre-veraison. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:				
	5'-ATTGATGAGTCCAGCGGAGATGCGCATTCAGCGCGG-3' and				
	5'-ATTCAGAGTCCAGCGGCGGCGGAGTGG-3' (30'NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."				
ORIGIN					
Query Match	25.7%	Score 329.8;	DB 14;	Length 831;	
Best Local Similarity	64.5%	Prod. No. 1.8e-38;			
Matches 509;	Conservative 0;	Mismatches 277;	Indels 3;	Gaps 1	
390	GTGGATTCGAGTCCATTGGGCTCTCTCAACCCCGATTTCTCTTGGAAATATAGCCAC	449			
1	GTGGCCTCATCTCAATCTCTCTCTCTTGTACTTCTCTCTCTGAAATATATGCCAT	60			
450	AGGATCCACGACGCCACACAATTCATCTGCATTAAGATGAAGTTTACATTTCTAAAGT	509			
61	CGCGGCATCATTTGTAATATACCGGTTCCCTCGAAGAAAGATGAAGTTTGTGCCCAAAAC	120			
510	AAATTCGAAGTCAAGATTATTTCCAAATCTTTTAAACATTCACCCGGCGAGTGTCTACT	569			
121	AAATTCGAAGTCAAGTGTACTTCCAAATATTCGAAACATTCACCTTGTGTCATTCATCA	180			

QY 570 TTGGTGTTCGGTTCAGTTAGATTTCGGTATACCTTTAATAATATCTCGGCAAG 629
 Db 181 CTCACCAATTCAACACACTCTAGGCTGGCTTTGTATCTAATGTTCACGTTTCAGGCAAG 240
 QY 630 AATAACGGGAGGTTTGGCAACCACTTTGATCCCATGAGTCCAAATTTTCAACGATGTGAA 689
 Db 241 CGCTACAGTATGATTTGCTTGGCACTTTGATCCCAATGTCCAATTTACTCAGATGTGAG 300
 QY 690 CGCGTTCAAGTTTGTATCCGATTTGGTCTTCGCTGATTTTATGCAATCAAGCTT 749
 Db 301 CGACTGCAGATATACATTTACAGATGCTGTGTTCTTGCATCACTATGACTTTACCGT 360
 QY 750 CTTGTAGCAGCAAAAGGGCAGCTTGGTAAATCAATGTACGCAATTCAGTACTAGGT 809
 Db 361 CTTGCAAGTATCAAAAGGCTCACAATGGTCTTGTGTGTTATGATGTCCCTGTGATTT 420
 QY 810 GTAAAGCGTGTCTTGCTTTGATCAATATTTGACACACACCCATCTCTCACTCCGTAT 869
 Db 421 GTGATGGATTTCTGTGCTGATTAAGTATTTGACGATACCCACCGCTCTCTGCCACAC 480
 QY 870 TATGATTCACCGAATGGAATGATCAAGGCGCTTATCAACATGATAGGATTTT 929
 Db 481 TATGATTCCTGTAGTGGACTGTGAGAGAGGCTTTGGCCACCATGATAGACTAT 540
 QY 930 GGGTTCCTGAATCGGCTTTTCCAGCAGTTCACACACTCAAGTCTTCATCATTTGATC 989
 Db 541 GGAATTCCTTAACAGGTTTTCATATTAACGATATCTCATGTGGCACACATTTGTTT 600
 QY 990 TCATACATTCACATTCATTCATGCAAAAGGACAAAGGATGCAATCAAGCCAGTGTGGGC 1049
 Db 601 TCAACATTCGCGCATTTATCATGCAATGAGGCTACAAAGGCCATTAAGCCAGTATTAGA 660
 QY 1050 GAGTACTATATAATCGACAGACTCCCAATTTTCAAGCAATGTATAGAGGCTTAAGAA 1109
 Db 661 GATTATATATCATGTTGATGAGACTTCATTTTACAAAGCAATGTGAAAGAGGCAAAAGAG 720
 QY 1110 TGCATCTACATCGAGCCGATGAGATAGCAGCAAAAGGTGTGTTCTGTACCAACAAG 1169
 Db 721 TGTGTCTATGTCCAGTGGATGTGA---CAAGGCAAAAGGTGTTTCTGTGTACCAAGAT 777
 QY 1170 ATGTAAATCA 1178
 Db 778 AAGTTTGA 786

Search completed: June 23, 2004, 14:43:21
 Job time : 2561 secs

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Qy 301 RVEHDVTHVHLHLISYIPHYHAKERDAIKPVIGEYKIDRTPIFKAMTREACECIYI 360
Db 299 SVLHDVTHVHMLHLSYIPHYHAKERDAINTVLGDPYKIDRTPIFKAMTREACECIPI 358
Qy 361 EPDESEHKGVFWYHKK 376
Db 359 EPEKRESKGVWYHKK 374

RESULT 2

US-09-059-769-4
Sequence 4, Application US/09059769
Patent No. 6329518
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lemman, Marit
APPLICANT: Stymer, Sten
TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-769-4

Query Match 78.1%; Score 1598.5; DB 4; Length 374;

Best Local Similarity 75.7%; Pred. No. 1e-160; Mismatches 46; Indels 5; Gaps 3;

Matches 286; Conservative 41; Mismatches 46; Indels 5; Gaps 3;

Qy 1 MGAGRMSDPSEGNILKRLVDP-PFTLSDLKKAIPHCERSYIRSSYYVHDLIYAY 59
Db 1 MGAGR--GRTSEKSVMERVSVDVPTFSLDKKAIPHCGRSVIRSSYYVQDLIYAY 58
Qy 60 VFYLIANTYIPLIPPLAYLAMPVYVFCOASITLGLMWIGHGCHHAFSDQLDIIYGF 119

Db 59 IFFYLIANTYIPLNHLPLAYLAMPVYVFCOASVLTGLMWIGHGCHHAFSNTWDDIYGF 118
Qy 120 VHSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKYKYSKLNNPGSVFTLVF 179
Db 119 IHSFLLTPYFSWKYSHRNHNSNTSIDNDEVYIPKRSKYKRIYKLLNPGSLVLVI 178
Qy 180 RLITGFPYLYLTNLSGKKYGFANHPDMSEIFNDRERVOYLLSDFGILAVFYAKLIVA 239
Db 179 MFTLGFPYLYLTNLSGKKYGRFANHPDMSEIFKEREFOVFLSDGLAVFYGIKAVA 238
Qy 240 AKGAWYINWYAIVLGVSVEFLITYLHHTLSLPHYDSTERNMIGALSTIORDFGFL 299
Db 239 NKGAWYACMGVVLGVTFEVDYITFLHTHSSPHYDSTERNMIGALSAIRDREGL 298
Qy 300 NRVEHDVTHVHLHLISYIPHYHAKERDAIKPVIGEYKIDRTPIFKAMTREACECIY 359
Db 299 NSVHDVTHVHMLHLSYIPHYHAKERDAIKPILGDFYVIDRTPIFKAMWREGRECMY 358
Qy 360 IEPDESEHKGVFWYHKK 377
Db 359 IEP--DSKLGKVWYHKK 374

RESULT 3

US-09-059-769-2
Sequence 2, Application US/09059769
Patent No. 6329518
GENERAL INFORMATION:
APPLICANT: Green, Allan
APPLICANT: Singh, Surinder
APPLICANT: Lemman, Marit
APPLICANT: Stymer, Sten
TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,769
FILING DATE: April 14, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06223
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU P06226
FILING DATE: 15-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/043706
FILING DATE: 16-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/050403
FILING DATE: 20-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 374 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-059-769-2

Query Match 77.7%; Score 1589.5; DB 4; Length 374;
Best Local Similarity 75.4%; Pred. No. 9e-160;
Matches 285; Conservative 40; Mismatches 48; Indels 5; Gaps 3;

QY 1 MGAGGRMSDPEGKILERVVD-P-PTLSDLKKAIPHCERSVIRSSYVVHDLIYAY 59
DB 1 MGAGGR--GRISKSVMKRSVDPVTFSLSELKQAIIPHCFORSVIRSSYVVODLIYAY 58
QY 60 VFYLYANTYIPLIPTPLAYLAMPVYVFCQASILTGLAWIGHCGHNAFSDYOLIDIYGF 119
DB 59 IFYLYANTYIPTLPTSLAYLAMPVYVFCQASVLTGLAWIGHCGHNAFSDYOLIDIYGF 118
QY 120 VLHSAFLTPTYSKMSKSHRNHANTNSLNDDEVYIPKRSKVKIYSKLANNPGRVFTLVF 179
DB 119 ILHSAFLTPTYSKMSKSHRNHANTNSLNDDEVYIPKRSKVKIYSKLANNPGRVFTLVF 178
QY 180 RLITGFPLIYLTNTSGKKYGRFANHPDMSPIFENDREVOVLSDGLAVFYAKLVA 239
DB 179 MPTLGFPLIYLTNTSGKKYGRFANHPDMSPIFENDREVOVLSDGLAVFYAKLVA 238
QY 240 AKGAWVINYAIIVLAGVVFVLTLYLHTHLSLPHYDSTEMWIKGALSTIDRDFGL 299
DB 239 NKGAAWVACVGVVLAGVFTFVDVITPLHHTHOSPHDSTEMWIKGALSAIDRDFGL 298
QY 300 NRVDVHTHTVYHLHLSIIPHYNAKEARDAIKPVLAGYIKIDRTPIFKAMYREKECIY 359
DB 299 NSVDVHTHTVYHLHLSIIPHYNAKEARDAIKPVLAGYIKIDRTPIFKAMYREKECIY 358
QY 360 IEPDESEKGVFWYHKM 377
DB 359 IEP--DSKLGKGYWYHKL 374

RESULT 4

US-08-872-302-4
Sequence 4, Application US/08872302
Patent No. 5846784

GENERAL INFORMATION:
APPLICANT: Hitz, William D
TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
TITLE OF INVENTION: Developing Seeds of Vernonia galamensis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. duPont de Nemours and Co.
STREET: 1007 Market Street
CITY: Wilmington
STATE: Delaware
COUNTRY: USA
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872.302
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Majarian, William R
REGISTRATION NUMBER: P-41,173
REFERENCE/DOCKET NUMBER: BB-1084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4926
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-872-302-4

Query Match 77.1%; Score 1578.5; DB 2; Length 384;
Best Local Similarity 76.5%; Pred. No. 1.4e-158;
Matches 280; Conservative 39; Mismatches 44; Indels 3; Gaps 2;

QY 15 NILSRVPVD--PEPTLSDLKKAIPHCERSVIRSSYVVHDLIYAVFYLYANTYIPLIP 73
DB 19 NINEAPVDAAPFSLSDLKKAIPHCERSVIRSSYVVHDLIYAVFYLYANTYIPLIP 78
QY 74 TPLAYLAMPVYVFCQASILTGLAWIGHCGHNAFSDYOLIDIYGFVLHSAFLTPTYSK 133
DB 79 PPLAYLAMPVYVFCQASILTGLAWIGHCGHNAFSDYOLIDIYGFVLHSAFLTPTYSK 138
QY 134 YSHRNHANTNSLNDDEVYIPKRSKVKIYS--KLANNPGRVFTLVRLITGFPLIYLT 191
DB 139 YSHRNHANTNSLNDDEVYIPKRSKVKIYS--KLANNPGRVFTLVRLITGFPLIYLT 198
QY 192 NISGKKYGRFANHPDMSPIFENDREVOVLSDGLAVFYAKLVAKGAWVINYA 251
DB 199 NISGKKYGRFANHPDMSPIFENDREVOVLSDGLAVFYAKLVAKGAWVINYA 258
QY 252 IIVLAGVVFVLTLYLHTHLSLPHYDSTEMWIKGALSTIDRDFGLNRFVHTV 311
DB 259 APVGLANAFIMITYLHHTHLSLPHYDSTEMWIKGALSTIDRDFGLNRFVHTV 318
QY 312 LHLHLSIIPHYNAKEARDAIKPVLAGYIKIDRTPIFKAMYREKECIYEPDESEKGV 371
DB 319 LHLHLSIIPHYNAKEARDAIKPVLAGYIKIDRTPIFKAMYREKECIYEPDESEKGV 378
QY 372 FWYHKM 377
DB 379 YWYHKM 384

RESULT 5

US-09-638-937-15
Sequence 15, Application US/09638937
Patent No. 6593514

GENERAL INFORMATION:
APPLICANT: Cahoon, Edgar B
APPLICANT: Hitz, William D
APPLICANT: Ripp, Kevin G
TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF CALENDIC ACID, AN UNUSUAL
TITLE OF INVENTION: FATTY ACID CONTAINING DELTA-8,10,12 CONJUGATED DOUBLE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/638.937
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: BB-1371-P1
PRIOR FILING DATE: 1999-08-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Microsoft Office 97
SEQ ID NO 15
LENGTH: 383
TYPE: PRT
ORGANISM: Borago officinalis
US-09-638-937-15
Query Match 68.2%; Score 1396.5; DB 4; Length 383;
Best Local Similarity 63.9%; Pred. No. 2.6e-139;
Matches 242; Conservative 62; Mismatches 70; Indels 5; Gaps 2;

[illegible]

RESULT 10
US-08-675-650B-2
; Sequence 2, Application US/08675650B
; Patent No. 5850026

```

GENERAL INFORMATION:
APPLICANT: DeBonte, L. et al.
TITLE OF INVENTION: CANOLA OIL HAVING INCREASED OLEIC ACID AND
TITLE OF INVENTION: DECREASED LINOLENIC ACID CONTENT
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C., P.A.
STREET: 60 South Sixth Street, Suite 3300
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,650B
FILING DATE: 03-JUL-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Lundquist, Ronald C.
REGISTRATION NUMBER: 37,875
REFERENCE/DOCKET NUMBER: 07148/042001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/335-5070
TELEFAX: 612/288-9696
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

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Query Match	64.4%	Score 1318;	DB 2;	length 384;
Best Local Similarity	61.2%;	Pred. No. 5.2e-131;		
Matches 253;	Conservative 61;	Mismatches 81;	Indels 6;	Gaps 4;

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Qy      1  MGAAGGMM--SDSSEGG--NIIERVAVD--PPTLSLDKKAIPTHCFFERSVIRSSYYVHDL    55
Db      1  MGAAGGMMQVSPSSKSESDTITKRVPCEHPPTVGEIKKAIIPHCFFKSIIPRSFSYLMDI    60

Qy      56  IYAVVYUANTYITPLIPPLAYLAMPVYWFQASILTGLVWIGHCGGHAFFSDYOLIDD    115
Db      61  IIASCYVAYATYFELLPHPLSYFAMPPLMYACOGCVLGLGVWVIAHECGGHAFFSDYQWLDD    120

Qy      116  IYGFVYHSLTLIPYFSWKYSHRNHNAANNSILDNEVYIPIKSKKYKYSYKLLNPPGRVF    175
Db      121  TVGLIRHSEGLVLPVYFSWKYSHRNHNSNGSLERDVPAPKKKSDIKMYGKYLNNPLGRIV    180

Qy      176  TVYFRLTLGFPYLLTLNIGSKKY--GRFANHFDPMSPIFNDRERQVULSDFGLLAYFAL    234
Db      181  MLTVQGTLLGPELXLLENVSGRPYDGGFACHHNPAPINDBERQIYISDAGILAVCYGL    240

Qy      235  KLLVAAGAAWYINMYAIPVLGVSVEFVLYITLYLHHHTLSLPHDYSTEMWNIKGAISTIDR    294
Db      241  FRVAAAGVAAWSCFYGVPLILVNGFLVLIITLYLQHTPSSLPHDYSSSEMDWIRGALATVDR    300

Qy      295  DGGFLARVHDVTHVYVLAHLISYIPHNAGKARDALKPVLGEYTKIDRPIPRAMWREA    354
Db      301  DYGLINKVPHNITDTHVAHHLFSTMPHYAMEATKAIKPIIGEYFQDGPVPAWAMREA    360

Qy      355  KECIYIEPDDESEHKGVFWYH    375
Db      361  KECIYIEPDDESEHKGVFWYH    381

```

RESULT 11
US-09-354-231B-14
; Sequence 14, Application US/09354231B
; Patent No. 6342658
; Grant of INVENTION

```

? GENERAL INFORMATION:
? APPLICANT: Debonte, Lorin R.
? APPLICANT: Shorrock, Basil S.
? TITLE OF INVENTION: FATY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
? FILE REFERENCE: 07148-063002
? CURRENT APPLICATION NUMBER: US/09/354,231B
? CURRENT FILING DATE: 1999-07-16
? PRIOR APPLICATION NUMBER: US 08/874,109
? PRIOR FILING DATE: 1997-06-12
? NUMBER OF SEQ ID NOS: 69
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 14
? LENGTH: 384
? TYPE: PR1
? ORGANISM: Brassica napus
? US-09-354-231B-14

```

Query Match	64.4%	Score 1318	DB 4	Length 384
Best Local Similarity	61.2%	Pred. No. 5.2e-131		
Matches 233; Conservative	61;	Mismatches 81;	Indels 6;	Gaps 4;

Qy	1	MAAGGMM--SDSEGG--NIIERVAVD--PPTSLDLSKKAIPTHCFEESVIRSSYYVHDL	55
		: : : : :	
Db	1	MGAGGMQVSPSSKSETDITIKRVPCENPPFVGBLTKAIIPPHCFKKSIPRSFSYLIWDI	60
Qy		: : : : :	
Db		: : : : :	
Qy	56	IVAVVYXYLANNYIPIIPPELAIYLAWPYVWQASIIITGLVATGHEGHHAFSPYQIID	115
		: : : : :	
Db	61	IISCFTYATYITFPLPPLPISITPMALYMAQCGVLGAVVIAHCGHNAFSYQIWD	120
Qy		: : : : :	
Db		: : : : :	
Qy	116	IVGFVLHSAALLTPYSGWKYSHRNHHNANNSLDNDEVYIIPKRSKVKIYSLKLNPPGRV	175
		: : : : :	
Db	121	TVGLIITFHSFLIAPYFESWKYSHRRHNSNGSLERDEVIPPKKSDIKIYWGXTLNPPERTV	180
Qy	176	TVLFRLLTGPPIYLITLNISGKKY--GRPNHNPDPSPFINDERIQVQLSDPGLLAVERAI	234
		: : : : :	
Db	181	MLTVQGTLLQWPIILANVSGRPYDGGFACHHPNAPFINDERIQIYISDGLIAYCYL	244
Qy		: : : : :	
Db		: : : : :	
Qy	235	KLLVAAKGAAMVIMNIAIPVLGVSPFVLITLYLHHHTLSLPHDYSTEMNMIKGLSLTDR	294
		: : : : :	
Db		: : : : :	

Db 241 FRVAAAGVASMCFYGVPLIYNGFLVLYLQHTHESLPHYDSSEMDWIRGALATVDR 300
 Qy 295 DFGFLNPFVDVTHVTHLHLISYIPHYHAKAARDAPKVLGEYKIDRPIFRAMYREA 354
 Db 301 DYGILNPFVFNHTIDTHVAHHLFSTMPHYHAKAATKALPIIGEYQDPGTIVVAKMREA 360
 Qy 355 KECIYIEPDEDESEHKGVFWYH 375
 Db 361 KECIYIEPDRQGEKKGVFWYN 381

RESULT 12
 US-09-128-602B-14
 ; Sequence 14, Application US/09128602B
 ; Patent No. 6414223
 ; GENERAL INFORMATION:
 ; APPLICANT: Kodali, Dharm
 ; APPLICANT: Fan, Zhongong
 ; APPLICANT: Debonte, Lorin R.
 ; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
 ; FILE REFERENCE: 07148-072001
 ; CURRENT APPLICATION NUMBER: US/09/128,602B
 ; CURRENT FILING DATE: 1998-08-03
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 384
 ; TYPE: PRT
 ; ORGANISM: Braessica napus
 US-09-128-602B-14

Query Match 64.4%; Score 1318; DB 4; Length 384;
 Best Local Similarity 61.2%; Pred. No. 5.2e-131;
 Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;
 Qy 1 MGAGRM--SDPSEK--NILERVPVD--PPTLSDLKKAIPTHCFERSVIRSSYYVHDL 55
 Db 1 MGAGRMQVSPSPKSESTDRIKVPCEPTPTVVELKKAIPHCFSKISIPRSFYLWDI 60
 Qy 56 IVAVFFYLLANTYIPLIPTPLAYLAMPVYVFCQASILTGLMWIGHEGCHAFSDYQILD 115
 Db 61 IASCFFYVATYTPPLPHPLSYFAMPVLYMACQCVLTGVVIAHEGCHAFSDYQWLD 120
 Qy 116 IVGFVLSALTTPFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKLLNPPGVF 175
 Db 121 TVGLIFHSFLVLPFSKYSIRRHNSNTGSLERDEVFPKKSIDIKMYGKILNPLGRTV 180
 Qy 176 TLVRLTLGFPYLLTLNIGSKY--GRFANHPDPMSPFNDREVOVLLSDFLAVFYAI 234
 Db 181 MLTVQFLGMPLYLAFVNSGRPYDGFACHFHPAIPYNDRELOIYISDAGILAVCYGL 240
 Qy 235 KLVAAAGAAVIMVYAPVGVSVFVLYLTHLHLSLPHYSTENWIKALSTIDR 294
 Db 241 FRVAAAGVASMCFYGVPLIYNGFLVLYLQHTHESLPHYDSSEMDWIRGALATVDR 300
 Qy 295 DFGFLNPFVDVTHVTHLHLISYIPHYHAKAARDAPKVLGEYKIDRPIFRAMYREA 354
 Db 301 DYGILNPFVFNHTIDTHVAHHLFSTMPHYHAKAATKALPIIGEYQDPGTIVVAKMREA 360
 Qy 355 KECIYIEPDEDESEHKGVFWYH 375
 Db 361 KECIYIEPDRQGEKKGVFWYN 381

RESULT 13
 US-09-995-297-14
 ; Sequence 14, Application US/0995297
 ; Patent No. 6649782
 ; GENERAL INFORMATION:
 ; APPLICANT: Kodali, Dharm
 ; APPLICANT: Fan, Zhongong
 ; APPLICANT: Debonte, Lorin R.

; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
 ; FILE REFERENCE: 07148-072002
 ; CURRENT APPLICATION NUMBER: US/09/995,297
 ; CURRENT FILING DATE: 2001-11-27
 ; PRIOR APPLICATION NUMBER: US 09/128,602
 ; PRIOR FILING DATE: 1998-08-03
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 14
 ; LENGTH: 384
 ; TYPE: PRT
 ; ORGANISM: Braessica napus
 US-09-995-297-14

Query Match 64.4%; Score 1318; DB 4; Length 384;
 Best Local Similarity 61.2%; Pred. No. 5.2e-131;
 Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;
 Qy 1 MGAGRM--SDPSEK--NILERVPVD--PPTLSDLKKAIPTHCFERSVIRSSYYVHDL 55
 Db 1 MGAGRMQVSPSPKSESTDRIKVPCEPTPTVVELKKAIPHCFSKISIPRSFYLWDI 60
 Qy 56 IVAVFFYLLANTYIPLIPTPLAYLAMPVYVFCQASILTGLMWIGHEGCHAFSDYQILD 115
 Db 61 IASCFFYVATYTPPLPHPLSYFAMPVLYMACQCVLTGVVIAHEGCHAFSDYQWLD 120
 Qy 116 IVGFVLSALTTPFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKLLNPPGVF 175
 Db 121 TVGLIFHSFLVLPFSKYSIRRHNSNTGSLERDEVFPKKSIDIKMYGKILNPLGRTV 180
 Qy 176 TLVRLTLGFPYLLTLNIGSKY--GRFANHPDPMSPFNDREVOVLLSDFLAVFYAI 234
 Db 181 MLTVQFLGMPLYLAFVNSGRPYDGFACHFHPAIPYNDRELOIYISDAGILAVCYGL 240
 Qy 235 KLVAAAGAAVIMVYAPVGVSVFVLYLTHLHLSLPHYSTENWIKALSTIDR 294
 Db 241 FRVAAAGVASMCFYGVPLIYNGFLVLYLQHTHESLPHYDSSEMDWIRGALATVDR 300
 Qy 295 DFGFLNPFVDVTHVTHLHLISYIPHYHAKAARDAPKVLGEYKIDRPIFRAMYREA 354
 Db 301 DYGILNPFVFNHTIDTHVAHHLFSTMPHYHAKAATKALPIIGEYQDPGTIVVAKMREA 360
 Qy 355 KECIYIEPDEDESEHKGVFWYH 375
 Db 361 KECIYIEPDRQGEKKGVFWYN 381

RESULT 14
 US-09-354-231B-10
 ; Sequence 10, Application US/09354231B
 ; Patent No. 6342658
 ; GENERAL INFORMATION:
 ; APPLICANT: Debonte, Lorin R.
 ; APPLICANT: Shorosh, Babil S.
 ; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
 ; FILE REFERENCE: 07148-063002
 ; CURRENT APPLICATION NUMBER: US/09/354,231B
 ; CURRENT FILING DATE: 1999-07-16
 ; PRIOR APPLICATION NUMBER: US 08/874,109
 ; PRIOR FILING DATE: 1997-06-12
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 384
 ; TYPE: PRT
 ; ORGANISM: Braessica napus
 US-09-354-231B-10

Query Match 64.3%; Score 1317; DB 4; Length 384;
 Best Local Similarity 61.3%; Pred. No. 6.7e-131;
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;

QY 1 MGAGRM-----SDPSGKNILERVVD-PPFTSLDKKALPTCFERSVIRSSYYVHD 54
 DB 1 MGAGRMQVSPSPSKSETDNI-KRVPCEPPTVGEELKALPPhCFKRSIPRSPSYLIMD 59
 QY 55 LIVAVFPLYANTYIPLIPPLAYLAMPVWFCOASITGLMVGHEGCHHAFSDYOLID 114
 DB 60 IILASCFTYVATTYFPPLPPLPPLSTFAMPLWACQCVLTGAVLWLAHEGCHHAFSDYOLID 119
 QY 115 DIVGFVLSALLTPYFWSKYSHRHMHANTNSLDNDEVYIPRKSQVLYSLNNPGRV 174
 DB 120 DTGGLIFHSFLVYFWSKYSHRHMHANTNSLERNDEVFVPRKKSQVLYSLNNPGRV 179
 QY 175 FTLYVRLTLGFPPLYLTLNLSGKTY-GRPANFDPMSPIFNDRERQVLLSPGLLAVFYA 233
 DB 180 VMLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHNPAPYNDRERLQIYISDAGILAVCYG 239
 QY 234 IKLLVAAKGAAMVNTMTALPVLAGSVFPLVLTLYLHHTLSLPHYDSTEMNIIKGLSTID 293
 DB 240 LYRYAAVQGVASWCFYGVPLLVNGFLVLTLYLQHTPSSLPHDSSMDWLRGLATVD 299
 QY 294 RDPFGLNRVFDVTHVTLHHLISYIPHYAKKARDAIKPVLAGSYKIDRTPIFKAMYRE 353
 DB 300 RDYGLLNKVFNNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEEYQDGTPIVYKAMWRE 359
 QY 354 AKECIYIEPDEDSHKGVFWYH 375
 DB 360 AKECIYVEPDRGEGKGVFWYH 381

RESULT 15

US-09-133-962A-4
 Sequence 4, Application US/09133962A
 Patent No. 6372965

GENERAL INFORMATION:

APPLICANT: JOHN JOSEPH OXLEY

TITLE OF INVENTION: GENES FOR MITOCHONDRIAL FATY ACID

DELTA-12 DESATURASES AND RELATED

ENZYMES FROM PLANTS

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESS: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: UNITED STATES OF AMERICA

ZIP: 19898

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.50 INCH

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95

SOFTWARE: MICROSOFT WORD VERSION 7.0A

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/133,962A

FILING DATE: 14-Aug-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. 07/977,339

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: CHRISTENBURY, LYNN M.

REGISTRATION NUMBER: 30,971

REFERENCE/DOCKET NUMBER: BB-1043-D

TELECOMMUNICATION INFORMATION:

TELEPHONE: (302)992-5481

TELEFAX: (302)773-0164

TELEX: 835420

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 384 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-133-962A-4

Query Match

Best Local Similarity 64.3%; Score 1317; DB 4; Length 384;
 Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;

QY 1 MGAGRM-----SDPSGKNILERVVD-PPFTSLDKKALPTCFERSVIRSSYYVHD 54
 DB 1 MGAGRMQVSPSPSKSETDNI-KRVPCEPPTVGEELKALPPhCFKRSIPRSPSYLIMD 59
 QY 55 LIVAVFPLYANTYIPLIPPLAYLAMPVWFCOASITGLMVGHEGCHHAFSDYOLID 114
 DB 60 IILASCFTYVATTYFPPLPPLPPLSTFAMPLWACQCVLTGAVLWLAHEGCHHAFSDYOLID 119
 QY 115 DIVGFVLSALLTPYFWSKYSHRHMHANTNSLDNDEVYIPRKSQVLYSLNNPGRV 174
 DB 120 DTGGLIFHSFLVYFWSKYSHRHMHANTNSLERNDEVFVPRKKSQVLYSLNNPGRV 179
 QY 175 FTLYVRLTLGFPPLYLTLNLSGKTY-GRPANFDPMSPIFNDRERQVLLSPGLLAVFYA 233
 DB 180 VMLTVQFTLGWPLYLAFNVSGRPYDGGFACHFHNPAPYNDRERLQIYISDAGILAVCYG 239
 QY 234 IKLLVAAKGAAMVNTMTALPVLAGSVFPLVLTLYLHHTLSLPHYDSTEMNIIKGLSTID 293
 DB 240 LYRYAAVQGVASWCFYGVPLLVNGFLVLTLYLQHTPSSLPHDSSMDWLRGLATVD 299
 QY 294 RDPFGLNRVFDVTHVTLHHLISYIPHYAKKARDAIKPVLAGSYKIDRTPIFKAMYRE 353
 DB 300 RDYGLLNKVFNNITDTHVAHHLFSTMPHYHAMEATKAIKPILGEEYQDGTPIVYKAMWRE 359
 QY 354 AKECIYIEPDEDSHKGVFWYH 375
 DB 360 AKECIYVEPDRGEGKGVFWYH 381

Search completed: June 18, 2004, 17:39:02

Job time : 24 secs

Result No.	Query			ID	Description
	Score	Match Length	DB		
1	1633.5	79.8	364	US-09-981-124-20	Sequence 20, Appl
2	1592	77.8	372	US-09-981-124-4	Sequence 4, Appl
3	1589.2	77.7	374	US-09-981-124-2	Sequence 2, Appl
4	136.5	68.2	383	US-10-464-631-15	Sequence 15, Appl
5	1356.5	66.3	383	US-10-424-599-266787	Sequence 266787,
6	1356.5	66.3	385	US-10-425-114-40643	Sequence 40643,
7	1348.5	65.9	382	US-09-981-124-12	Sequence 12, Appl
8	1346.5	65.8	392	US-10-425-114-56017	Sequence 56017,
9	1332.5	65.1	383	US-09-837-751-6	Sequence 6, Appl
10	1325.5	64.8	383	US-09-837-751-31	Sequence 31, Appl
11	1333.5	64.7	383	US-09-852-999-4	Sequence 4, Appl
12	1318	64.4	384	US-09-995-297-14	Sequence 14, Appl
13	1318	64.4	384	US-09-771-904-14	Sequence 14, Appl
14	1318	64.4	384	US-10-715-100-10	Sequence 10, Appl
15	1317	64.3	384	US-09-995-297-10	Sequence 10, Appl

QY 1 MGAGGRMSDPEG-KNILERVPVD-PPFTLSDLKKAIPTHCFERSVIRSSYYVHDLIVA 58

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QY      1 MGAGGRMSDSEEG-KNILLERVPD-PPPTLSDLKKAIPHCFERSTIRSSYYVVDLIA 56
      |||||:  : ||: :|||  |||: :||| |||: :||| |||: :|||

```

Db 1 MGAGRMNTTDDQKNLFRQVPAKPPFSLADLKKAIPHCFOBSLSSYYVVDLVVA 60
Qy 59 VFYFLANTYIPLIPTPLAY-LAMPVYFCQASILTGLMVIHGECGHHAFSDYQIDDIY 117
Db 61 VFYFLANTYIPLIPSLAYLAMPVYFCQASILTGLMVIHGECGHHAFSDYQIDDIY 120
Qy 118 GFVLHSAALTPYFSWKYSHRNHNANTNSLDNDEVYIPKSKVKIYKSLNPPGRVFTL 177
Db 121 GFILHSALFTYFSGWKYSHRNHNANTNSLDNDEVYIPKSKVKIYKSLNPPGRVFTL 180
Qy 178 VFRLTGLPVLNTNISKKKYGRFANHPDMSPIFNDREVOYLLSDGLAVFAIKLL 237
Db 181 AFRLIVGPELPLFTNVSCKYERFANHPDMSPIFTEREHVOLLSDGLAVFAIKLL 240
Qy 238 VAAKGAAMVIMVYAIPLVGVSVFVLITLHTHTLSLPHYDSTEMWIKALSTIDRDFG 297
Db 241 VLAAGGAMVVICIYGVPLAVNAFLLITLHTHTLSLPHYDSTEMWIKALSTIDRDFG 300
Qy 298 FLNFVFDVTHVHLHLISYIPHYHAKARDAIKPLVGEYKIDRTPIFKAMVREAK 355
Db 301 FLNFVFDVTHVHLHLISYIPHYHAKARDAIKPLVGEYKIDRTPIFKAMVREAK 358

RESULT 2

US-09-981-124-4
; Sequence 4, Application US/09981124
; Patent No. US2002016144A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lemman, Marit
; APPLICANT: Styume, Sten
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
; FILE REFERENCE: 26-98A
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/043706
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: AU P06223
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 60/050403
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Crepis sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (292)..(292)
; OTHER INFORMATION: The 'Xaa' at location 292 stands for Arg, or Ser.
; NAME/KEY: misc_feature
; LOCATION: (937)..(937)
; OTHER INFORMATION: N is any nucleotide residue
; LOCATION: (901)..(901)
; OTHER INFORMATION: N is any nucleotide residue
US-09-981-124-4

Query Match 77.8%; Score 1592; DB 9; Length 373;
Best Local Similarity 75.9%; Pred. No. 4e-154;
Matches 287; Conservative 40; Mismatches 45; Indels 6; Gaps 4;

Qy 1 MGAGRMDSPEGKNIILERVVDP-PFTLSDLKKAIPHCERSVIRSSYYVVDLIYAY 59
Db 1 MGAGGR--GRSE-KSVMERVSVDVPTLSLKLKAIIPHCFORSVIRSSYYVVDLIYAY 57

Qy 60 VFYFLANTYIPLIPTPLAYLAMPVYFCQASILTGLMVIHGECGHHAFSDYQIDDIY 119
Db 58 IFYFLANTYIPLIPSLAYLAMPVYFCQASVLTGLMVIHGECGHHAFSDYQIDDIY 117
Qy 120 VLSHALLTPYFSWKYSHRNHNANTNSLDNDEVYIPKSKVKIYKSLNPPGRVFTL 179
Db 118 IHSFLLTPYFSWKYSHRNHNANTNSLDNDEVYIPKSKVKIYKSLNPPGRVFTL 177
Qy 180 RLITGFPLYLNTNISKKKYGRFANHPDMSPIFNDREVOYLLSDGLAVFAIKLLVA 239
Db 178 MFTLGFPLYLNTNISKKKYGRFANHPDMSPIFNDREVOYLLSDGLAVFAIKLLVA 237
Qy 240 AKGAAMVIMVYAIPLVGVSVFVLITLHTHTLSLPHYDSTEMWIKALSTIDRDFG 299
Db 238 NKGAAVAMVIMVYAIPLVGVSVFVLITLHTHTLSLPHYDSTEMWIKALSTIDRDFG 297
Qy 300 NRVFDVTHVHLHLISYIPHYHAKARDAIKPLVGEYKIDRTPIFKAMVREAKC 359
Db 298 NSVFHDVTHVHLHLISYIPHYHAKARDAIKPLVGEYKIDRTPIFKAMVREAKC 357
Qy 360 IEPDESEHKGVFWYHKM 377
Db 358 IEP--DSKKGVWYHKL 373

RESULT 3

US-09-981-124-2
; Sequence 2, Application US/09981124
; Patent No. US2002016144A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lemman, Marit
; APPLICANT: Styume, Sten
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
; FILE REFERENCE: 26-98A
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/043706
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: AU P06223
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 60/050403
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Crepis palaestina
US-09-981-124-2

Query Match 77.7%; Score 1589.5; DB 9; Length 374;
Best Local Similarity 75.4%; Pred. No. 7.3e-154;
Matches 285; Conservative 40; Mismatches 48; Indels 5; Gaps 3;

Qy 1 MGAGRMDSPEGKNIILERVVDP-PFTLSDLKKAIPHCERSVIRSSYYVVDLIYAY 59
Db 1 MGAGGR--GRSEKSVMERVSVDVPTLSLKLKAIIPHCFORSVIRSSYYVVDLIYAY 58
Qy 60 VFYFLANTYIPLIPTPLAYLAMPVYFCQASILTGLMVIHGECGHHAFSDYQIDDIY 119
Db 59 IFYFLANTYIPLIPSLAYLAMPVYFCQASVLTGLMVIHGECGHHAFSDYQIDDIY 118
Qy 120 VLSHALLTPYFSWKYSHRNHNANTNSLDNDEVYIPKSKVKIYKSLNPPGRVFTL 179
Db 119 IHSFLLTPYFSWKYSHRNHNANTNSLDNDEVYIPKSKVKIYKSLNPPGRVFTL 178

QY 180 RLTLGFPYLTLTNGSKKYGFRANHPDMSPIFNDRERVOVLLSDFGLLAVFAIKLVA 239
 DB 179 MFTLGFPYLTLTNGSKKYGFRANHPDMSPIFNDRERVOVLLSDFGLLAVFAIKLVA 238
 QY 240 AKGAAYINMVAIPVGLVSVFVLITLTHLTHLSLPHYSTENWIKALSTIDRDFGL 299
 DB 239 NKGAWACWGVGLVGFTEFEDVITFHHTHQSSPHYDSTENWIRGALSIRDFFGL 298
 QY 300 NRVPHDVTHVTHLTHLSYIPHYAKEARDAIKPVLAGREYIDRPTPKAMYREAKECIGY 359
 DB 299 NSVPHDVTHVTHLTHLSYIPHYAKEARDAIKPVLAGREYIDRPTPKAMYREAKECIGY 358
 QY 360 IEPDESEHKGVEWYHQM 377
 DB 359 IEP--DSKLGKGVYVYHKL 374

RESULT 4
 US-10-464-631-15
 ; Sequence 15, Application US/10464631
 ; Publication No. US2003020487A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cahoon, Edgar B
 ; APPLICANT: Hitz, William G
 ; APPLICANT: Rapp, Kevin G
 ; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF CALENDIC ACID, AN UNSUOL
 ; TITLE OF INVENTION: FATTY ACID CONTAINING DELTA-8,10,12 CONJUGATED DOUBLE
 ; TITLE OF INVENTION: BONDS
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/10/464,631
 ; CURRENT FILING DATE: 2003-06-18
 ; PRIOR APPLICATION NUMBER: US/09/638,937
 ; PRIOR FILING DATE: 2000-08-15
 ; PRIOR APPLICATION NUMBER: BR-1371-P1
 ; PRIOR FILING DATE: 1999-08-16
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 15:
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Boreago officinalis
 ; US-10-464-631-15

Query Match 68.2%; Score 1396.5; DB 12; Length 383;
 Best Local Similarity 63.9%; Pred. No. 4.3e-114;
 Matches 242; Conservative 62; Mismatches 70; Indels 5; Gaps 2;

QY 1 MGAGGRMSDSEBGR---NILERVPVD-PPETLSDLKKAIPTHCFERSVIRSSYYVVDL 55
 DB 1 MGAGGRMPVPTKGGKSDVDFQVPSSEKPPETVGLDKKVIIPHCFOGVSFVSVYYVDL 60
 QY 56 IVAVFFYLLANTYPIPIPTPLAYLAMPVYWCQASITLGLVIGHGCHNAFSYQYOLD 115
 DB 61 VIAAFYLLANTYPIPIPTPLAYLAMPVYWCQASITLGLVIGHGCHNAFSYQYOLD 120
 QY 116 IVGFVLSALTLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKLLNPPGRVF 175
 DB 121 TVGLLHLSALLVYFYSKYSIRRHSTGSLERDEVIPKRSKVSISSEVLNPPGRVL 180
 QY 176 TLVERLTGFPYLTLTNGSKKYGFRANHPDMSPIFNDRERVOVLLSDFGLLAVFAIK 235
 DB 181 VLVOLTLGMPVLYLMPVNSGRPYDRFACHDPKSPYVDRERLQIYISDAIVAMVGLY 240
 QY 236 LIVAAGAAVYINMVAIPVGLVSVFVLITLTHLTHLSLPHYSTENWIKALSTIDR 295
 DB 241 RLVAAGAAVYINMVAIPVGLVSVFVLITLTHLTHLSLPHYSTENWIKALSTIDR 300
 QY 296 FGFLNRVPHDVTHVTHLTHLSYIPHYAKEARDAIKPVLAGREYKIDRTPIFKAMREAK 355
 DB 301 YGFLNKVFNHITTDHVAHHLFSTMPHYNAMEATKAIKPIIGSEYRFDPTPVKAMREAR 360
 QY 356 ECIYIEPDESEHKGVEWY 374
 DB 359 IEP--DSKLGKGVYVYHKL 374

DB 361 ECIYIEADEGDNKKGVFWY 379

RESULT 5
 US-10-424-599-266787
 ; Sequence 266787, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 266787
 ; LENGTH: 383
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_8292C.1.Dep
 ; US-10-424-599-266787

Query Match 66.3%; Score 1356.5; DB 12; Length 383;
 Best Local Similarity 62.4%; Pred. No. 5.4e-130;
 Matches 237; Conservative 61; Mismatches 77; Indels 5; Gaps 2;

QY 1 MGAGGRMSDSEBGR---NILERVPVD-PPETLSDLKKAIPTHCFERSVIRSSYYVVDL 55
 DB 1 MGAGGRMPVPTKGGKSDVDFQVPSSEKPPETVGLDKKVIIPHCFOGVSFVSVYYVDL 60
 QY 56 IVAVFFYLLANTYPIPIPTPLAYLAMPVYWCQASITLGLVIGHGCHNAFSYQYOLD 115
 DB 61 VIAAFYLLANTYPIPIPTPLAYLAMPVYWCQASITLGLVIGHGCHNAFSYQYOLD 120
 QY 116 IVGFVLSALTLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKVKIYSKLLNPPGRVF 175
 DB 121 TVGLLHLSALLVYFYSKYSIRRHSTGSLERDEVIPKRSKVSISSEVLNPPGRVL 180
 QY 176 TLVERLTGFPYLTLTNGSKKYGFRANHPDMSPIFNDRERVOVLLSDFGLLAVFAIK 235
 DB 181 TIAATLTLGMPVLYLMPVNSGRPYDRFACHDPKSPYVDRERLQIYISDAIVAMVGLY 240
 QY 236 LIVAAGAAVYINMVAIPVGLVSVFVLITLTHLTHLSLPHYSTENWIKALSTIDR 295
 DB 241 RLMAAGAAVYINMVAIPVGLVSVFVLITLTHLTHLSLPHYSTENWIKALSTIDR 300
 QY 296 FGFLNRVPHDVTHVTHLTHLSYIPHYAKEARDAIKPVLAGREYKIDRTPIFKAMREAK 355
 DB 301 YGFLNKVFNHITTDHVAHHLFSTMPHYNAMEATKAIKPIIGSEYRFDPTPVKAMREAR 360
 QY 356 ECIYIEPDESEHKGVEWY 375
 DB 361 ECIYIEPDQSTESKGVFWY 380

RESULT 6
 US-10-425-114-40643
 ; Sequence 40643, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53113)B

```

; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40643
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: clone ID: LIB3028-001-B9_FLI.pep
US-10-425-114-40643

Query Match      66.3%; Score 1356.5; DB 12; Length 395;
Best Local Similarity 62.4%; Pred. No. 5,6e-130;
Matches 237; Conservative 61; Mismatches 77; Indels 5; Gaps 2;

QY 1 MGAGGRMSDPSGK---NILERVVD--PPTLSDLKAIPTGCEERSVIRSSYYVVDL 55
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 13 MGAGRTDVPANRKRSEVDPLKRVFEPKPSLSQIKVIPPCHQRSVPSFSYVVDL 72
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 56 IVAVFFYIANTYIPLIPTLAYLAMPYVWFCQASILGLWVIGHGCHHAFSDYQILD 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 73 TIAFCLYVAATHYTHLPSPLFLAMPYMAVQGCILGWVIAHEGCHHAFSDYQILD 132
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 IVGFVLSALLTPYFSWKYSHRNHNHANSIDNDEYV1PKRKSRYKYSKLIANNPGRVF 175
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 133 IVGLVHSGGLVFPVSMKYSRRHSHSNTGSLERDEVFPVKQSKCIKWSKLIANNPGRV 192
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 176 TLVFLRLTGFPVLYLTINISGKKYGRFANHPDMSPIFNDREVRQVLSDFGLAVFAIK 235
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 193 TLAVLTLTGMPLYLALANVSGRYPDFACHYDPGYISDRELRQIYISDAGVLAVCYGLF 252
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 236 LIVAAGAAWYINMYAIPVLGVSEFVLTITVHTHLSLPHYDSTENMWIKALSTIRD 295
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 253 RLAAKAGLAWVVCYGVPLVNGFLVITFLQHTHSPALPHYTSEMDMLRGALATVRD 312
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 296 FGLVRVHDVTHYTHVHLHSYIPTYHAKEDARDAIKVLGEYYKIDRTPIFKAMYREAK 355
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 313 YGLINKVFNHTIDTHVAHLFSITMHPVAMATYAKIKELGTYRFDETPFVKAAMREAR 372
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 356 ECIYIEPDESEHKGVFWYH 375
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 373 ECIYIEPDQSTESKGVFWYH 392
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-981-124-12
; Sequence 12, Application US/09981124
; Patent No. US20020161441
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surlinder
; APPLICANT: Lemman, Marit
; APPLICANT: Steyane, Sten
; TITLE OF INVENTION: PATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
; FILE REFERENCE: 26-98A
; CURRENT APPLICATION NUMBER: US/09/981,124
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/043706
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: AU P06223
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 60/050403
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 383
; TYPE: PRT
```

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; ORGANISM: Solanum commersonii
US-09-981-124-12

Query Match      65.9%; Score 1348.5; DB 9; Length 383;
Best Local Similarity 61.2%; Pred. No. 3,6e-129;
Matches 232; Conservative 65; Mismatches 77; Indels 5; Gaps 2;

QY 1 MGAGGRMSDPS---EGKNILERVVD--PPTLSDLKAIPTGCEERSVIRSSYYVVDL 55
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 MGAGGRMSAPNGETEVKNPQKVPSPPTVBDIKAIIPPHCFORSLIRSFYVVDL 60
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 56 IVAVFFYIANTYIPLIPTLAYLAMPYVWFCQASILGLWVIGHGCHHAFSDYQILD 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 ILVSIIMVYANTYIHTLPSPICTIAMPYIMCQGCCTGIVWNAHEGCHHAFSDYQVVD 120
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 116 IVGFVLSALLTPYFSWKYSHRNHNHANSIDNDEYV1PKRKSRYKYSKLIANNPGRVF 175
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 121 TVGILHLSALLVFPVSMKYSRRHSHSNTGSLERDEVFPVKQSKQIGWYSKLIANNPGRV 180
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 176 TLVFLRLTGFPVLYLTINISGKKYGRFANHPDMSPIFNDREVRQVLSDFGLAVFAIK 235
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 181 SLITTLTGMPLYLAFVNSGRYPDFACHYDPGYPIYNNRRLQIFISDAGVLGVCYLLY 240
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 236 LIVAAGAAWYINMYAIPVLGVSEFVLTITVHTHLSLPHYDSTENMWIKALSTIRD 295
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 241 RLAAVGLAWVVCYGVPLVNGFLVITFLQHTHSPALPHYDSTENMDMLRGALATCRD 300
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 296 FGLVRVHDVTHYTHVHLHSYIPTYHAKEDARDAIKVLGEYYKIDRTPIFKAMYREAK 355
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 301 YGLINKVFNHTIDTHVAHLFSITMHPVAMATYAVKVLDDYQFDQTPYIKEMWREAR 360
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 356 ECIYIEPDESEHKGVFWY 374
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 361 ECLYVEKDESSQKGVFWY 379
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-10-425-114-56017
; Sequence 56017, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 56017
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: clone ID: 701211444_FLI.pep
US-10-425-114-56017

Query Match      65.8%; Score 1346.5; DB 12; Length 392;
Best Local Similarity 62.1%; Pred. No. 5,9e-129;
Matches 236; Conservative 61; Mismatches 78; Indels 5; Gaps 2;

QY 1 MGAGGRMSDPSGK---NILERVVD--PPTLSDLKAIPTGCEERSVIRSSYYVVDL 55
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 MGAGRTDVPANRKRSEVDPLKRVFEPKPSLSQIKVIPPCHQRSVPSFSYVVDL 69
   ||||| : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 56 IVAVFFYIANTYIPLIPTLAYLAMPYVWFCQASILGLWVIGHGCHHAFSDYQILD 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 70 TIAFCLYVAATHYTHLPSPLFLAMPYMAVQGCILGWVIAHEGCHHAFSDYQILD 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

QY 116 IVGVLHSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKYKYSKLNNPGRVF 175
DB 130 IVGLVHSGLLVYPYFSWKYSHRRHNSNTGSLERDEVFPKXSCIKWYSKYLNMLPGRYL 189
QY 176 TLVRLTLGFPYLLTNTSGKKYGRFANHPDMSIFPDRERVOYLLSDPGLAVFAIK 235
DB 190 TLAVTLTGMPLYLALNVSGRPYDPFACHYDPGYISYDRELOQYISDAGVLAICYLF 249
QY 236 LTVAKGAAMVYNNVAPVLGVSVFVLITVLIHTHLSLPHYDSTEMWIKGALSTDRD 295
DB 250 RLMAKGLAMVVCYGVPLVNGFLVITFLQHTHPALPHYTSEMDWMLGALATVDRD 309
QY 296 FGLNRFVHDVTHVHLHLSYIPHYAKARDAIKFVLGEYKIDRTPIFKAMYREAK 355
DB 310 YGILNKVFHNITDTHVAHHLFSTMPHYAMEATKAIKILGEYVFPDETPIVKAMWREAR 369
QY 356 ECIYIEPDESEHKGVFWYH 375
DB 370 ECIYIEPDQSTESKGVFWYN 389

RESULT 9

US-09-837-751-6
; Sequence 6, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 383
; TYPE: PRT
; ORGANISM: *Gossypium* sp.
US-09-837-751-6

Query Match 65.1%; Score 1332.5; DB 9; Length 383;
Best Local Similarity 60.7%; Pred. No. 1.5e-127;
Matches 230; Conservative 70; Mismatches 74; Indels 5; Gaps 2;

QY 1 MGAGRMSDPESEK---NILERVVD--PPTLSDLKKAIFTHCFERSVIRSSYYVVDL 55
DB 1 MGAGRMSVPTSPPKPEBNSLKRVDYSKPPTLSBIKKAIPPHCFORSVLSFSYLLDYF 60
QY 56 IVAVFFYLLANTYPLIPTPLAYLAMPYWFCQASILTLGWLVIHGECHNAFSDYQLIDD 115
DB 61 ILASLFYHVAANTYFENLPQALSNVAMPYWMQCGILGVWVIAHECHNAFSDYQMLDD 120
QY 116 IVGVLHSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKYKYSKLNNPGRVF 175
DB 121 TVGLIHSLSLVLPYFSWKYSHRRHNSNTGSLERDEVFPKXSCIKWYSKYLNMLPGRYL 180
QY 176 TLVRLTLGFPYLLTNTSGKKYGRFANHPDMSIFPDRERVOYLLSDPGLAVFAIK 235
DB 181 SITQTLTGMPLYLALNVSGRPYDPFACHYDPGYISYDRELOQYISDAGVLAICYLF 240
QY 236 LTVAKGAAMVYNNVAPVLGVSVFVLITVLIHTHLSLPHYDSTEMWIKGALSTDRD 295
DB 241 RLVAKGLAMVVCYGVPLVNGFLVITFLQHTHPALPHYTSEMDWMLGALATVDRD 300
QY 296 FGLNRFVHDVTHVHLHLSYIPHYAKARDAIKFVLGEYKIDRTPIFKAMYREAK 355
DB 301 YGILNKVFHNITDTHVAHHLFSTMPHYAMEATKAIKILGEYVFPDETPIVKAMWREAR 360
QY 356 ECIYIEPDESEHKGVFWY 374
DB 370 ECIYIEPDQSTESKGVFWYN 389

DB 361 ECIYIEPDQSGKGVFWY 379

RESULT 10

US-09-837-751-31
; Sequence 31, Application US/09837751
; Patent No. US20020104124A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qing
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 383
; TYPE: PRT
; ORGANISM: *Glycine* max
US-09-837-751-31

Query Match 64.8%; Score 1325.5; DB 9; Length 383;
Best Local Similarity 61.3%; Pred. No. 8e-127;
Matches 233; Conservative 62; Mismatches 80; Indels 5; Gaps 2;

QY 1 MGAGRMSDPESEK---NILERVVD--PPTLSDLKKAIFTHCFERSVIRSSYYVVDL 55
DB 1 MGAGRTDVPNANKSEVDPLKRVPEKPFSLQIKKAIPPHCFORSVLSFSYVVDL 60
QY 56 IVAVFFYLLANTYPLIPTPLAYLAMPYWFCQASILTLGWLVIHGECHNAFSDYQLIDD 115
DB 61 TIAFLYVATHYTHLHLPUSFRGMATYMWQCGILGVWVIAHECHNAFSDYQLIDD 120
QY 116 IVGVLHSALLTPYFSWKYSHRNHANTNSLDNDEVYIPKRSKYKYSKLNNPGRVF 175
DB 121 IVGLIHSLSLVLPYFSWKYSHRRHNSNTGSLERDEVFPKXSCIKWYSKYLNMLPGRYL 180
QY 176 TLVRLTLGFPYLLTNTSGKKYGRFANHPDMSIFPDRERVOYLLSDPGLAVFAIK 235
DB 181 TLAVTLTGMPLYLALNVSGRPYDPFACHYDPGYISYDRELOQYISDAGVLAICYLF 240
QY 236 LTVAKGAAMVYNNVAPVLGVSVFVLITVLIHTHLSLPHYDSTEMWIKGALSTDRD 295
DB 241 RLMAKGLAMVVCYGVPLVNGFLVITFLQHTHPALPHYTSEMDWMLGALATVDRD 300
QY 296 FGLNRFVHDVTHVHLHLSYIPHYAKARDAIKFVLGEYKIDRTPIFKAMYREAK 355
DB 301 YGILNKVFHNITDTHVAHHLFSTMPHYAMEATKAIKILGEYVFPDETPIVKAMWREAR 360
QY 356 ECIYIEPDESEHKGVFWYH 375
DB 361 ECIYIEPDQSTESKGVFWYN 380

RESULT 11

US-09-852-399-4
; Sequence 4, Application US/09852399
; Patent No. US20020045232A1
; GENERAL INFORMATION:
; APPLICANT: Otsu, Xiao
; TITLE OF INVENTION: PRODUCTION OF CONJUGATED LINOLEIC AND
; FILE REFERENCE: BNZ-002
; CURRENT APPLICATION NUMBER: US/09/852,399
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: USSN 60/203,027
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4
LENGTH: 383
TYPE: PRT
ORGANISM: Calendula officinalis
US-09-852-399-4

Query Match 64.7%; Score 123.5; DB 9; Length 383;
Best Local Similarity 61.3%; Pred. No. 1.3e-126;
Matches 233; Conservative 57; Mismatches 83; Indels 7; Gaps 2;

QY 1 MGAGGRMDPSEKGIILRRVVD-----PPETLSDLKKAIPTHCFERSVIRSSYYVHD 54
DB 1 MGAGGRMDPRTNGAKTPEPPIQVPHKPEPTVDIDKAIIPHCFTNSVIRSSYYVVD 60
QY 55 LIVAVFYIANTYIPLIPTPLAYLAMPVYVFCQASILTLGLWVIGHECGHAFSDYQI 114
DB 61 LTIASILYIANNTYISTPLSPLAYVAMPVYVACQCVLTGVVLAHECGHAFSDHQYLD 120
QY 115 DIVGFLVLSALLTPFSKWKYSHRNHNANTNSLDNDVYIIPKRSKYKISKLANPPGRV 174
DB 121 DTGVLVLSPLVFPFSWKYSHRRHSNTGSIHDEVEFVPLKSGVRSSTARYLNNPPGRI 180
QY 175 FTLVRLLTGFPFLYLTNLSGKKYGRFANHPDPMSPIFNDRERVOVLSDGFLAVFYAI 234
DB 181 LTLVTLTLGMPLYLTFVNSGRYIRFACHDENSPIYSKERRAQIFISDAGILAVFVL 240
QY 235 KLVAAKGAAMVIMMYAIPVLGVSFVFLITYLHHTLSLPHYDSTEMNMIKALSTIDR 294
DB 241 FRLANRVFHDVYTHVLAHLISYIPHYHAKAADAIKPVIGEYKIDRTPIFKAMREA 300
QY 295 DFGFLANRVFHDVYTHVLAHLISYIPHYHAKAADAIKPVIGEYKIDRTPIFKAMREA 354
DB 301 DYGLINKVFHNIITDTHVAHLFSTMPHYHAMEATKAIKPIIGEYQFGDTISFKAMRET 360
QY 355 KECIYEDEDESEHKGVFWY 374
DB 361 KECIYVDDEEVK-DGVYVY 379

RESULT 12

US-09-995-297-14
Sequence 14, Application US/09995297
Patent No. US20020092038A1

GENERAL INFORMATION:
APPLICANT: Kodali, Dharma
APPLICANT: Fan, Zhegong
APPLICANT: Debonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
FILE OF INVENTION: PATTY ACID CONTENT
FILE REFERENCE: 07148-072002
CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 384
TYPE: PRT
ORGANISM: Brassica napus
US-09-995-297-14

Query Match 64.4%; Score 1318; DB 9; Length 384;
Best Local Similarity 61.2%; Pred. No. 4.7e-126;
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

QY 1 MGAGGRM--SDPSSEK--NILERVVD--PPETLSDLKKAIPTHCFERSVIRSSYYVHD 55
DB 1 MGAGGRMVSPPSKSESTDITIKRVPCETPPFTVGLKKAIPHCFTNSVIRSSYYVVD 60
QY 56 IVAVFYIANTYIPLIPTPLAYLAMPVYVFCQASILTLGLWVIGHECGHAFSDYQI 115
DB 61 IIASCFYVATTYIFPLBPLSTYFAMPVYVACQCVLTGVVLAHECGHAFSDYQI 120

QY 116 IVGFLVLSALLTPFSKWKYSHRNHNANTNSLDNDVYIIPKRSKYKISKLANPPGRV 175
DB 121 TVGLIFHSFLVLPFSWKYSHRRHSNTGSIHDEVEFVPLKSGVRSSTARYLNNPPGRI 180
QY 176 TFLVRLTLGFPFLYLTNLSGKKY--GRFANHPDPMSPIFNDRERVOVLSDGFLAVFYAI 234
DB 181 MLTVQFTLGMPLYLAFVNSGRPYDGFACHHPAPAIYNDREKQIYISDAGILAVCYGL 240
QY 235 KLVAAKGAAMVIMMYAIPVLGVSFVFLITYLHHTLSLPHYDSTEMNMIKALSTIDR 294
DB 241 FRVAAQGVASMWCFGVPLIIVNGFLVLTLYLQHTHPSLPHYDSEMDMLRGALATVDR 300
QY 295 DFGFLANRVFHDVYTHVLAHLISYIPHYHAKAADAIKPVIGEYKIDRTPIFKAMREA 354
DB 301 DYGLINKVFHNIITDTHVAHLFSTMPHYHAMEATKAIKPIIGEYQFGDTISFKAMREA 360
QY 355 KECIYEDEDESEHKGVFWY 375
DB 361 KECIYEDROGCKGVFWIN 381

RESULT 13
US-09-771-904-14
Sequence 14, Application US/09771904
Publication No. US20030131379A1

GENERAL INFORMATION:
APPLICANT: Debonte, Lorin R.
APPLICANT: Fan, Zhegong
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
FILE REFERENCE: 07148-063003
CURRENT APPLICATION NUMBER: US/09/771,904
CURRENT FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 384
TYPE: PRT
ORGANISM: Brassica napus
US-09-771-904-14

Query Match 64.4%; Score 1318; DB 10; Length 384;
Best Local Similarity 61.2%; Pred. No. 4.7e-126;
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

QY 1 MGAGGRM--SDPSSEK--NILERVVD--PPETLSDLKKAIPTHCFERSVIRSSYYVHD 55
DB 1 MGAGGRMVSPPSKSESTDITIKRVPCETPPFTVGLKKAIPHCFTNSVIRSSYYVVD 60
QY 56 IVAVFYIANTYIPLIPTPLAYLAMPVYVFCQASILTLGLWVIGHECGHAFSDYQI 115
DB 61 IIASCFYVATTYIFPLBPLSTYFAMPVYVACQCVLTGVVLAHECGHAFSDYQI 120
QY 116 IVGFLVLSALLTPFSKWKYSHRNHNANTNSLDNDVYIIPKRSKYKISKLANPPGRV 175
DB 121 TVGLIFHSFLVLPFSWKYSHRRHSNTGSIHDEVEFVPLKSGVRSSTARYLNNPPGRI 180
QY 176 TFLVRLTLGFPFLYLTNLSGKKY--GRFANHPDPMSPIFNDRERVOVLSDGFLAVFYAI 234
DB 181 MLTVQFTLGMPLYLAFVNSGRPYDGFACHHPAPAIYNDREKQIYISDAGILAVCYGL 240
QY 235 KLVAAKGAAMVIMMYAIPVLGVSFVFLITYLHHTLSLPHYDSTEMNMIKALSTIDR 294
DB 241 FRVAAQGVASMWCFGVPLIIVNGFLVLTLYLQHTHPSLPHYDSEMDMLRGALATVDR 300
QY 295 DFGFLANRVFHDVYTHVLAHLISYIPHYHAKAADAIKPVIGEYKIDRTPIFKAMREA 354
DB 301 DYGLINKVFHNIITDTHVAHLFSTMPHYHAMEATKAIKPIIGEYQFGDTISFKAMREA 360
QY 355 KECIYEDEDESEHKGVFWY 375

Db 361 KECIYEPDROGKKGWFWYN 381

RESULT 14

US-10-715-100-14
; Sequence 14, Application US/10715100
; Publication No. US20040083503a1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharm
; APPLICANT: Pan, Zhegong
; APPLICANT: Debonite, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; FILE REFERENCE: 07148-072002
; CURRENT APPLICATION NUMBER: US/10/715,100
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US/09/995,297
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US/09/128,602
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Brassica napus
US-10-715-100-14

Query Match 64.4%; Score 1318; DB 16; Length 384;
Best Local Similarity 61.2%; Pred. No. 4.7e-126;
Matches 233; Conservative 61; Mismatches 81; Indels 6; Gaps 4;

Qy 1 MGAGRM--SDPSEK--NILERVVD--PPTLSDLKKAIPPTCFERSVRSYVVDL 55
Db 1 MGAGRMQVSPSPSKSSEDTNKRVCETPPFTVGEKKAIPPHCFKRSIPRSFSTYLWDI 60
Qy 56 IVAVVFYLLANTYIPLIPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQIJD 115
Db 61 IIASCFYVATYTFPLPHPLSTYFAMPPLYACQCVLTGVWVAHECGHAFSDYQIJD 120
Qy 116 IVGFVLSALLTPYFSWKYSHRNHANTNSLNDDEVYIPKRSKVKYISKLNPPGRV 175
Db 121 TVGILFHSFLVYFWSKYSRHRHNSNTGSLERDEVFPKKSIDIKWYGYKLNPPGRV 180
Qy 176 TLVFRULTGFPPLYLNTNISKKY--GRFANHDPMSPIFNDREROVLLSDGLAVFAI 234
Db 181 MLTVQFTLGPPLYLAFNVSGRPYDGGFACHFNAPNAPYNDRERLQIYISDAGILAVCYG 240
Qy 235 KILVAAGAAMVIMYAIPLVGVSVFVLTITLHHTLSLPHYDSTEMNWKIGALSTIDR 294
Db 241 FRYAAAGVAVSMVCYGVPLIYNGFLVLTITLQHTHPSLPHYDSEMDLKGALATYDR 300
Qy 295 DPGFLNRVFDVTHVTHVHLISYIPHYAKKARDAIKPVLSGYKIDRTPIFKAMYRE 354
Db 301 DYGLINKVFENITDTHVAHHLFSTMPHYAMEATKAIKPIIGXYQDGTVPVYKAMRE 360
Qy 355 KECIYIEPDDESEHKGVFWYH 375
Db 361 KECIYIEPDROGKKGWFWYN 381

RESULT 15

US-09-995-297-10
; Sequence 10, Application US/09995297
; Patent No. US20020092038A1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharm
; APPLICANT: Pan, Zhegong
; APPLICANT: Debonite, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; FILE REFERENCE: 07148-072002

; CURRENT APPLICATION NUMBER: US/09/995,297
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US/09/128,602
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Brassica napus
US-09-995-297-10

Query Match 64.3%; Score 1317; DB 9; Length 384;
Best Local Similarity 61.3%; Pred. No. 6e-126;
Matches 234; Conservative 58; Mismatches 82; Indels 8; Gaps 4;

Qy 1 MGAGRM-----SDPSEKNIILERVVD--PPTLSDLKKAIPPTCFERSVRSYVVDH 54
Db 1 MGAGRMQVSPSPSKSSEDTN--KRVPCETPPFTVGEKKAIPPHCFKRSIPRSFSTYLWD 59
Qy 55 LIAVVFYLLANTYIPLIPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQIJD 114
Db 60 IIASCFYVATYTFPLPHPLSTYFAMPPLYACQCVLTGVWVAHECGHAFSDYQIJD 119
Qy 115 DIVGFVLSALLTPYFSWKYSHRNHANTNSLNDDEVYIPKRSKVKYISKLNPPGRV 174
Db 120 DTGILFHSFLVYFWSKYSRHRHNSNTGSLERDEVFPKKSIDIKWYGYKLNPPGRV 179
Qy 175 FTVFRULTGFPPLYLNTNISKKY--GRFANHDPMSPIFNDREROVLLSDGLAVFYA 233
Db 180 VMLTVQFTLGPPLYLAFNVSGRPYDGGFACHFNAPNAPYNDRERLQIYISDAGILAVCYG 239
Qy 234 IKLVAAGAAMVIMYAIPLVGVSVFVLTITLHHTLSLPHYDSTEMNWKIGALSTID 293
Db 240 LYRYAAAGVAVSMVCYGVPLIYNGFLVLTITLQHTHPSLPHYDSEMDLKGALATVD 299
Qy 294 RDPFGLNRVFDVTHVTHVHLISYIPHYAKKARDAIKPVLSGYKIDRTPIFKAMYRE 353
Db 300 RDYGLINKVFENITDTHVAHHLFSTMPHYAMEATKAIKPIIGXYQDGTVPVYKAMRE 359
Qy 354 AKECIYIEPDDESEHKGVFWYH 375
Db 360 AKECIYIEPDROGKKGWFWYN 381

Search completed: June 18, 2004, 17:43:53
Job time : 49 secs

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OM protein - protein search, using sw model

Run on: June 18, 2004, 17:34:22 ; Search time 20 Seconds
(without alignments)
1813.210 Million cell updates/sec

Title: US-10-069-772-2
Perfect score: 2047
Sequence: 1 MGAGGRMSDSEKGVFVYTHKM 377

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 78: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1348.5	65.9	383	2 T10480	Delta12 fatty acid
2	1336	65.3	382	2 T15042	omega-6 fatty acid
3	1332.5	65.1	383	2 T10789	omega-6 desaturase
4	1325.5	64.8	383	2 T07688	omega-6 desaturase
5	1296.5	63.3	385	2 T09880	omega-6 desaturase
6	1273.5	62.2	387	2 T09839	oleate 12-hydroxyl
7	1241.5	60.6	383	2 T15043	funeral elictor-in
8	1237.5	60.5	387	2 T07687	omega-6 desaturase
9	1220	59.6	378	2 T14269	Delta12 fatty acid
10	1160.5	56.7	333	2 T07009	omega-6 fatty acid
11	926.5	45.3	376	2 JC7871	stearyl-CoA 9-des
12	658.5	32.2	359	2 AG2005	omega-3 fatty acid
13	653	31.9	359	2 SS2650	omega-3 fatty acid
14	645	31.5	441	2 T10063	omega-3 fatty acid
15	639.5	31.2	460	2 T10063	omega-3 fatty acid
16	632.5	30.9	381	2 T03923	probable omega-3 f
17	627	30.6	431	2 T07685	omega-3 fatty acid
18	620.5	30.3	386	1 JC2335	omega-3 fatty acid
19	612	29.9	379	2 JC2555	omega-3 fatty acid
20	607	29.7	398	2 T01686	omega-3 fatty acid
21	607	29.7	404	2 PQ0812	omega-3 fatty acid
22	606	29.6	418	2 JC7872	stearyl-CoA 9-des
23	606	29.6	446	1 T02336	omega-3 fatty acid
24	604.5	29.5	443	2 T01697	omega-3 fatty acid
25	602.5	29.4	453	1 T02339	omega-3 fatty acid
26	593.5	29.0	380	2 T10898	probable omega-3 f
27	593	29.0	438	2 T15039	omega-3 fatty acid
28	590.5	28.8	377	1 JC2337	omega-3 fatty acid
29	590.5	28.8	383	2 T06238	omega-3 fatty acid

30	588.5	28.7	383	1 A44227	omega-3 fatty acid
31	585	28.6	380	2 T06238	omega-3 fatty acid
32	574	28.0	380	2 T02335	omega-3 fatty acid
33	428.5	20.9	376	2 T26075	hypothetical prote
34	339	16.6	350	2 A43772	phosphatidylcholin
35	339	16.6	350	2 A42005	phosphatidylcholin
36	330	16.1	424	2 JC5891	omega 6 desaturase
37	319	15.6	347	2 S43771	phosphatidylcholin
38	316.5	15.5	447	2 S53309	n-6 fatty acid des
39	309.5	15.1	351	2 S11519	phosphatidylcholin
40	306	14.9	349	2 S43770	phosphatidylcholin
41	306	14.9	424	2 T07742	omega-6 desaturase
42	301	14.7	448	2 D85362	hypothetical prote
43	293.5	14.3	443	2 T08136	probable omega-6 d
44	292	14.3	351	2 S54259	Delta12 fatty acid
45	214	10.5	352	2 B69901	fatty-acid desatur

ALIGNMENTS

RESULT 1									
T10480	Delta12 fatty acid desaturase (EC 1.14.99.-) [imported] - Commerson's wild potato								
C:Species:	Solanum commersonii (Commerson's wild potato)								
C:Date:	16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jun-2000								
C:Accession:	T10480								
R:Consiglio, F.; Amatruda, M.R.; Leone, A.; Costa, A.; Grillo, S.									
submitted to the EMBL Data Library, November 1995									
A:Reference number:	Z17044								
A:Accession:	T10480								
A:Status:	preliminary; translated from GB/EMBL/DBJ								
A:Molecule type:	mRNA								
A:Residues:	1-383 <CON>								
A:Cross-references:	EMBL:X92847; NID:g1054842; PID:g1054843								
A:Experimental source:	clone ScDes D11								
C:Superfamily:	omega-3 fatty acid desaturase								
C:Keywords:	oxidoreductase; unsaturated fatty acid biosynthesis								
Query Match									
Best Local Similarity	61.2%	Score	1348.5;	DB 2;	Length	383;			
Matches	232;	Conservative	65;	Mismatches	77;	Indels	5;	Gaps	2;
QY	1	MGAGGRMSDPS-----EGKNIIRVPVD-PPTLSDLKKAIPTHGFEBSVIRSSYYVVDL	55						
DB	1	MGAGGRMSAPNGEIEVKNRNPLOKVPSTKPEPTVGDIKAIIPKCFQRLISFVYVDL	60						
QY	56	IVAVFYVYLLANTYIPLIPTPLAYLAMPYWFQASILTGLWVIGHCCHAFSDYQLID	115						
DB	61	ILVSIWYVANTYTHLLPSFYCYLAMPYWCQGCCTGIVWNAHCGHAFSDYQWDD	120						
QY	116	IVGVVLSALITPFPSWKYSRRNHANTSLDNDENVYIPKSKVKYISKLNPPRGVIF	175						
DB	121	TVGILHSALIVPFPSWKYSRRHNSVTSLEBEVFPKPKSGLGWYSKYLNNPPGVL	180						
QY	176	TLVRLTGFPLYLTLNISKCKYGRFANHPDPMSPIFDRBRVOVLLSDFGLAVFYAIX	235						
DB	181	SLTTLTGMPLYLAFNVSGRPRDFACHDPYGRPIINRRLOIFISDAVLYGVYLLY	240						
QY	236	LLVNAKGAWVNNYALPVLGVSVEFVLITVLAHTTHSLPHYDSTENWIMKALSTIDRD	295						
DB	241	RIALVKGIAWVCYGVPLAVNNGFVLITLQHTHSLPHYDSTENWIMKALATCRD	300						
QY	296	FGFLNRYFHDVTHVTHVLAHLISYIPHYAKARDAIKPVLCGYIKIDTPIFKMYRBAK	355						
DB	301	YGVINKGFVHNTDTHVHHLFSTPHYAMATRAYVPLDYYQFDGTPIYKEMWBAK	360						
QY	356	ECIYIPDESEKGVFVY 374							
DB	361	ECLYVEKDESQKGVFVY 379							
RESULT 2									

T15042
 omega-6 fatty acid desaturase (EC 1.14.99.-) - parsley
 C|Species: Petroselinum crispum (parsley)
 C|Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C|Accession: T15042
 R|Kirsch, C.; Hahlbrock, K.; Somssich, I.E.
 Plant Physiol. 115: 283-289, 1997
 A|Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desaturase
 A|Reference number: Z18274; MUID:97451781; PMID:9306702
 A|Accession: T15042
 A|Status: preliminary; translated from GB/EMBL/DBD
 A|Molecule type: mRNA
 A|Residues: 1-382 <KIR>
 A|Cross-references: EMBL:U086072; NID:g2501789; PIDN:AA808696.1; PID:g2501790
 C|Superfamily: omega-3 fatty acid desaturase
 C|Keywords: oxidoreductase

Query Match	Similarity	65.3%	Score 1336	DB 2	length 382
Best local	Similarity	61.2%	Pred. No. 1.7e-104		
Matches	Conservative	69	Mismatches	74	Indels
					Gaps
					2
QY	1	MGAGGRMSDPSEGNK--ILERVPVD-PPFTLSDIKKAIPTHCFSERVIRSSYYVHHDI	56		
DB	1	MGAGGRMPINPGCKSEEVTLGRVPSPKPFPTGDIKKAIIPHCFSRVIRSSYYVYDL	60		
QY	57	VAVVYYIYANTYIPIPTPLATLAPVYVFCQASLTGLMVTGHCCHHAFSDYOLIDI	116		
DB	61	IASIIYPAATNTIQLPPHPLSTIAMPINGEVQCFELTGIWVAHSCGHAHAFSDYMLDT	120		
QY	117	VGFLVSLALTPFYSFMKYSRHHNHNNTSLDNDDEVYIPRKSXKVIYSKTLNPPGRVFT	176		
DB	121	VGLIHSSLSLVYFSEMKYSRHHNHNNTSLDNDDEVYFVPRKPSKELDSVAKYTNNPGRVLT	180		
QY	177	LVFRLTLGEPYVYLNNISGKTKGRPAHFDEPMSPIFNDREYQVLSDFGLLAVFYAIKL	236		
DB	181	LVLTTLTQMPYLTLFNVSGRHYERFACHYDPKSPYISDRERAKIILVSDAGVLAIVSGYLR	240		
QY	237	LVAAAGAMVIMVMVAPIVLGVVFVLLTYLHHTHLSLPHYOSTEMNTKGLSTIDRDF	296		
DB	241	LAVAKGLTWLVCYGGPILLVYNGFVLVLTFLDHTHPALPHINSSENDWIKGLAIYVDRDY	300		
QY	297	GFUNRFVDVTVTHVLAHLISYIIPHYHAKAADAIKPVLGEEYKIDRTPIFFAMTREAKE	356		
DB	301	GIUNRFVLTNITDTTHVAHHLFTSMPIYHNAETKAIKPIIGDYRRDFDVFVYKAMTREAKE	360		
QY	357	CIYLEDDEDESHKGVFWYH	375		
DB	361	CIYVEPDGDDQCKGILFWYN	379		

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RESULT 3
T10789
omega-6 desaturase, microsomal - upland cotton
C|Species: Gossypium hirsutum (upland cotton)
C|Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C|Accession: T10789
R|Lit, Q.; Singh, S.P.; Green, A.; Sharp, P.J.; Marshall, D.R.
submitted to the EMBL Data Library, March 1999
A|Description: Isolation and characterisation of two different microsomal omega-6 desat
A|Reference number: Z17145
A|Accession: T10789
A|Status: preliminary; translated from GB/EMBL/DBD
A|Molecule type: mRNA
A|Residues: 1-383 <Lit>
A|Cross-references: EMBL:Y10112
A|Experimental source: subspecies Delcaine-16
C|Function:
A|Description: involved in production of polyunsaturated lipids
C|Superfamily: omega-3 fatty acid desaturase

Query Match      65.1%; Score 1332.5; DB 2; Length 383;
Best Local Similarity 60.7%; Pred. No.3.4e-104;
Matches 230; Conservative 70; Mismatches 74; Indels 5; Gaps 2;

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QY      1 MGAGGRMSDPSGK----NIIEKRVVD--PPTLSDLKKAIPHCIFERSVIRSGSYVVDL 55
QY      1 MGAGGRMSDPSGK----NIIEKRVVD--PPTLSDLKKAIPHCIFERSVIRSGSYVVDL 55
Db      1 MGAGGRMSVPTSPKPKPEBSLSKRVYSKRPPTLSEIKKAIPEHCORSLVRSSTYLLYDF 60
QY      56 IVAAYFYLYLANTYIEPLPTPLAYLAMPVYVFCOASLITGLMWYIGHGCHHAFSDYQOLD 115
Db      61 ILASLFHYVATNYFPNLPQALSNVAMPPLYMAMQGCILTGVMYIAHGCHHAFSDYQOLD 120
QY      116 IVGPLYHSAALTPTYSWKYSHRNHNHANTSLDNDEYIIPKRSKVKIYKSLANPFGKRV 175
Db      121 IVGLIHSSLLVPYFSYWKYSHRRHNSNGSLDERDEVFVKKSGGLMWAHKNFNNPGRFL 180
QY      176 TLVPLTLTGFPPLYLLTNTISGKKYGRFANHPDMSPIFNDRERQVLLSPDGLLAAYALK 235
Db      181 STTIDLTIGMPLYLAFNVAGRPYDPACHYDYGPIFSRERLQIYISDAGVLAAYALK 240
QY      236 LLVAAGKAWVIMYAIPIVLGSVVEFVLLTYLHHTLSLPHYDSTEMNMIKGLASTIDRD 295
Db      241 RLVLAKGVMVISYVGVLPLVYNAFLWMTIYQHTHPSLPHYDSEMDMWRGALSTVDRD 300
QY      296 FGLNLRVHDVTHVTHVHLHLISYIPIHTAKKARDAIKPIVLGEYKIKDRPIPFAMTREA 355
Db      301 YGILNKKVFNINIDIVAHHLFSTMPHYAMVATKAIKPIVLGEYQDFDGMFVYKAIWREA 360
QY      356 ECIYIEPDDESEHKGVFW 374
Db      361 ECLIVPEPDGKOKGVFW 379

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RESULT 4
T07688
omega-6 desaturase FAD2-2, microsomal - soybean
C1Species: Glycine max (soybean)
C1Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
C1Accession: T07688
R1Hepbard, E.P.; Kliney, A.J.; Stecca, K.L.; Miao, G.H.
Plant Physiol. 110, 311-319, 1996
A1Title: Developmental and growth temperature regulation of two different microsomal ome
A1Reference number: Z16095; KUID:96151506; PMID:8587990
A1Accession: T07688
A1Status: preliminary; translated from GB/EMBL/DDJ
A1Residues: 1-383 <HR>
A1Molecule type: mRNA
A1Cross-references: EMBL:L43921; NID:G904153; PIDN:AA08060.1; PID:G904154
A1Experimental source: epicotyl
C1Genetics:
A1Gene: FAD2-2
C1Function:
A1Description: involved in production of polyunsaturated lipids
A1Note: constitutively expressed in both vegetative tissues and developing seeds
C1Superfamily: omega-3 fatty acid desaturase

Query Match      64.8%; Score 1325.5; DB 2; Length 383;
Best Local Similarity 61.3%; Pred. No. 1.3e-103;
Matches 233; Conservative 62; Mismatches 80; Indels 5; Gaps 2;

QY      1 MGAGGMSDPSSEK---NILERVPVD-PEPTLSDLKALPTGCFERSVIRSSYYVVDL 55
      |||||      :      :      :      :      :      :      :      :      :      :
DB      1 MGAAGRTDVPANRKRSEVDLKRVPPEKQPSLSQIKKAIIPHCQFRSLVLSFSYVVDL 60
      |||||      :      :      :      :      :      :      :      :      :      :

QY      56 IVAAYFYIANTYIPIPIPLAYLAMPVWFQQAIIITGLWVIGHECGHAFSDYQIIDD 115
      :      :      :      :      :      :      :      :      :      :
DB      61 TIAFCLYVAATHYFHLLPGELSPFGMAIYVAVQGCIIITGVWVIAHECGHAFSDYQIIDD 120
      :      :      :      :      :      :      :      :      :      :

QY      116 IYGFVTHSLTPPYFSKWSYHRNHNANTSLNDENVYIPKRSKVYISKXILNPPGRVF 175
      :      :      :      :      :      :      :      :      :      :
DB      121 IYGLIHSAIIVPYFSWKSHRRHSNTGSLERBEVVPKQKSCIKWYSKIANNPPGRVL 180
      :      :      :      :      :      :      :      :      :      :

QY      176 TVFVRLTLPPLLTINISGKTKYGRFANHPDPMSPIFENDREVRVQVILSDFGILAVFYAIK 235
      |||||      :      :      :      :      :      :      :      :      :      :
DB      181 TLAIVTITLMPYLIANVSGRPYDRACHYDIPGYIYSDRRLQIYISDAGVLAVYGLF 240

```

Qy 236 LVAAGAAVYNNATPVLGVSFVLTITLHTHTLSLPHYDSTERNWIKALSTDRD 295
 Db 241 RLAAAGAAVAVCVGYPVLVNGPLVLTPLQHTHPLPHYTSEEMWMLGALATVDRD 300
 Qy 296 GFLNRPVHDVTHVTHLHLSYIPHYAKARDAIKVLSYXVYIDRTPIFKAMVREAK 355
 Db 301 YGILNKVFHNTIDTHVAHLSSTMPHYAMBATKAIKILGEYIKFDETPVYKAMWREAK 360
 Qy 356 ECIYIEPDESEHKGVFWMY 375
 Db 361 ECIYIEPDESEHKGVFWMY 380

RESULT 5

T09880
 omega-6 desaturase - upland cotton
 C:Species: Gossypium hirsutum (upland cotton)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
 C:Accession: T09880
 R:Lit, Q.
 submitted to the EMBL Data Library, March 1996
 A:Reference number: Z16895
 A:Accession: T09880
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-385 <Lit>
 A:Cross-references: EMBL:X97016
 A:Experimental source: cultivar Deltapine-16
 C:Function:
 A:Description: introduces a cis double bond at omega-6 position of oleic acids
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 63.3%; Score 1296.5; DB 2; Length 385;
 Best Local Similarity 59.6%; Pred. No. 3.6e-101;
 Matches 227; Conservative 61; Mismatches 66; Indels 7; Gaps 3;
 Qy 1 MGAGGRM---SDPSEGNILERVVD-PEFTLSDLKKAIPTHCFERSVIRSSYYVHDL 56
 Db 1 MGAGGRMPIDGIIKENRGSVNRVPLEKPPFTLGQIKKAI PPHCFERSILRSFSYVHDL 60
 Qy 57 VAVYFYLLANTYIPLIPPLAYLAMPVYVFCQASITLGLMTVIGHECGHNASDYQLIDI 116
 Db 61 LASFFYYIATSYFHFLLPQFSYIAMPVYVVLQGLTGVWVIAHEGHAERDYQWVD 120
 Qy 117 VGFLHSALTLPYFSKWSHRNHNANTSLNDEYVYIPKRSKVYKYSKLNPPGRVET 176
 Db 121 VGLILHSALTLPYFSKWSHRNHNANTSLNDEYVYIPKRSKVYKYSKLNPPGRVET 180
 Qy 177 LVFRLTIGFPLVLTNLSGKRYGRFANFPDMSPIFNDRERVOVLLSDPGLAVFYAKL 236
 Db 181 LVVTLTIGFMPVYLAFNVSGRYDRLASHYNYGPIYSRERLQVYISDTGIFAVIYVLYX 240
 Qy 237 LVAAGAAVYNNATPVLGVSFVLTITLHTHTLSLPHYDSTERNWIKALSTDRD 296
 Db 241 IAAKAGAAVYNNATPVLGVSFVLTITLHTHTLSLPHYDSTERNWIKALSTDRD 300
 Qy 297 GFLNRPVHDVTHVTHLHLSYIPHYAKARDAIKVLSYXVYIDRTPIFKAMVREAK 356
 Db 301 GVLNRPVHDVTHVTHLHLSYIPHYAKARDAIKVLSYXVYIDRTPIFKAMVREAK 360
 Qy 357 CIIYIEPD---EDSEHKGVFWMY 374
 Db 361 CIIYIEPD---EDSEHKGVFWMY 381

RESULT 6

T09839
 oleate 12-hydroxylase - castor bean
 C:Species: Ricinus communis (castor bean)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: T09839
 R:van de Loo, F.J.; Brown, P.; Turner, S.; Somerville, C.R.
 Proc. Natl. Acad. Sci. U.S.A. 92, 6743-6747, 1995

A>Title: An oleate 12-hydroxylase from Ricinus communis L. is a fatty acyl desaturase ho
 A:Reference number: Z16877; MUID:95350145; PMID:7624314
 A:Accession: T09839
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-387
 A:Cross-references: EMBL:U23378; NID:9722350; PIDN:AAC9010.1; PID:9722351
 A:Experimental source: strain Baker 296; tissue-type developing endosperm
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 62.2%; Score 1273.5; DB 2; Length 387;
 Best Local Similarity 56.9%; Pred. No. 3.1e-99;
 Matches 218; Conservative 68; Mismatches 88; Indels 9; Gaps 2;

Qy 1 MGAGGRM-----SDPSEGNILERVVD-PEFTLSDLKKAIPTHCFERSVIRSSYYV 51
 Db 1 MGAGGRMSTVITSNSEKGGSSHLKAPRHPFTLGLDRLAIPPHCFERSVIRSSYYV 60
 Qy 52 VHDIVAVFYLLANTYIPLIPPLAYLAMPVYVFCQASITLGLMTVIGHECGHNASDYQ 111
 Db 61 AYDVLSTFLFYSIATNFPYISSPLSYAVMLVYVFCQASITLGLMTVIGHECGHNASDYQ 120
 Qy 112 LIDIVGVHLSALTLPYFSKWSHRNHNANTSLNDEYVYIPKRSKVYKYSKLNPP 171
 Db 121 LADIVGLVHLSALTLPYFSKWSHRNHNANTSLNDEYVYIPKRSKVYKYSKLNPP 180
 Qy 172 GRVFLVRLTIGFPLVLTNLSGKRYGRFANFPDMSPIFNDRERVOVLLSDPGLAVF 231
 Db 181 GRVTLTALTIGFPLVLTNLSGKRYGRFANFPDMSPIFNDRERVOVLLSDPGLAVF 240
 Qy 232 YAIKLVAAGAAVYNNATPVLGVSFVLTITLHTHTLSLPHYDSTERNWIKALST 291
 Db 241 FVLQATAAKGLAVWMLVGVPLLVNCFVMTVLTGHTHPALIDRYGSSSEMDWLRGAVT 300
 Qy 292 IDRPGRFLNRPVHDVTHVTHLHLSYIPHYAKARDAIKVLSYXVYIDRTPIFKAM 351
 Db 301 VDRDYGVLNRPVHDVTHVTHLHLSYIPHYAKARDAIKVLSYXVYIDRTPIFKAM 360
 Qy 352 REAKCIYIEPDESEHKGVFWMY 374
 Db 361 REAKCIYIEPDESEHKGVFWMY 383

RESULT 7

T15043
 fungal elicitor-induced protein - parsley
 C:Species: Petroselinum crispum (parsley)
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: T15043
 R:Kirsch, C.; Hahlbrock, K.; Somschich, I.E.
 Plant Physiol. 115, 283-289, 1997
 A>Title: Rapid and transient induction of a parsley microsomal delta 12 fatty acid desat
 A:Reference number: Z18274; MUID:97451781; PMID:9306702
 A:Accession: T15043
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-383 <KIR>
 A:Cross-references: EMBL:U86374; NID:92501791; PIDN:AAB80697.1; PID:92501792
 C:Genetics:
 A:Gene: EL112
 C:Superfamily: omega-3 fatty acid desaturase

Query Match 60.6%; Score 1241.5; DB 2; Length 383;
 Best Local Similarity 58.2%; Pred. No. 1.5e-96;
 Matches 221; Conservative 64; Mismatches 88; Indels 7; Gaps 4;

Qy 1 MGAGGRMSDSESGK---NIIERVVD-PEFTLSDLKKAIPTHCFERSVIRSSYYVHDL 55
 Db 1 MGAGGRMSDSESGKTAABALKRAHPKPTTIDLKKAIPHCFERSVIRSSYYVHDL 60
 Qy 56 IVAVFYLLANTYI-PLIPPLAYLAMPVYVFCQASITLGLMTVIGHECGHNASDYQLID 114
 Db 61 FMAAYLVAVYNTYIDQYLTPTPFNVYVMAAYIAVQGVLTGAMVVGHCCHDAFNTYWIN 120

Oy	115	IIVGVLVHSHALLTPVPSMKYSHRNHNHANNLSLDNDSVYI PKRSXYKYSKLINDPGRV	174
Dd	121	DIVGLVHSSHLVPFWSKI SHRRHHANQOSLENDVYDPRFKSNIRNYIKLINDPGRV	180
Oy	175	FTLVERLTIGFPLUYLLTNISGKKYGRFANHFDMSDIPENDREVOYLSDFGLLAVFYAI	234
Dd	181	LVMLTLLTILGFPLYLMFNVSCHKYEBSWTSHYDPSFLYSRKEKXIIIVSDIALIAVYDL	240
Oy	235	KLVAAKGAAWJINMYAIPVLGVSVRFVLIYTHLHHNLSLPHVDSTEMNNIKALSTIDR	294
Dd	241	YQVLTAKEGAMWF CYIGGPLVAVNGFVLYTTILNHHPSLPIYDOSTBMDLRKALCTVDR	300
Oy	295	DGFLNRRVFHDVTHTVLHLLSYIPIBHAKEARDAIKPVLGBEYKXIDRTPIKAMYREA	354
Dd	301	DYGILNKVFHNVCMNAVCHIFSMIPHYGLTESTEAMKRPILGYYQYGDGTPIIKAMYREM	360
Oy	355	KECITYEPDESEHKGVFWY	374
Dd	361	KECIYVEKDE-GETKGVWY	379

RESULT 8

omega-6 desaturase FAD2-1, microsomal - soybean
 C:Species: Glycine max (soybean)
 C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000
 C:Accession: T07687
 R:Heppard, E.P.; Kinney, A.J.; Stecca, K.L.; Miao, G.H.
 plant Physiol. 110, 311-319, 1996
 A:Title: Developmental and growth temperature regulation of two different microsomal
 A:Reference number: Z16095, PMID:96151506, PMID:8587990
 A:Accession: T07687
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-387 <HEP>
 A:Cross-references: EMBL:L43920, NID:g904151, PIDD:AA00859.1, PIR:g904152
 A:Experimental source: seed
 C:Genetics:
 A:Gene: FAD2-1
 C:Function:
 A:Description: involved in production of polyunsaturated lipids; plays a major role in c
 A>Note: strongly expressed in developing seeds
 C:Superfamily: omega-3 fatty acid desaturase

Query Match	60.5%	Score 1237.5;	DB 2;	Length 387;
Best Local Similarity	56.6%	Pred. No. 3.3e-56;		
Matches 213;	Conservative 70;	Mismatches 90;	Indels 3;	Gaps 3

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QY 1 GGAGGRMSDPS-EGKNILIERVP-VDPPTSLSDKKAITTHCEESVIRSSVVYVHDLIVA 58
Db 9 MGRGRVAKVEQGGKPPSLRVPNTKKPPTVQLKKAIPPHCFQBSLLTFSFYVYDLSFA 68
QY 59 YVYFYANTYIPLIPTPLAFLAMPYWFQOASILGLVWIGHCEGHAFSPYOLIDPIVG 118
Db 69 FIF-YIATTYTHLLOPFSLIAMPITWLOGLLGWAVIAHECGHAFSXIOWVDVWG 127
QY 119 FVLHSALLTPYFSWCKSHRNHHANTNSLNDNEVYIPKRSKVKIYSKLIANNPGSRFVLT 178
Db 128 LTHSHTLVPIYFSWCKSHRRHSHNSGSLDRBVEYIPKRSKSKYAMPSTKIANNPLORAASLL 187
QY 179 FRLTGLPFLYLLTNSGKKYGRFANHPDPSPIENDREVRVOLLSDFCGLLAVFYAIKLLV 238
Db 188 VLTIGWEMYLAFNVSGRPYDSFASHYHPYAPIENRRLLIYSDVALFVYISLYRVA 247
QY 239 AAKGAAMVIMNTAIVLGVSVFVLITYLHHTHLSLPHYDSTENWIKGALSTIDRDEGF 298
Db 248 TLKGIVMLTLCYGVAPLLVINGELVITIYLQHTHFALPHYDSEMDMLKGALATMDRDYGI 307
QY 299 LNRVHDVTHTHVHLHLSYIPHNHAKARDAIKRVAGEYVKIDRTPIFKMYAEAKECI 358
Db 308 LNRVHNHTDTHVHHLFSTYMPHYAMEATYNAIKRILGEYVOFDTPRYKALMBARCEL 367

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QY	359	YIEPDESEHKGVFWY	374
		: : : : : : :	
Db	368	YVEPDEGTSEKGVWY	383

RESULT 9

Delta12 fatty acid desaturase (EC 1.4.99.-) [imported] - common sunflower
 C\$Species: Helianthus annuus (common sunflower)
 C\$Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
 A\$Accession: T14269
 R\$Hombstrakul, V.; Slabaugh, M.B.; Knapp, S.J.
 submitted to the EMBL Data Library, February 1997
 A\$Description: Sunflower delta-12 oleate desaturase.
 A\$Reference number: Z17949
 A\$Accession: T14269
 A\$Status: preliminary; translated from GB/EMBL/DBJ
 A\$Molecule type: mRNA
 A\$Residues: 1-378 <HON>
 A\$Cross-references: EMBL:U91341; NID:g2290403; PTD:g2290404
 A\$Experimental source: Strain Mammoth
 C\$Function:
 A\$Description: desaturates oleic acid to linoleic acid
 C\$Superfamily: omega-3 fatty acid desaturase
 C\$Keywords: oxidoreductase; unsaturated fatty acid biosynthesis

Query Match	59.6%	Score 1220;	DB 2;	Length 378;
Best Local Similarity	56.7%	Pred. No. 9.4e-95;		
Matches 215;	Conservative 69;	Mismatches 91;	Indels 4;	Gaps 4

[illegible]

RESULT 10

omega-6 fatty acid desaturase (EC 1.14.99.-) defense-related - tomato
C|Species: Lycopersicon esculentum (tomato)
C|Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000
C|Accession: T07009
R|Gadea, J.; Mayda, E.; Conejero, V.; Vera, P.
Mol. Plant Microbe Interact. 9, 409-415, 1996
A|Title: Characterization of defense-related genes ectopically expressed in virid-infected
A|Reference number: Z15859; PMID:96252900; PMID:8672818
A|Accession: T07009
A|Status: preliminary; translated from GB/EMBL/DDJ
A|Molecule type: mRNA
A|Residues: 1-333 <GAD>

A:Cross-references: EMBL:X94944, NID:g1161567, PIDN:CAA64414.1, PID:g1161568
A:Experimental source: cultivar Rutgers; leaf
C:Genetics:
A:Gene: cev119
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 56.7%; Score 1160.5; DB 2; Length 353;
Best Local Similarity 55.1%; Pred. No. 8e-90;
Matches 209; Conservative 54; Mismatches 61; Indels 55; Gaps 5;

QY 1 MGAGRM-----SDSEGNILIERVVD--PPTLSLKKALIPHCERSVISSYVVDL 55
DB 1 MGGGNNAMTSKNEQKNPLERVPSSKRPPTLGVKKAIPHCERSLVXSFSLIDL 60
QY 56 IVAVFYIANTYIPLIPPLAYLAMPYVFCQASILGLMWIGHCNHAFSDYQLD 115
DB 61 ILVYIFYYIANTYIHLITPFRYVANTYVIAQGCVCIGVIGHGCHGFSDIQVDD 120
QY 116 IVGFVLSALLTPYFWMKYSRHHNANTSLDNDEVYIPKRSKYVSKLLNPPGRVF 175
DB 121 IVGLILHSALLTPYFAMGSHRRHANTGSLNDEIYIPRLKSKLR----- 166
QY 176 TLVRLTLGFLYLLTNSGKYGFRANHPMSPIFNDREVOYLLSDFLAVFAIK 235
DB 167 -----GKKYRFACHYDPSIYNRRRLQIYISDVIVATVYLLY 207
QY 236 LIVAAGAAWVINYAIPLVGVSVFVLTLYLHHTLSLPHYDSEKMWIKALSTDRD 295
DB 208 RVTITQGLAG-----FVITLHHTHSLPHYDSEMDHLGALATVDRD 253
QY 296 FGLNRFVHDVTHVHLHLSYIPHYAKARDAIKVLEGGYKIDRTPIPKMYREAK 355
DB 254 YGLNKFVHNVDTHVHLHPSYISHYAMEAKAIKVLDEYKYDDTPIKAMWMDTK 313
QY 356 ECIYIEPDESEHKGVFYH 374
DB 314 ECIYIEPDESEHKGVD 329

RESULT 11

JC7871
stearyl-CoA 9-desaturase (EC 1.14.19.1), FAD2 - *Chlorella vulgaris*
N:Alternate names: acyl-CoA desaturase; delta12 stearyl-CoA desaturase; delta9-desaturase
C:Species: *Chlorella vulgaris*
C>Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 31-Mar-2003
A:Accession: JC7871
R:Stuga, K.; Honjoh, K.; Furuya, N.; Shimizu, H.; Nishi, K.; Shinohara, F.; Hirabaru, Y.;
BioSci. Biotechnol. Biochem. 66, 1314-1327, 2002
A:Title: Two low-temperature-inducible *Chlorella* genes for delta12 and omega-3 fatty acid
desaturase, and expression of omega-3 fad in *Nicotiana tabacum*.
A:Reference number: JC7871, MUID:22152186, PMID:12162554
A:Accession: JC7871
A:Molecule type: mRNA
A:Residues: 1-376 <SUG>
A:Cross-references: DDBJ:AB075526
C:Comment: This enzyme is involved in low temperature adaptation, and is also involved in
A:Gene: fad2
C:Keywords: oxidoreductase

Query Match 45.3%; Score 926.5; DB 2; Length 376;
Best Local Similarity 45.9%; Pred. No. 4.1e-70;
Matches 175; Conservative 76; Mismatches 117; Indels 13; Gaps 8;

QY 3 AGGMSDPSSEGNILIERVVD--PPTLSLKKALIPHCERSVISSYVVDL 60
DB 2 AATRRASABG---WTRQPVVTKPAFSVSTLRKAIIPACWQSRSPRCAYLAADLALAA 58
QY 61 FYIYANTYIPLIPPLA--YLA-WPVYVFCQASILGLMWIGHCNHAFSDYQLD 117
DB 59 LVW-ASTFIDAPVPAVPAVWALMPAYWILAGAVATGIVIAHCGHAFSDYQAVNDGV 117

QY 118 GPTLHSALLTPYFWMKYSRHHNANTSLDNDEVYIPKRSKYVSKLLNPPGRVFTL 177
DB 118 GLVILHSLLVYVYWMKYSRHHNANTGVDVAVPEVPTREBVDKMLBQAWPRLVKL 177
QY 178 VFRITLGPFLYLLTNSGKYGFRANHPMSPIFNDREVOYLLSDFLAVFAIKL 236
DB 178 FITLGLPFLYLLNVAASRPFEKSVNHPDMSPIFSKRELVEVAASDAALVACGRQ 237
QY 237 LVAAGAAWVINYAIPLVGVSVFVLTLYLHHTLSLPHYDSEKMWIKALSTDRD 296
DB 238 LAASFGRMLVKTMLVPLVNVNFWLVTITMLQSHPELPHIGEDMDLRLGALLTVDDY 297
QY 297 GF-LNRFVHDVTHVHLHLSYIPHYAKARDAIKVLEGGYKIDRTPIPKMYREAK 355
DB 298 GMLNLSLHHTHIAOTHVAHLFSQMPHYAQAETALKVLDDYRSDSRPILQAIWDFG 357
QY 356 ECIYIEPDESEHKGVFYH 376
DB 358 SCRVAADPTGD--GVLMFRK 376

RESULT 12

AG2005
omega-3 fatty acid desaturase [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. PCC 7120
A:Notes: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
A:Accession: AG2005
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasaoto, S.; Watanabe, A.; Iriiguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
A:Reference number: AB1807, MUID:21595285, PMID:11759640
A:Accession: AG2005
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA877963.1; PID:g17135417; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all1597
C:Superfamily: omega-3 fatty acid desaturase

Query Match 32.2%; Score 658.5; DB 2; Length 359;
Best Local Similarity 35.7%; Pred. No. 1.2e-47;
Matches 121; Conservative 76; Mismatches 123; Indels 19; Gaps 6;

QY 25 PFTLSLKKALIPHCERSVISSYVVDLIVAVFYIANTYIPLIPPLAYLAMPVY 84
DB 24 PFTLQDLKALIPACFPQPNVSKSLFYFPRDVLVGLLYAVAH-YLD-----SWYFWDIF 76
QY 85 WFCQASILGLMWIGHCNHAFSDYQLDIVEFVLHSALLTPYFWMKYSRHHNANTN 144
DB 77 WLIGTWFMAFLFVVGHCQHSFQKXKMLNDLIGHLTHITFLVYHOMRISHRTHNKTG 136
QY 145 SLNDDEVYIPKRSKYVSKLLNPPGRVFTLVRITLGPFLYLLTNSGKYGFRANH 204
DB 137 NINDSEWYPTQSYK-----EMPLGQKIGRYVLLAVPLVLPKRSPEK-----GSH 186
QY 205 FDPMSPIFNDREVOYLLSDFLAVFAIKLIVAAGAAWVINYAIPLVGVSVFVLI 264
DB 187 FLPESSLFKPSSEKMDVITSLVMSGVGLGFLVYQGMWMLKYVAAPYLVFVITWDLV 246
QY 265 TYLHHTLSLPHYDSEKMWIKALSTDRDVGFLNRFVHDVTHVHLHLSYIPHYA 324
DB 247 TFLHHTRADLPWRGSEMDTFLKGAISSIDRYGLVNHNIHDI-GTHVAHHIPLNI PHYNL 305
QY 325 KEARDAIKPVLEGGYKIDRTPIPKMYREAKECYIEPD 363
DB 306 LKATKAIKPVWGGYIKRSSEPIKSLMRSCVSCHFV-PD 343

RESULT 13

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A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-441 <HAM>
A:Cross-references: EMBL:D79979; NID:G1694624; PIDs:BA11475.1; PID:G1694625
A:Experimental source: cultivar SRI
C:Genetics:
A:Gene: PAD7
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match      31.5%; Score 645; DB 2; Length 441;
Best Local Similarity 35.6%; Pred. No. 2,Je-46;
Matches 137; Conservative 56; Mismatches 113; Indels 40; Gaps 9;

QY 3 AGGMSPPSEKGNLIERVPDPPETLSDLKAIPTHCFEFSVIRSSYYVHDLIVAVF- 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 82 SGGFFPRPG-----APPPKSLDIAIKIKHCWKNPKMSNSVYRD--VALVFG 129
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 62 ----YYIANTYIPLIEPTPLAYIAMPYVWFCQASILGLWVIGECGHAFSDYQIDDI 116
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 130 LAAAAAFENN-----WVWVPLWYFAQSTMFALFVLGHDCHGSGFSNNHKLNSV 178
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 117 VGFVLHSAALLTPYFSWKYSRHNHNHANTSLDNDENVYIPKRSKRYIKSKLANPGRVET 176
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 179 VGHILHSSILVPYQWGRISHRTHQNHGHVENDSMHPHE--KYNSLDLATKRLFT 235
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 177 LVPELTGLFPIYLLTNTLSGKKYGFPAHFDPMSIPFNDREVOYLLSDPGLIAVFAIKL 236
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 236 LPFPL-LAPYPRPLVSRSPGKK---GSHFDPNSDLFPESEKDYMTSLCTNPAALIVG 290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 237 LVAAGAAWVYINMYAIVLVGVSVFVLLITLHN--THSLPHYDSTENWIKALSTIDR 294
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 291 LSPWGPFOYAKYLGIFYWGVWMLDLVTYLHHGHGDKLPMYRGEEVSYLRGGLTIDR 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 295 DFGFLANVFHDVTHVLAHLHILSTIPHYAKAADAIKPVIGEYK 340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 351 DYGINNIHHD1-GTHVILHLPQIPHYHLVEATEAKPVLGKYK 395
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 15
T11063
omega-3 fatty acid desaturase (EC 1.14.99.-) PAD7 - caetor bean
N:Alternate names: 1lnoleoyl desaturase
C:Species: Ricinus communis (castor bean)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T11063
R:ide Loo, F.J.; Somerville, C.
Plant Physiol. 105, 443-444, 1994
A:Title: Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis.
A:Reference numbers: Z16930; MUID:94302177; PMID:8029360
A:Accession: T11063
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-160 <DBJ>
A:Cross-references: EMBL:L25897; NID:G414731; PIDs:AAA73511.1; PID:G414732
A:Experimental source: cultivar Baker 296; tissue-type seed
C:Genetics:
A:Gene: PAD7
C:Function:
A:Pathway: fatty acid biosynthesis
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match      31.2%; Score 639.5; DB 2; Length 460;
Best Local Similarity 35.5%; Pred. No. 6,5e-46;
Matches 134; Conservative 72; Mismatches 134; Indels 37; Gaps 9;

QY 12 EGNKILERVYDPPPTLSDLKAIPTHCFEFSVIRSSYYVHDLIVAVF----VYYIANT 67
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 96 EKGGEFFPDAGAPPFPTLADIPAAIPKHCWKNPKMSNSVYLRDVVVVVGGLAAVAFENN- 154
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 68 YIPLIPFLAYIAMPYVWFCQASILGLWVIGECGHAFSDYQIDYIDIVGFLHSAIILT 127
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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Db 155 -----WVAMPWYECQGTMEWALFVLGHDCGHSFSNNPKLNSVGHLLHSSILV 204
Qy 128 PYFSMKYSHRHHANTNSLDNDEVYIPKRSKVKIYSKLNNPGRVFTLVFRLTIGPPL 187
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 PYHGRISHRTHQHNGHVENDESGHPLSE---KIFKSLDNVTYKTLRFSLPFPM-LAYPF 260
Qy 188 YLLTNISGKKYGRFANHPDPMSPIFNDRERVQLISDFGLLAVFYAIKLVAAKGAAMVI 247
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 261 YLMRSRPGKK-----GSHFHPDGLFVPERKDIITSTACWTAMALLVYLNFSGMPVQML 316
Qy 248 NMVAIPVLGVSVFVLITYLH--THLSLPHYDSTENNMKIGALSTIDRSGFLNRVFD 305
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 317 KLYGIPYWI FVWMLDFVYLHHGHEDKLPWYRGKAMS YLRGGLTTLDRDYGWINNIHD 376
Qy 306 VTHHTVHLHLISYIPHYHAKAARDAIKPVLGEYKIDRTP-----IFKAMYREAKECIY 359
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 377 I-GTHVTHHLFPQIPHYHLVATEAKAPVMGKYIREPKSGPLPLHLGLSLVRSMKEDHY 435
Qy 360 IEPDESEHKGVFWYHK 376
    ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 436 VSDTGD-----VYVYOK 447

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Search completed: June 18, 2004, 17:38:26
 Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 18, 2004, 17:30:33 ; Search time 18 seconds
(without alignments)
1090.580 Million cell updates/sec

Title: US-10-069-772-2
Perfect score: 2047
Sequence: 1 MGACGRMSDBSEGNILERV.....IYIEPDESEHKGVFWYHKM 377

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1629	79.6	375	D12_CREAL	O81931 crepis alpi
2	1325.5	64.8	383	PD62_SOYN	P48631 glycine max
3	1301	63.6	384	PD6E_BRAYU	Q32877 brassica ju
4	1300.5	63.5	383	PD6E_BRAYU	P46313 arabidopsis
5	1237.5	60.5	387	PD61_SOYN	P48630 glycine max
6	782	38.2	400	PD12_MORIS	P53668 mortierella
7	781	38.2	400	PD12_MORAP	Q97855 mortierella
8	642	31.4	447	PD3C_SESIN	P48620 sesamum ind
9	639.5	31.2	460	PD3C_RICCO	P48619 ricinus com
10	620.5	30.3	386	PD3E_ARATH	P48623 arabidopsis
11	612	29.9	379	PD3E_TOBAC	P48626 nicotiana t
12	607	29.7	404	PD3C_BRANA	P48618 brassica na
13	606	29.6	446	PD3C_ARATH	P46310 arabidopsis
14	602.5	29.4	451	PD3C_SOYN	P48621 glycine max
15	598.5	29.2	435	PD3D_ARATH	P48622 arabidopsis
16	593.5	29.0	380	PD3E_PHAVU	P33291 phaseolus a
17	588.5	28.7	383	PD3E_BRANA	P48624 brassica na
18	574	28.0	380	PD3E_SOYN	P48625 glycine max
19	316.5	15.5	447	PD3C_SPIOL	P48625 spinacia ol
20	309.5	15.1	351	PD3A_SYNY3	P20388 synchocyst
21	306	14.9	424	PD3C_SOYN	P48628 glycine max
22	301	14.7	448	PD6C_ARATH	P46312 arabidopsis
23	293.5	14.3	443	PD6C_BRANA	P48627 brassica na
24	292	14.3	351	PD3A_SYNY3	Q54794 spirulina p
25	169.5	8.3	359	LI2D_SYNY3	Q08871 synchocyst
26	110	5.4	1191	S122_SYNY3	P55013 equalus aca
27	101	4.9	1212	S122_HUMAN	P55011 homo sapien
28	97	4.7	320	CR2W_HABPL	Q39982 haemacococc
29	96.5	4.7	390	ARP2_SCHPO	Q9U011 schizosacch
30	95.5	4.7	711	FR33_YEAST	Q08957 schizosacch
31	95.5	4.7	1044	YAF3_SCHPO	Q08957 schizosacch
32	94	4.6	313	CCSA_TOBAC	P12216 nicotiana t
33	94	4.6	794	POT2_ARATH	O22881 arabidopsis

34	94	4.6	973	1	HYPA_CLOPE	Q46205 clostridium
35	93	4.5	888	1	POL_SMRVA	P03364 squitrel mo
36	93	4.5	1205	1	S1205_MOUSE	P55012 mus musculu
37	92.5	4.5	514	1	MYIN_BUCAP	Q8K913 buchnera ap
38	92	4.5	1353	1	CYAS_MOUSE	P51830 mus musculu
39	91.5	4.5	359	1	ACOD_BOVIN	Q8T94 bos taurus
40	91	4.4	444	1	FADS_BRARE	Q9DEX7 brachydiano
41	91	4.4	1353	1	CYAS_HUMAN	O60503 homo sapien
42	90.5	4.4	346	1	FMLR_MACMU	P79189 macaca mula
43	89.5	4.4	1026	1	EXSB_CHLMU	Q9PL18 chlamydia m
44	89	4.3	870	1	POL_TSRV	P31623 sheep pulmo
45	88	4.3	499	1	PTRA_ECOLI	P37308 escherichia

ALIGNMENTS

RESULT 1
ID- D12_CREAL STANDARD; PRT; 375 AA.
AC O81931;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Delta(12) fatty acid dehydrogenase (EC 1.14.99.33) (Crepennate synthase) (Delta-12 fatty acid acetylase).
OS Crepis alpina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; OC Campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
OC Crepis.
OX NCBI_TaxID=72610;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96239771; PubMed=9572738;
RA Lee M., Lemman M., Banas A., Bator M., Singh S., Schweizer M.,
RA Nilsson R., Liljenberg C., Dahlqvist A., Gummesson P.O., Sjodahl S.,
RA Green A., Stymer S.;
RT "Identification of non-heme diiron proteins that catalyze triple bond and epoxy group formation";
RL Science 280:915-918(1998).
CC -1- FUNCTION: Changes the delta-12 double bond of linoleic acid into a triple bond in the biosynthesis of crepennic acid.
CC -1- CATALYTIC ACTIVITY: Linoleate + AH(2) + O(2) = crepennate + A + H(2)O.
CC -1- COFACTOR: Iron.
CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Seed.
CC -1- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.
CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
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CC -----
DR EMBL, Y16285; CAAT6158.2; -;
DR InterPro, IPR005804; FA_desat_fam.
DR Pfam, PF00487; FA_desat_fam; 1.
DR ProDom, PD001081; FA_desat_fam; 2.
KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Iron.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 77 97 POTENTIAL.
FT TRANSMEM 110 130 POTENTIAL.
FT TRANSMEM 172 192 POTENTIAL.
FT TRANSMEM 218 238 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
FT DOMAIN 98 102 HISTIDINE BOX-1.

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. 651-2-5-7-4;
 RA Singh S.P., van der Heide T., McKinney S., Green A.;
 RT "Nucleotide sequence of a cDNA from *Brassica juncea* encoding a
 RL microsomal omega-6 desaturase.";
 CC (in) Plant Gene Register PGR95-107.
 CC -1- FUNCTION: ER (microsomal) omega-6 fatty acid desaturase introduces
 CC the second double bond in the biosynthesis of 18:3 fatty acids;
 CC important constituents of plant membranes. It is thought to use
 CC cytochrome b5 as an electron donor and to act on fatty acids
 CC esterified to phosphatidylcholine and, possibly, other
 CC phospholipids (by similarity).
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL/ X91139; CAA62578.1; -;
 DR InterPro; IPR005804; FA_desat. fam.
 DR Pfam; PF00487; FA_desaturase; 1.
 DR ProDom; PD001081; FA_desat. fam; 2.
 DR KEGG; 01000; Fatty acid biosynthesis; Endoplasmic reticulum;
 KM Transmembrane.
 FT TRANSMEM 56 76 POTENTIAL.
 FT TRANSMEM 84 104 POTENTIAL.
 FT TRANSMEM 117 137 POTENTIAL.
 FT TRANSMEM 180 200 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 253 273 POTENTIAL.
 FT DOMAIN 105 109 HISTIDINE BOX-1.
 FT DOMAIN 141 145 HISTIDINE BOX-2.
 FT DOMAIN 316 320 HISTIDINE BOX-3.
 SQ SEQUENCE 384 AA; 44315 MW; 43AF77CE9861A492 CRC64;
 Query Match 63.6%; Score 1301; DB 1; Length 384;
 Best Local Similarity 60.6%; Pred. No. 2e-97;
 Matches 231; Conservative 60; Mismatches 84; Indels 6; Gaps 4;
 QY 1 MGAGGRMS-DESEK--NILERVVD-PPTLSLKKAIPTHCERSVIRSSYYVHDL 55
 DB 1 MGAGGRMQVSPSPKSEETDTLKRVCCEPPTVGLKKAIPPHCKRSISPSFYLWIDI 60
 QY 56 IVAVFVYLANITYPLIPTLALAYLAWPYWFCQASILGLWVIGHCCHNAFSDQLDD 115
 DB 61 IVASCFYVATYPLPLPLPPLPLPLPLPLPLPLPLPLPLPLPLPLPLPLPLPL 120
 QY 116 IVGEVLASALTPEFSWKSHRNHNANTSLDNDEVYIPKRSKYKYSKLLNPPGRVF 175
 DB 121 TVGLIFHSFLVLPFSWKSHRNHNANTSLDNDEVYIPKRSKYKYSKLLNPPGRVF 180
 QY 176 TLVRLTLFPLLYLTNLSGKKYGR-FANHPDMSPIFNDESRVOLLSDFGLLAVFYAI 234
 DB 181 MLTVQFTLGMPLLYANFVNSGRPRGACHFPNAPFIYNDERLQIYVSDGIIAVCYGL 240
 QY 235 KLVLAAGKAAMVIMMYALPVGVSEFTLYLTHHTHLSLPHYSTENWIKGALSTIDR 294
 DB 241 YRYAAAGQVAVCVLYGVPLLVANFLVLTLYLQHTHSLPLHYSSSEMDLKGALATADR 300
 QY 295 DFGELNRFVDVTVTHVLAHLISYPRYHAKARDAIPVAGEYKIRTPIFKAMVREA 354
 DB 301 DYGILNKYFNHTIDTHVAHHLFSTMPKHNHAMEVTKAIRIIGDYQFPGTVMYRAMREA 360
 QY 355 KECIYIEPDDESEHKGVFWYN 375
 |||||:|||||:|||||:

DB 361 KECIYIEPDDESEHKGVFWYN 381
 RESULT 4
 PDBE_ARATH STANDARD; PRT; 383 AA.
 ID_PDBE_ARATH
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-)
 DE (Delta-12 desaturase).
 GN FAD2 OR AT3G12120 OR T23B7.6 OR T21B14.6 OR T21B14_107.
 OS Arabidopsis thaliana (mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OK NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94176997; PubMed=7907506;
 RX Okuley J., Lightner J., Feldmann K.A., Yadav N., Lark E., Browne J.;
 RT "Arabidopsis FAD2 gene encodes the enzyme that is essential for
 RL polyunsaturated lipid synthesis.";
 RL Plant Cell 6:1147-1158(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=20363099; PubMed=10907853;
 RA Kaneo T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
 RT and BAC clones.";
 RL DNA Res. 7:217-221(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Anseorge W., Unseid M.,
 RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
 RA Delseny M., Bouty M., Grivell L.A., Maché R., Puigdomenech P.,
 RA De Simone V., Choisme N., Artiguenave F., Robert C., Brocletier P.,
 RA Wincker P., Catalillo L., Weissenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Mumbach R., Drzonek H., Erle H., Jordan N., Bandert P.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nykatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordiek J.,
 RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-liauro C., Purnelle B., Masny D.,
 RA de Haan M., Maaree A.C., Alcaraz J.-P., Cottet A., Casacubeta B.,
 RA Monfort A., Argitlou A., Flores M., Liguori R., Vitale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Uteback T., Fujii C.Y., Shea T.P.,
 RA Crasy T.H., Haas B., Maizi R., Wu D., Peterson J., Van Aken S.,
 RA Pai G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
 RA Preuss D., Lin X., Nijman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant *Arabidopsis*
 RT *thaliana*.";
 RT Nature 408:820-822(2000).
 CC -1- FUNCTION: ER (microsomal) omega-6 fatty acid desaturase introduces
 CC the second double bond in the biosynthesis of 18:3 fatty acids;
 CC important constituents of plant membranes. It is thought to use
 CC cytochrome b5 as an electron donor and to act on fatty acids
 CC esterified to phosphatidylcholine and, possibly, other
 CC phospholipids.

CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC -----
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 CC -----
 CC EMBL: L26296; AA32782.1; -
 CC EMBL: AP002063; BAB01960.1; -
 CC EMBL: AC069473; AAG51042.1; -
 CC InterPro: IPR005804; FA_desat_fam.
 CC Pfam: PF00487; FA_desaturase; 1.
 CC ProDom: PD001081; FA_desat_fam; 2.
 CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 CC Transmembrane.
 CC TRANSMEM 56 76 POTENTIAL.
 CC TRANSMEM 117 137 POTENTIAL.
 CC TRANSMEM 179 199 POTENTIAL.
 CC TRANSMEM 225 245 POTENTIAL.
 CC TRANSMEM 252 272 POTENTIAL.
 CC DOMAIN 105 109 HISTIDINE BOX-1.
 CC DOMAIN 141 145 HISTIDINE BOX-2.
 CC DOMAIN 315 319 HISTIDINE BOX-3.
 CC SEQUENCE 383 AA; 44047 MW; 8815ADD2D3B8C982 CRC64;

Query Match 63.5%; Score 1300.5; DB 1; Length 383;
 Best Local Similarity 59.5%; Pred. No. 2.2e-97;
 Matches 226; Conservative 65; Mismatches 84; Indels 5; Gaps 2;

QY 1 MGAGGRMDPSRCK---NILERVVD--PPTFLSDLKALPHCEBSVIRSYVHDL 55
 DB 1 MGAGGRMPVPTSSKSEDTTKRVCCKPSPFVGDLKAIIPHCKRSIPRFSYLSIDI 60
 QY 56 IVAVFFYLLANTYIPILPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQLIDD 115
 DB 61 IIAFCFYVATNYFSLPQLPQLSTYLAMPYLMACQGVLTGVIWIAHECGHAFSDYQLIDD 120
 QY 116 IVGFVLSALLTPYRSWKYSRRNHNANTNSLDNDEVYIPKRSKYKYSKILNPPGVE 175
 DB 121 TVGLTFHSFLVLPYFSWKYSRRNHNANTNSLDNDEVYIPKRSKYKYSKILNPPGVE 180
 QY 176 TLVPLTLGFPYLTLTNSGKKYGRFANHPDMSPIFNDRERVOYLSDFGLLAVFAIK 235
 DB 181 MLTVQFVLGWPVLYLAFNVSGRPYDGPACHFFPNADPIYNDRELTQYLSDDAGILLAVCFGLY 240
 QY 236 LLVAAGAMVINVMAIPVLGVSVFVLITVYLLHHTLSLPHYDSEEMNIGALSTIIRD 295
 DB 241 RYAAAGMAMSMICLXGVPLILVNAFLVILITVYQHHTPSLPHDSSSEMDLRAALTVDRD 300
 QY 296 FGLNRFVHDVTHVHLHLISYIPHYAKKARDAIKPVLAGYKIDRTPIFKANYREAK 355
 DB 301 YGILNKVFHNITDTVAHHLFSTMPHYNAMEATKAIKPLGDYQYQDFGTPWVANYREAK 360
 QY 356 ECIYEPEDESEHKGVFWYH 375
 DB 361 ECIYVEPRREGDKGVWYWN 380

RESULT 5
 ID_FDB1_SOYBN STANDARD; PRT; 387 AA.
 AC P48630;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 1

DN (EC 1.14.19.-).
 OS Glycine max (Soybean).
 GN Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=96151506; PubMed=8587990;
 RA Heppard E.P., Kinney A.J., Stecca K.L., Miao G.H.;
 RT "Developmental and growth temperature regulation of two different
 RL microsomal omega-6 desaturase genes in soybeans";
 RL Plant Physiol. 110:311-319(1996).
 CC -1- FUNCTION: ER (microsomal) omega-6 fatty acid desaturase introduces
 CC the second double bond in the biosynthesis of 18:3 fatty acids,
 CC important constituents of plant membranes. It is thought to use
 CC cytochrome b5 as an electron donor and to act on fatty acids
 CC esterified to phosphatidylcholine and, possibly, other
 CC phospholipids.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum.
 CC -1- TISSUE SPECIFICITY: Strongly expressed in developing seeds.
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC -----
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 CC -----
 CC EMBL: L43920; AAB00859.1; -
 CC PIR: T07687; T07687.
 CC InterPro: IPR005804; FA_desat_fam.
 CC Pfam: PF00487; FA_desaturase; 1.
 CC ProDom: PD001081; FA_desat_fam; 2.
 CC Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;
 CC Transmembrane.
 CC TRANSMEM 54 74 POTENTIAL.
 CC TRANSMEM 87 107 POTENTIAL.
 CC TRANSMEM 121 141 POTENTIAL.
 CC TRANSMEM 183 203 POTENTIAL.
 CC TRANSMEM 227 247 POTENTIAL.
 CC TRANSMEM 251 271 POTENTIAL.
 CC DOMAIN 109 113 HISTIDINE BOX-1.
 CC DOMAIN 145 149 HISTIDINE BOX-2.
 CC DOMAIN 319 323 HISTIDINE BOX-3.
 CC SEQUENCE 387 AA; 44662 MW; 49068805C21A1C31 CRC64;

Query Match 60.5%; Score 1237.5; DB 1; Length 387;
 Best Local Similarity 56.6%; Pred. No. 2.6e-92;
 Matches 213; Conservative 70; Mismatches 90; Indels 3; Gaps 3;

QY 1 MGAGGRMDPS-EGKNILERV-VDPPTFLSDLKALPHCEBSVIRSYVHDLIVA 58
 DB 9 MGGRGVAKVAVQGGKPSRVPNTKPTPTVQLKKAIPHCFQSLTSPSYVAVDLFA 68
 QY 59 YVFFYLLANTYIPILPTPLAYLAMPVYWFQASILTGLWVIGHECGHAFSDYQLIDDIVG 118
 DB 69 FIF-YIATTFPHLLPQPSLAMPYLVWLQGCCLLTGLVWVIAHECGHAFSKQWDDVVG 127
 QY 119 FVLHSALLTPYRSWKYSRRNHNANTNSLDNDEVYIPKRSKYKYSKILNPPGVEFTLV 178
 DB 128 LTLHSTLLVLPYFSWKYSRRNHNANTNSLDNDEVYIPKRSKYKYSKILNPPGVEFTLV 187
 QY 179 FRITLGFPLYLTLTNSGKKYGRFANHPDMSPIFNDRERVOYLSDFGLLAVFAIKLV 238
 DB 188 VTLTIGWPMVLYLAFNVSGRPYDGPASHYHPAPVYISNRRERLTIYSDVALFSVTYLSLYRA 247

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QY 239 AAKGAAMVANNYALPVLGVSVEFVLLITLHHTLSLPHYDSTENWIKALSTIDRDPG 298
DB 248 TLKGIVMLLCYGVFLILVNGFLVITLQHTHFALPHYDSEMDWLKALATMDRDYGI 307
QY 299 LNRVHDVTHVHLHLISYIPHYAKARDAIKRVGLGEYKIDTPTFKMYRAKACGI 358
DB 308 LNRVFNHTDTHVHHLSTMPHYAMEATNAIKPILGEYQFDPTPFYKALMREARBL 367
QY 359 YIEPDESEHKGVFWY 374
DB 368 YVEDEGTSEKGVWY 383

RESULT 6
FD12 MORIS
ID _FD12 MORIS STANDARD; PRT; 400 AA.
AC PS9668;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella isabellina (Umbelopsis isabellina).
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mucorales;
OC Mucorales incertae sedis; Umbelopsis.
OX NCBI_TaxID=91625;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M6-22;
RA Liu L., Li M., Xing L., Hu G.;
RL "Delta 12 fatty acid desaturase mRNA of Mortierella isabellina."
CC Submitted (SFP-2001) to the EMBL/Genbank/DBJ databases.
CC -1 FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
CC to linoleic acid (delta9, delta12-18:2) (by similarity).
CC -1 PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1 DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -1 SIMILARITY: Belongs to the fatty acid desaturase family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF417245; AAL1301.1;
DR InterPro; IPR005804; FA_desat_fam.
DR Pfam; PF00487; FA_desaturase; 1.
DR ProDom; PD001081; FA_desat_fam; 1.
KM Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.
FT TRANSMEM 91 111 POTENTIAL.
FT TRANSMEM 199 219 POTENTIAL.
FT TRANSMEM 245 265 POTENTIAL.
FT TRANSMEM 277 297 POTENTIAL.
FT DOMAIN 112 116 HISTIDINE BOX-1.
FT DOMAIN 148 152 HISTIDINE BOX-2.
FT DOMAIN 339 343 HISTIDINE BOX-3.
SQ SEQUENCE 400 AA; 46016 MW; F5512D3F8210DBD2 CRC64;

Query March 38.2%; Score 782; DB 1; Length 400;
Best Local Similarity 39.8%; Pred. No. 1.2e-55;
Matches 156; Conservative 63; Mismatches 135; Indels 38; Gaps 6;
QY 10 PSEGNLIERVVPPTLSDKKAIPTHCEFSYIRSSYYVVDLIVAVFYFLANYI 69
DB 22 PTKAKPAERNYQPEFTIKERICIPAHCFERSGLRGLCHVAIDLWTASLL-FLAAQI 80
QY 70 PLITPL-AYLAWVYVFCQASILTLGVLVIGHCGHAHAFSYQYLIDIVGVLSALITP 128
DB 81 DKFENPLIRYLAWPAYWIMQIGVCTGIWVLAHCEGHOSFSTSKTLNNTVGWILHSMILVP 140

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QY 129 YFSWKYSHRNHANTNSLDNDEVYIPKRKSKVYIKLNNPGR----- 173
DB 141 YHSWRISHSKHKHAKTGHMTKDQVFPVKRSQVGL-----PKKSAANAAGEEDMSVHL 193
QY 174 -----VFLVRLITLGFLLYLTINISGKKYGFANHPFPMSTIFNDRERQVLTSLDF 225
DB 194 DEBAPVTLFVWVVIQFLGWPAYLIMNASGDYGRWSTHFTYSPFEPBRPFDDIISDL 253
QY 226 GLLAVFVAIKLVAAGAAVYNNYALPVLGVSVEFVLLITLHHTLSLPHYDSTENWI 285
DB 254 GVLNALGALITYASQSLITLTKYIIPYLVNFWMLITLQHTDPLPHYBSAAMFQ 313
QY 286 KQALSTIDRDPG-FLNRVHDVTHVHLHLISYIPHYAKARDAIKRVGLGEYKIDT 344
DB 314 RQALCTVDRSFGKFLDHFHFGIVHTHVAHHLFSGQWPFHAEATYHKLKLGYYVYDPS 373
QY 345 PIFKAMTRAEKCIYIEPDESEHKGVFWYHK 376
DB 374 PIVVAWRSFRCRFVE-----DHQDVVFPKK 400

RESULT 7
FD12 MORAP
ID _FD12 MORAP STANDARD; PRT; 400 AA.
AC Q9Y8H5; Q96TH3; Q9UVV4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Delta-12 fatty acid desaturase (EC 1.14.99.-).
OS Mortierella alpina.
OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Mortierellales;
OC Mortierellaceae; Mortierella.
OX NCBI_TaxID=64516;
RN [1]
RP SEQUENCE FROM N.A. AND FUNCTION.
RC STRAIN=IS-4;
RA MEDLINE=99234062; PubMed=10215899;
RA Sakurudani E., Kobayashi M., Ashikari T., Shimizu S.;
RT "Identification of delta12-fatty acid desaturase from arachidonic
RT acid-producing Mortierella fungus by heterologous expression in the
RT yeast Saccharomyces cerevisiae and the fungus Aspergillus oryzae."
RL Eur. J. Biochem. 261:812-820(1999).
RN [2]
RP SEQUENCE FROM N.A. AND FUNCTION.
RC STRAIN=ATCC 32221;
RX MEDLINE=99406036; PubMed=10478922;
RA Huang Y.-S., Chaudhary S., Thurmond J.M., Bobik E.G. Jr., Yuan L.,
RA Chan G.M., Kirchner S.J., Mukerji P., Knutson D.S.;
RT "Cloning of delta12- and delta6-desaturases from Mortierella alpina
RT and recombinant production of gamma-linolenic acid in Saccharomyces
RT cerevisiae."
RL Lipids 34:649-659(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 16266;
RA Liu L., Li M., Xing L., Hu G.;
RL "Delta 12 fatty acid desaturase gene of Mortierella alpina."
CC Submitted (SFP-2001) to the EMBL/Genbank/DBJ databases.
CC -1 FUNCTION: Catalyzes the desaturation of oleic acid (delta9-18:1)
CC to linoleic acid (delta9, delta12-18:2).
CC -1 PATHWAY: C20 polyunsaturated fatty acid biosynthesis.
CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1 DOMAIN: The histidine box domains may contain the active site
CC and/or be involved in metal ion binding.
CC -1 SIMILARITY: Belongs to the fatty acid desaturase family.
CC -----
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CC -----

DR EMBL; AB020033; BAA81754.1; -

DR EMBL; AF110509; AAF08684.1; -

DR EMBL; AF117244; AAL13300.1; -

DR GO; GO:0016021; C: integral to membrane; NAS.

DR GO; GO:0006633; P: oxidoreductase activity; IDA.

DR InterPro; IPR005804; FA_desat_1fam.

DR Pfam; PF00487; FA_desaturase; 1.

DR Prodom; P0001081; FA_desat_fam; 1.

KW Oxidoreductase; Fatty acid biosynthesis; Transmembrane; Repeat.

FT TRANSMEM 91 111 POTENTIAL.

FT TRANSMEM 199 219 POTENTIAL.

FT TRANSMEM 245 265 POTENTIAL.

FT TRANSMEM 277 297 POTENTIAL.

FT DOMAIN 112 116 HISTIDINE BOX-1.

FT DOMAIN 148 152 HISTIDINE BOX-2.

FT DOMAIN 339 343 HISTIDINE BOX-3.

FT CONFLICT 17 19 STS -> TTT (IN REF. 3).

FT CONFLICT 21 23 APT -> PN (IN REF. 2).

FT CONFLICT 95 95 A -> V (IN REF. 2).

FT CONFLICT 107 107 I -> V (IN REF. 2).

FT CONFLICT 179 179 N -> S (IN REF. 3).

FT CONFLICT 180 182 AAA -> VAV (IN REF. 1).

FT CONFLICT 261 261 A -> T (IN REF. 1).

FT CONFLICT 280 280 V -> I (IN REF. 3).

FT CONFLICT 358 358 Y -> H (IN REF. 2).

FT CONFLICT 392 392 H -> Q (IN REF. 2).

SC SEQUENCE 400 AA; 46001 MW; 40B2FCLC1E01E93F CRC64;

Query Match 38.2%; Score 781; DB 1; Length 400;

Best Local Similarity 40.3%; Pred. No. 1.5e-55;

Matches 156; Conservative 64; Mismatches 139; Indels 28; Gaps 6;

QY 10 PSEGNILERVVDPEFTLSDKKAIPTHCERSVIRSSYVVDLIYAVYVYIANTYI 69

DB 22 PLSAKPAERKYQDPEFTIKRECIPTACFERSGLRGICHAIDLTVASL-FLAAIOTI 80

QY 70 PLIPPL-AYLAMPYVFCQASILTGLWVIGHECGHHAESDYQLIDIVGVFASALTP 128

DB 81 DKFENPLRLYLAMPYVIMOGIVCTGIWVLAHCEGHQSISKTLNNTVGMVILHSMILVP 140

QY 129 YFSWKYSRHNHANTNSLDNDEVYIPKRSKYIYSKLIIN-----P 170

DB 141 YHSWISHSKHKAKGHMTKQVFPVKTRSGVGLPPK--ENAAAVOEEDMSVHLDEAP 198

QY 171 PGRVETLPLRLTGLPFLVLTNLSGKKYGRFANHPDMSPIFNDRERVOVLSDPGLAV 230

DB 199 IYTLWMVYIQLFEGPAILIMNASGQDYGRTSHHTYSPLEPPNFDITISDLGLAA 258

QY 231 FYAIFLVAAGAAVIMMYAIPVLGVSVFVLYLYLHHTHLSLPHYDSTEMNWKIGALS 290

DB 259 LGAALVAMQSLVLTVTYKYIVPYLPVFWVLILIFLQHTDPKLPHYREGAMNPGRLALC 318

QY 291 TIDRDFG-FLNRVPHDVTHTVLHLLISYIPHYAKARDAIKPVLGSIYKIDRTPIKA 349

DB 319 TVDRFEGFLDMHFGIIVTHVAHLLFQMPFYHAEEATYHLKLLGEEYVVDPSPIVA 378

QY 350 MYRAKECIYTERPDDSEHKGVFWYHK 376

DB 379 VWRSEFRCRFEV-----DHGDVVFPEKK 400

RESULT 8

FD3C_SESIN STANDARD; PRT; 447 AA.

AC P46620;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).

GN PAD7.

OS Sesamum indicum (Oriental sesame) (gingelly).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Lamiales; Pedaliaceae; Sesamum.

OC NCBI_TaxID=4182;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. 4294; TISSUE=Cotyledon;

RA Shoji K.;

RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the third double bond in the biosynthesis of 16:3 and 18:3 fatty acids, important constituents of plant membranes. It is thought to use ferredoxin as an electron donor and to act on fatty acids esterified to galactolipids, sulfolipids and phosphatidylglycerol.

CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).

CC -1- DOMAIN: The histidine box domains may contain the active site and/or be involved in metal ion binding.

CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.

CC -----

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CC -----

DR EMBL; U25817; AAA70334.1; -

DR InterPro; IPR005804; FA_desat_1fam.

DR Pfam; PF00487; FA_desaturase; 1.

DR Prodom; P0001081; FA_desat_fam; 2.

KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;

KW Trans peptide.

FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).

FT CHAIN 2 447 OMEGA-3 FATTY ACID DESATURASE.

FT DOMAIN 167 171 HISTIDINE BOX-1.

FT DOMAIN 203 207 HISTIDINE BOX-2.

FT DOMAIN 370 374 HISTIDINE BOX-3.

SC SEQUENCE 447 AA; 51116 MW; 4E76250DD6DA6B1 CRC64;

Query Match 31.4%; Score 642; DB 1; Length 447;

Best Local Similarity 38.2%; Pred. No. 2.5e-44;

Matches 132; Conservative 63; Mismatches 109; Indels 42; Gaps 10;

QY 4 GRRMSDPSEGNILERVVDPEFTLSDKKAIPTHCERSVIRSSYVVDLIYAVYVYIANTYI 59

DB 88 GGEERDFG-----APPFTKLSDRERAIPTHCWKDWRMSGVYVVDVAVVFGSLAA 137

QY 60 VFYIYANTYIPLIPTPLAYLAMPYVFCQASILTGLWVIGHECGHHAESDYQLIDIVGF 119

DB 138 VAAAYNN-----WVWVPLVWFQASITFMVLFVLGHDCGHSFSDNPKLSVVGH 186

QY 120 VLHSAALLTPYFSWKYSRHNHANTNSLDNDEVYIPKRSKYIYSKLIINPPRGVFTLVF 179

DB 187 ILHSSILVPGYGMRSHTTHQNGHVENDSWHPLS--KIKKINDTATKRLRFTLPF 243

QY 180 RLTLGFLYLTNLSGKKYGRFANHPDMSPIFNDRERVOVLSDF---GLAVFYAIFL 236

DB 244 PL-LAYPIYLMRSRPGKO---GSHFHDSDLFPNEKVDYITSVCTMALALLVGLSF 298

QY 237 LVAAKGAAMVIMMYAIPVLGVSVFVLYLYLHHTHLSLPHYDSTEMNWKIGALSTDR 294

DB 299 VI---GVQLLKVLKGIPIYLGVMVMDLVTVLHHGHEDKLLPMYRGKEWSYLRGLTTLDR 355

QY 295 DFGPLNRVPHDVTHTVLHLLISYIPHYAKARDAIKPVLGSIYKIDRTPIKA 340

DB 356 DYGMINNIHDI-GTHVILHLPOLPHYLLEATEAAKPVIGKYR 400

RESULT 9

FD3C_RICCO

ID FD3C_RICCO STANDARD; PRT; 460 AA.
 AC P48619;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 GN PAD7A-1.
 OS Ricinus communis (Castor bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae;
 OC Ricinus.
 OC NCBI_TaxID=3988;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Baker 296; TISSUE=seed;
 RX MEDLINE=94302177; PubMed=8029360;
 RA van de Loo P.J., Somerville C.R.;
 RT "Plasmid omega-3 fatty acid desaturase cDNA from Ricinus communis";
 RL Plant Physiol. 105:443-444(1994).
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the
 CC third double bond in the biosynthesis of 16:3 and 18:3 fatty
 CC acids, important constituents of plant membranes. It is thought to
 CC use ferredoxin as an electron donor and to act on fatty acids
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLY).
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC -----
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 CC -----
 DR EMBL: L25897; AAA73511.1; -.
 DR PIR: L10063; T10063.
 DR InterPro: IPR005804; FA_desat_fam.
 DR Pfam: PF00487; FA_desaturase; 1.
 DR ProDom: PD001081; FA_desat_fam; 2.
 KM Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KM Transic peptide.
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN ? 460 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 177 181 HISTIDINE BOX-1.
 FT DOMAIN 213 217 HISTIDINE BOX-2.
 FT DOMAIN 380 384 HISTIDINE BOX-3.
 SQ SEQUENCE 460 AA; 52561 MW; 8365929046F3C7B0 CRC64;
 Query Match 31.2%; Score 639.5; DB 1; Length 460;
 Best Local Similarity 35.5%; Pred. No. 4.2e-44;
 Matches 134; Conservative 72; Mismatches 134; Indels 37; Gaps 9;
 QY 12 EGGKILRVPVDPFTSLDKKAPTHCFERSVRSYVVVHDLIVAX---VETYLANT 67
 DB 96 EGKEEPDAGAPPTLADIRALPKQGVKNPWRMSYVARDVVVGLAAVAAYERN- 154
 QY 68 YIPLIPLPLAVLVVFWFQASILITGLVIGHEGCHHAFSDYOLIDIVGFVLSALIT 127
 DB 155 -----WVAAPLVWFGCGTFMFLFVLGHGCHGHSFNNPKLNSVGHLLHSSITLV 204
 QY 128 PYFSWKYSHRNHNANTSLNDEVYIIPKSKVKIYSLKLNPPGRVFTLVRLTLGEP 187
 DB 205 PYHGMRIASHRTNHNQGHVNDSEWHPLSE---KIFSLDVTYTLRSLPFPV-LAYPF 260
 QY 188 YLTNIGSKKKYGRANHFDPKSPIFNDREVOVLSDGLLAVYAYITLVAAGAAMVI 247
 DB 261 YLMSRSFGK---GSHFHPDUGLFPVKERKDIITSTACTMAALLVTLNFSGPOVOML 316

QY 248 NMAIPLVGVSEFVLLITLHH--THLSLPHYDSTENWIKALSTIDRDGFLNRPVHD 305
 DB 317 KLYGIPYWI FVMWIDFVYLLHHGHEDKLPYRGRKAWSYLGGTLTIDRDGWINNTHHD 376
 QY 306 VTHNHLHHLISYIPHYHAKERDAIKPVGEYKIDRT-----IFKAYREKECIY 359
 DB 377 I-GTHVHLHLPQILPHHLVLEATEAPKVMGKTYRBPKSGPLPLHLGSLVRSKEDHY 435
 QY 360 IEPDESEHKGVFWYHK 376
 DB 436 VSDTGD-----VYVYOK 447
 RESULT 10
 FD3E_ARATH STANDARD; PRT; 386 AA.
 ID FD3E_ARATH
 AC P48623;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Omega-3 fatty acid desaturase, endoplasmic reticulum (EC 1.14.19.-).
 GN FAD3 OR ATG29980 OR F23F1.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Seedling;
 RX MEDLINE=94302147; PubMed=8029334;
 RA Yadav N.S., Wierzbicki A., Aegerter M., Caeter C.S., Perez-Grau L.,
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
 RA Feldmann K.A., Pierce J., Browne J.;
 RT "Cloning of higher plant omega-3 fatty acid desaturases";
 RL Plant Physiol. 103:467-476(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;
 RA Wataniki M.C., Yamamoto K.T.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94345020; PubMed=8066143;
 RA Nishinchi T., Nishimura M., Aroniel V., Iba K.;
 RT "Genomic nucleotide sequence of a gene encoding a microsomal omega-3
 RT fatty acid desaturase from Arabidopsis thaliana";
 RL Plant Physiol. 105:767-768(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat C.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
 RA Talton L.J., Gill J.B., Adams M.D., Carrera A.J., Craasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Niernan W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:761-768(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Phan P.K., Cheuk R.F.,
 RA Katlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

Db	119	GHILHSFIILVPHYGRKISRHTHQNHGVHENDSVPLPE	---	RVYKRLPHS	-----	TR	169
Qy	178	VEPLT	-----	LGPEYLTLNNTSGKGYGFANFPDMSPIFNDRRVOYLISDFGLAVFY	2322		
Db	170	MEATVPLPMLAVPYLCLCRSGKE	---	SGHFNPYSLFPASRSKLIATSTCWSIMFV	225		
Qy	233	AKRLVAAGAAVMVIMNTAIPVLGVSVFVILTYLHR	---	THLSLPHYDSTFEMNWKALS	290		
Db	226	SLIALFVFGPPLAVLKVGVPIIIFVMM	---	LDVLYLHHGHDEKLPWGRGKWSYLRGLT	2855		
Qy	291	TIDRDGFLNRFFHVHTHTVYLAHLISVTPHYAKKARDAKPLGSGYKIDRT	-----	3448			
Db	286	TIDRDGIFNNYHHBDI	---	GTHVHHLFPOLPHHLVDATKAKHAGVYRBPKTSICAIP	3444		
Qy	345	-----	PIFRAMY	---	REAKECIYIEPPDD	365	
Db	345	HLVESLVAISKDHYSDGDI	---	VFPETPD	374		
RESULT 11							
FD3E	TOBAC						
ID	FD3E	TOBAC	STANDARD;	PRT;	379	AA.	
AC	P48626;						
DT	01-FEB-1996	(Rel. 33,	Created)				
DT	01-FEB-1996	(Rel. 33,	Last sequence update)				
DT	28-FEB-2003	(Rel. 41,	Last annotation update)				
DE	Omega-3 fatty acid desaturase,	endoplasmic reticulum	(EC 1.14.19.-).				
GN	FAD3.						
OC	Nicotiana tabacum	(Common tobacco).					
OC	Eubacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asteride;						
OC	lamiales; Solanales; Solanaceae; Nicotiana.						
OX	NCBI_TaxID=4097;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	STRAIN=cv. SR1; TISSUE=Leaf;						
RC	MEDLINE=95011632; PubMed=796817;						
RA	Hamada T., Kodama H., Nishimura M., Iba K.;						
RL	Gene 147:293-294(1994).						
CC	-1- FUNCTION: ER (microsomal) omega-3 fatty acid desaturase introduces						
CC	the third double bond in the biosynthesis of 18:3 fatty acids,						
CC	important constituents of plant membranes. It is thought to use						
CC	cytochrome b5 as an electron donor and to act on fatty acids						
CC	esterified to phosphatidylcholine and, possibly, other						
CC	phospholipids.						
CC	-1- PATHWAY: Polyunsaturated fatty acid biosynthesis.						
CC	-1- SUBCELLULAR LOCATION: Endoplasmic reticulum.						
CC	-1- DOMAIN: The histidine box domains may contain the active site						
CC	and/or be involved in metal ion binding.						
CC	-1- SIMILARITY: Belongs to the fatty acid desaturase family.						

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CC	entities requires a license agreement (see http://www.isdb-sib.ch/announce						
CC	or send an email to license@isdb-sib.ch).						

DR	EMBL; D26509; BAA05515.1; -						
DR	PIR; JC2555; JC2555.						
DR	InterPro; IPR005804; PA_deeat_fam.						
DR	pfam; PF00487; PA_deeat_fam.1.						
DR	ProDom; PD001081; PA_deeat_fam.2.						
KM	Oxidoreductase; Fatty acid biosynthesis; Endoplasmic reticulum;						
KM	Transmembrane.						
FT	TRANSMEM	52	72	POTENTIAL.			
FT	TRANSMEM	213	233	POTENTIAL.			
FT	TRANSMEM	236	256	POTENTIAL.			
FT	DOMAIN	97	101	HISTIDINE BOX-1.			
FT	DOMAIN	133	137	HISTIDINE BOX-2.			
FT	DOMAIN	300	304	HISTIDINE BOX-3.			

SQ SEQUENCE 379 AA; 44149 MW; 87221A21AB02EB2 CRC64;
 Query Match 29.9%; Score 612; DB 1; Length 379;
 Best local similarity 34.7%; Pred. No. 5.4e-42;
 Matches 125; Conservative 73; Mismatches 128; Indels 34; Gaps 8;
 QY 9 DPSEGNILERVPPPTSLDLKKAIPTHCFERSVIRSSYYVHDLVAVFYVYANTY 68
 DB 23 DPS-----APPEPLAIBIRNVPKHCWVDPRLSLSYVRDVI-----PVATL 65
 QY 69 IPLIPLPLAYLAWVYVFCQASILGLWVIGHEGHAFFSYDOLIDIVGVLHSAITLP 128
 DB 66 IGLIHDSWLFYELVYALQCTMFMAIFVLGHDCGHGFSFSDOLNNVVGIIHLSALIVP 125
 QY 129 YFSKYSGRNHNATNSLDNDEVYIPKRSKVKIYKILNPPGKVFETLRLTGPFPLY 188
 DB 126 YHGRIKSHKTHQHNQVETDESVPME--KLNKVGYSYTKRLRYKIPPL-LAIPMY 181
 QY 189 LLTNISGKXGFRANFDPSPIRNDRVOVLLSDPGLAVFAIKLVAAGAAVYN 248
 DB 182 LMKSPGKS---GSHFNPYSDLFQPHRKRYVVTSLCWTMAALLVLCFAFGSLQWFK 237
 QY 249 MYAIPVGVSVFPLITYLH--THLSLPHYDSTEMWIKALSTIRDPGFLARVFHDV 306
 DB 238 IYGAPLYIFVWMLDFVYTLHHNGYEKGLPWYRGKMSYLRGGLTVYRDYGLFNNIHDI 297
 QY 307 THTVHLHLISYIPHYAKKARDAIKPYLGEYKIDRTP-----IFKAWYREAKECYI 360
 DB 298 -GTHVHHLFPQIHYHLRETKAAKPVLGKTYRBPKSGIPPHLVKDLTRSMKQDHY 356
 RESULT 12
 FD3C BRANA STANDARD; PRT; 404 AA.
 ID ID3C BRANA STANDARD; PRT; 404 AA.
 AC P46310;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-)
 DE (Fragment).
 GN PAD7.
 OS Brassica napus (Rape).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3708;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=94302147; PubMed=8029334;
 RA Yadav N.S., Wierzbicki A., Aegeer M., Caeter C.S., Perez-Grau L.,
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweizer B., Stecca K.L.,
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
 RA Feldmann K.A., Pierce J., Browse J.;
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";
 RL Plant Physiol. 103:467-476(1993).
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the
 CC third double bond in the biosynthesis of 16:3 and 18:3 fatty
 CC acids, important constituents of plant membranes. It is thought to
 CC use ferredoxin as an electron donor and to act on fatty acids
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST; MEMBRANE-BOUND (PROBABLY).
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC
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 CC -----
 CC EMBL:J22963; AAA61774.1; ALT_INIT.
 DR PIR; P00812; P00812.
 DR InterPro; IPR005804; FA_desat_fam.
 DR Pfam; PF00487; FA_desaturase_1.
 DR ProDom; PD001081; FA_desat_fam; 2.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transf. peptide.
 FT NON TER 1 1
 FT TRANSIT 1 1
 FT CHAIN 1 404
 FT DOMAIN 121 125
 FT DOMAIN 157 161
 FT DOMAIN 324 328
 SQ SEQUENCE 404 AA; 46617 MW; 4858FB2F36ZED54 CRC64;
 Query Match 29.7%; Score 607; DB 1; Length 404;
 Best local similarity 38.0%; Pred. No. 1.5e-41;
 Matches 123; Conservative 58; Mismatches 115; Indels 28; Gaps 8;
 QY 24 PPFTSLDLKKAIPTHCFERSVIRSSYYVHDLVAVYF---XYLANTYILITPLAYL 79
 DB 52 PPFTSLDLKKAIPTHCFERSVIRSSYYVHDLVAVYF---XYLANTYILITPLAYL 100
 QY 80 AMPYVFCQASILGLWVIGHEGHAFFSYDOLIDIVGVLHSAITLPYFSKYSGRNHN 139
 DB 101 VMLPYLWLAQCTMFMAIFVLGHDCGHGFSFSDPRLNSVGHIIHLSILVPHYGMWISRTH 160
 QY 140 HANTNSLDNDEVYIPKRSKVKIYKILNPPGKVFETLRLTGPFPLYLTNISGKY 198
 DB 161 HONGHVENDESMHMPSE---KIYKSL--DKPTFFFTPLVLMVAVFYVYANTY 214
 QY 199 GRFANFDPSPIRNDRVOVLLSDPGLAVFAIKLVAAGAAVYNVATPVLGVS 258
 DB 215 ---GSHVNPDSDLFPERNDVLTSTACWTMAALLVLCFAFGSLQWFK 271
 QY 259 VFPVLYLYLH--THLSLPHYDSTEMWIKALSTIRDPGFLARVFHDVTHVHLHI 316
 DB 272 MMLDFVYTLHHNGHEDLPWYRGKMSYLRGGLTVYRDYGLFNNIHDI-GTHVHHLF 330
 QY 317 SYIPHYAKKARDAIKPYLGEYK 340
 DB 331 PQIPIHYLVETEAKEKVLGKYR 354
 RESULT 13
 FD3C ARATH STANDARD; PRT; 446 AA.
 ID ID3C ARATH STANDARD; PRT; 446 AA.
 AC P46310;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-)
 GN FAD7 OR FADD OR ATG31170 OR F9F8.4 OR F11B9.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;
 RX MEDLINE=94302147; PubMed=8029334;
 RA Yadav N.S., Wierzbicki A., Aegeer M., Caeter C.S., Perez-Grau L.,
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweizer B., Stecca K.L.,
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
 RA Feldmann K.A., Pierce J., Browse J.;
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";
 RL Plant Physiol. 103:467-476(1993).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=cv. Columbia; TISSUE=Arerial parts;

RA MEDLINE=94043239; PubMed=8226956;
 RA Iba K., Gibson S., Nishitani T., Fuse T., Nishimura M., Aronow V.,
 RA Hugly S., Somerville C.R.;
 RT "A gene encoding a chloroplast omega-3 fatty acid desaturase
 RT complements alterations in fatty acid desaturation and chloroplast
 RT copy number of the fad7 mutant of Arabidopsis thaliana.";
 RU J. Biol. Chem. 268:24099-24105 (1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;
 RA Watanabe M., Yamamoto K.;
 RU Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,
 RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermair B.,
 RA Delaney M., Bouty M., Griwell L.A., Mache R., Pulgomech P.,
 RA De Simone V., Cholme N., Artiguenave F., Robert C., Brothier P.,
 RA Wincker P., Catolico L., Weisenbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Murbach E., Drzenek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Verzi A., D'Angelo M., Pallavicini A., Toppi S., Simonati B.,
 RA Conrad A., Hornigshagen K., Kauer O., Loehner T.-H., Nordliek G.,
 RA Reichelt J., Schaefer M., Schoen O., Barques M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Oltenswelder B., Duchemin D.,
 RA Cooke R., Landie M., Berger-Liauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maare A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argitrou A., Flores M., Liguori R., Valtale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Utechtack T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Walts R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Mlischner J., Sellers P., Gill J.R., Feldblyum T.V.,
 RA Preuss D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Friser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Aamizu Z.,
 RA Saegami S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shimo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RA "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RA thaliana.";
 RT Nature 408:820-822 (2000).
 RL -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces
 CC the third double bond in the biosynthesis of 16:3 and 18:3 fatty
 CC acids, important constituents of plant membranes. It is thought
 CC to use ferredoxin as an electron donor and to act on fatty acids
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- TISSUE SPECIFICITY: Most abundant in leaves and seedlings.
 CC -1- DOMAIN: The histidine box domain may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC -----
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 CC -----
 CC EMBL, L22961; AAA61773.1; -
 DR EMBL, D14007; BAA03106.1; -
 DR EMBL, D26019; BAA05040.1; -
 DR EMBL, AC009991; AAF01508.1; -
 DR EMBL, AC073395; AAG50977.1; -
 DR PIR, J02336; J02336.
 DR InterPro, IPR005804; FA_desat_fam.
 DR Pfam, PF00487; FA_desaturase; 1.

DR ProDom, PD001081; FA_desat_fam; 2.
 KW Oxidoreductase; Fatty acid biosynthesis; Chloroplast; Membrane;
 KW Transmembrane protein;
 FT TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 FT CHAIN 1 446 OMEGA-3 FATTY ACID DESATURASE.
 FT DOMAIN 163 167 HISTIDINE BOX-1.
 FT DOMAIN 199 203 HISTIDINE BOX-2.
 FT DOMAIN 366 370 HISTIDINE BOX-3.
 FT DOMAIN 446 AA; 51174 MW; 121125F634553D35 CRC64;
 SQ SEQUENCE
 Query Match 29.6%; Score 606; DB 1; Length 446;
 Best Local Similarity 34.7%; Pred. No. 2e-41;
 Matches 135; Conservative 67; Mismatches 129; Indels 58; Gaps 13;
 QY 16 ILERVPD-----PPTLSIDKAIPTHCERSYRSYVVDLVAAYF-- 61
 DB 74 IFESPLEDNKKORFPCAPPEPNLADIRALIPKHCWKNPKWSLSYVDVAIVFALAA 133
 QY 62 --YYLANTYILPLPLAYLAWPYWPCQASILGLWVIGEGCHHNSDQIDDIYGF 119
 DB 134 GAAYLNN-----WIWMPYWLQGTWFMALFVLGDCGHSFSDPKLSNVGH 182
 QY 120 VLHSAALTPYPMKYSRHHNANTSLDNDENVYIPKRSKYIKLNPGRVFTLVF 179
 DB 183 LHSILVPIYGMKLSRTHQNHGVNDSSWPMSE--KIINTL--DKPTFRFTL 237
 QY 180 RLTLGPFLYLLTNISGKCYFRANHPDPMSPFNDRRVOYLLSDFGLAVFAIKLV 238
 DB 238 PLVWLAYFYLWAPSPGK-----SSHVPSDLFLPKRKQVLTSTACWTMAALVCLN 293
 QY 239 AAKGAAVYNNYALPVLCVSVFVLITYLHN--THLSIPHDSYEMWIKALSTIDPF 296
 DB 294 FTIPIDQMLKLYGIPYWNWMLDPLVYLLHNGHEDKLPWRGKWSYLRGLTTLDYD 353
 QY 297 GLRLRVFVDYHTVTHLHLLISYIPYAKKARDIKPLAGSYKIDRTF-----IF 347
 DB 354 GLINNIHDI-GTHVYHLLFQPIRYHLLVETRAKPLVGLTY--REPDSSGLPLHL 409
 QY 348 KMYREAKKCYIIPDEDESEKGVFWYHK 376
 DB 410 ELAKSIKEDHYVS-DE-----GEVWYK 432
 RESULT 14
 ID PD3C SOYBN STANDARD; PRT; 453 AA.
 AC P48621;
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Omega-3 fatty acid desaturase, chloroplast precursor (EC 1.14.19.-).
 GN FAD7.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustroids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Seed;
 RX MEDLINE=94302147; PubMed=8029334;
 RA Yadav N.S., Wierzbicki A., Aegeerter M., Gaeter C.S., Perez-Grau L.,
 RA Kinney A.J., Hitz W.D., Booth J.R. Jr., Schweiger B., Stecca K.L.,
 RA Allen S.M., Blackwell M., Reiter R.S., Carlson T.J., Russell S.H.,
 RA Feldmann K.A., Pierce J., Browne J.;
 RT "Cloning of higher plant omega-3 fatty acid desaturases.";
 RL Plant Physiol. 103:467-476 (1993).
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the
 CC third double bond in the biosynthesis of 16:3 and 18:3 fatty
 CC acids, important constituents of plant membranes. It is thought to
 CC use ferredoxin as an electron donor and to act on fatty acids
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.

CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; L22965; AAA61776.1; -
 CC PIR; J02339; J02339.
 CC InterPro: IPR005804; FA_desat_fam.
 CC Pfam; PF00487; FA_desaturase_1.
 CC ProDom; PD001081; FA_desat_fam_2.
 CC Oxidoreductase; fatty acid biosynthesis; Chloroplast; Membrane;
 CC Transact peptide.
 CC TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 CC CHAIN 1 ? OMEGA-3 FATTY ACID DESATURASE.
 CC DOMAIN 171 175 HISTIDINE BOX-1.
 CC DOMAIN 207 211 HISTIDINE BOX-2.
 CC DOMAIN 374 378 HISTIDINE BOX-3.
 CC SEQUENCE 453 AA; 51362 MW; 9DC2FDB28522C018 CRC64;
 Query Match 29.4%; Score 602.5; DB 1; Length 453;
 Best local similarity 36.8%; Pred. No. 3,9e-41;
 Matches 128; Conservative 64; Mismatches 117; Indels 39; Gaps 10;
 QY 9 DPSEGNKIL--ERVV-----VDPPTSLDLKKAIPFHGFERSVSSYYVVDLI-----V 57
 DB DLITNGTNGVEHEKLPEDPDPGAPPPNLDIPRAIRKHCWVDPMMSMRYVVDVAVVGL 139
 QY 58 AYVYVYLYANTYVPLIPPLAYLAMPVWPCQASITGLMTVIGHECGHAFSDYQIIDIY 117
 DB 140 AAAAAYLYNN-----WLVWPLWYAAQCTWMAFLVGHDCGHSFNSKSLNSV 188
 QY 118 GFVLSALTLPYFSGKVSRRHNNHNTSLDNDEVYIP--KRSKVKYKYSKLNNPPGRV 174
 DB 189 GHLHSSITLVYHGRISHRTHOHGHAENDESNHPRPEKLFSLDTVTNLR----- 242
 QY 175 FTLVFRLLTLPPLYLTLNISGKGRFANHFDPSPPIFNDRERVVLSDGLAVFYAI 234
 DB 243 FTAPFPL-LAFPVYLFSSPKRT---GSHDPSSDLFVPERKQVITSTACMAMLGL 297
 QY 235 KLVAAKGAAMVNNYALPVLGVSFVLYLTLAH--THLSLPHYDSTENWIKGALSTI 292
 DB 298 VGLGFVWGPIDLLKLYGVVYLFVWMLDLVTLVHGHGHEKLPYRKGEMSYLRGLTTL 357
 QY 293 DRDGFGLNRVFDVTHVTHVHLISYIPHYAKERDAIKPVLEGYYK 340
 DB 358 DRDGYMINNIHDI-GTHVHHLPPQIPHYHLVEXTEAKPVFGCYR 404
 RESULT 15
 FD3D_ARATH STANDARD; PRT; 435 AA.
 AC P46622;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Temperature-sensitive omega-3 fatty acid desaturase, chloroplast
 DE precursor (EC 1.14.19.-).
 GN PAD8 OR ATSG05580 OR MOP10.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eucoside II; Brassicales; Brassicaceae; Arabidopsiis.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia; TISSUE=Aerial parts;
 RA MEDLINE=95148742; PubMed=7846164;
 RX Gibson S., Arondel V., Iba K., Somerville C.R.;
 RT "Cloning of a temperature-regulated gene encoding a chloroplast
 RT omega-3 desaturase from Arabidopsis thaliana";
 RL Plant Physiol. 106:1615-1621 (1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Hypocotyl;
 RA Marahki M.C., Yamamoto K.T.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=97471969; PubMed=9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
 RA Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 RT features of the 1.6 Mb regions covered by twenty physically assigned
 RT P1 clones";
 RL DNA Res. 4:215-230 (1997).
 CC -1- FUNCTION: Chloroplast omega-3 fatty acid desaturase introduces the
 CC third double bond in the biosynthesis of 16:3 and 18:3 fatty
 CC acids, important constituents of plant membranes. It is thought to
 CC use ferredoxin as an electron donor and to act on fatty acids
 CC esterified to galactolipids, sulfolipids and phosphatidylglycerol.
 CC -1- PATHWAY: Polyunsaturated fatty acid biosynthesis.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST, MEMBRANE-BOUND (PROBABLE).
 CC -1- INDUCTION: BY LOW TEMPERATURE.
 CC -1- DOMAIN: The histidine box domains may contain the active site
 CC and/or be involved in metal ion binding.
 CC -1- SIMILARITY: Belongs to the fatty acid desaturase family.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL; L27158; AAA65621.1; -
 CC EMBL; U08216; AAB0302.1; -
 CC EMBL; D17578; BAA04504.1; -
 CC EMBL; AB005241; BAB11547.1; -
 CC InterPro: IPR005804; FA_desat_fam.
 CC Pfam; PF00487; FA_desaturase_1.
 CC ProDom; PD001081; FA_desat_fam_2.
 CC Oxidoreductase; fatty acid biosynthesis; Chloroplast; Membrane;
 CC Transact peptide.
 CC TRANSIT 1 ? CHLOROPLAST (POTENTIAL).
 CC CHAIN 1 ? TEMPERATURE-SENSITIVE OMEGA-3 FATTY ACID
 CC DESATURASE.
 CC DOMAIN 156 160 HISTIDINE BOX-1.
 CC DOMAIN 192 196 HISTIDINE BOX-2.
 CC DOMAIN 359 363 HISTIDINE BOX-3.
 CC SEQUENCE 435 AA; 50136 MW; 3D7A803A56214E1 CRC64;
 Query Match 29.2%; Score 598.5; DB 1; Length 435;
 Best local similarity 34.9%; Pred. No. 7.8e-41;
 Matches 126; Conservative 67; Mismatches 127; Indels 41; Gaps 9;
 QY 24 PPFLSLDKKAIIPHGFERSVSSYYVVDLIYAY-----VFYLIANTYILIPPLAYL 79
 DB 87 PPFLSLDKKAIIPHGFERSVSSYYVVDLIYAY-----VFYLIANTYILIPPLAYL 135
 QY 80 AMPVWPCQASITGLMTVIGHECGHAFSDYQIIDIYGFVLSALTLPYFSGKVSRRH 139
 DB 136 LMPLYWFGQGMFPAALFVGHDCGHSFNSKSLNSVLPYHGMISIRH 195
 QY 140 HANTSLDNDEVYIPKRSKVKYKYSKLNNPPGRVFTLVPLTGLFPYLYLTNISGKYYG 199
 DB 196 HONHGHVENDESNHPRPEKLFSLDTVTNLR-LAYPVYLNRRSPGK-- 249

[illegible]

DR WP1: 2001-283028/30.
 DR P-PSDB: AAB70946.
 PT New nucleic acid sequence encoding *Calendula officinalis* calendulic acid
 PT desaturase, useful for e.g. producing transgenic plants having oil with
 PT an increased unsaturated fatty acid content.
 XX
 PS Claim 1b, Page 13-15, 22pp; German.
 XX
 CC This invention describes a novel isolated nucleic acid sequence (I)
 CC encoding a *Calendula officinalis* calendulic acid desaturase polypeptide.
 CC The invention also describes (1) a process for producing unsaturated
 CC fatty acids, comprising introducing at least one copy of (I) or (II) into
 CC an oil-producing organism, growing the organism, isolating oil from the
 CC organism and releasing fatty acids from the oil; (2) a process for
 CC producing triglycerides with an increased unsaturated fatty acid content,
 CC comprising introducing at least one copy of (I) or (II) into an oil-
 CC producing organism, growing the organism and isolating oil from the
 CC organism; (3) a process for producing saturated fatty acids, comprising
 CC introducing at least one nonfunctional copy of (I) or (II) into an oil-
 CC producing organism, growing the organism, isolating oil from the organism
 CC and releasing fatty acids from the oil; (4) a process for producing
 CC triglycerides with an increased saturated fatty acid content, comprising
 CC introducing at least one nonfunctional copy of (I) or (II) into an oil-
 CC producing organism, growing the organism and isolating oil from the
 CC organism; (5) an enzyme capable of converting a diunsaturated fatty acid
 CC of to a triunsaturated fatty acid. Transgenic organisms (especially
 CC plants) containing one or more copies of (I) are useful for producing
 CC oils with an increased unsaturated fatty acid content. Transgenic
 CC organisms (especially plants) containing one or more nonfunctional copies
 CC of (I) are useful for producing oils with an increased saturated fatty
 CC acid content. (I) and fragments of (I) are also useful for isolating
 CC genomic sequences by homology screening. This sequence encodes the
 CC calendulic acid desaturase described in the method of the invention
 XX
 SQ Sequence 1285 BP; 364 A; 294 C; 253 G; 374 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 3,12e-212 Length: 1285
 Score: 2047.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0
 US-10-069-772-2 (1-377) x AAF88311 (1-1285)
 QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyIleValIleLeuGluAlaVal 20
 DB 42 ATGGGTGCTGGTGGATGCGATGCGATCATCTGAGGAAAAAACAATCTTGAACGTGTG 101
 QY 21 ProValAspPropheThrIleuSerAspLeuValIleValIleProThrIleCysPhe 40
 DB 102 CCACTCATTCACCGCTTACGCTTAAGCATCTGAAGAAAGACATTCCTACCATTCCTT 161
 QY 41 GluArgSerValIleArgSerSerTyrTyrValValIleAspLeuIleValAlaTyrVal 60
 DB 162 GAGCGATCTGTCATCCGCTCATCATATGTTGTTCAATGATCTGTTGCTATGTC 221
 QY 61 PheTyrTyrLeuAlaSerThrTyrIleProLeuIleProThrProLeuAlaTyrLeuAla 80
 DB 222 TTCTACTACCTTGAACACGATATCCCTCTTATCTTACACCTCTGCTTACCTACCA 281
 QY 81 TrpProValIleTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTyrValIleGlyHis 100
 DB 282 TGGCCCGTTTACTGCTTTTGTTCACGCTACGATCTCCACCGGCTCTGGGTATCGGTAC 341
 QY 101 GluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAspIleValGlyPheVal 120
 DB 342 GAATGTGTGTCACCATGATTTAGCAGTACCGATGATGATGATGATGATGATGATGATG 401
 QY 121 LeuHisSerAlaLeuLeuThrProTyrPheSerTyrPheTyrSerHisArgAsnHisHis 140

DB 402 CTCGATTCGGCTCTCTCACCCCGATTTCTTGAAATATACGACAGGATCACAC 461
 QY 141 AlaSerThrAsnSerLeuAspAspGluValIlePheProIleArgGlySerLeuVal 160
 DB 462 GCCAACCAAAATTCATCTGATTAACGATGATGATGATGATGATGATGATGATGATG 521
 QY 161 LysIleTyrSerIleLeuAsnAsnProProGlyArgValIlePheThrLeuValPheArg 180
 DB 522 AAGATTTATTCACCAATCTTAAACATCCACCGGAGGTGTCTGCTGCTGCTGCTG 581
 QY 181 LeuThrLeuGlyPheProLeuTyrIleLeuThrAsnIleSerGlyIleValIleVal 200
 DB 582 TTGACTTTAGATTTCCGTTTACTTACTCTTAATATCTGGGCAAGAAATACGGAGG 641
 QY 201 PheAlaSerHisPheAspProMetSerProIlePheAsnAspArgGluArgValIleVal 220
 DB 642 TTTCGCAACCACTTGTGATCCCATAGTCAATTTTCAACGATCGTGAACGGGTTCAAGTT 701
 QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleValIleLeuValIleAla 240
 DB 702 TTGCTATCCGATTCGCTCTCTGCTGATTTTATGCAATCAAGCTTCTGTGACAGCA 761
 QY 241 LysGlyAlaAlaIleTyrValIleAsnMetTyrAlaIleProValIleGlyValSerValPhe 260
 DB 762 AAAGGGGACGCTTGGGTATACATGATGATGATGATGATGATGATGATGATGATG 821
 QY 261 PheValIleuIleThrTyrLeuHisHisThrHisLeuSerLeuProHisIleTyrAspSerThr 280
 DB 822 TTCGTTTATGATCATATTTTGCACACACCCATCTCTCATCTCATATGATGATCAACC 881
 QY 281 GluTrpAsnThrPheIleValIleLeuSerThrIleAspArgAspPheGlyPheLeuAsn 300
 DB 882 GAATGGAACGTGATCAAAAGGCGCTTATCAACAATCAATAGGATGATTCGGGTCTCGAAT 941
 QY 301 ArgValIlePheHisAspValThrHisThrHisValLeuHisIleLeuIleSerTyrIlePro 320
 DB 942 CGGCTTTCCACGACGATTCACACATCAGCTCTTGATATCTTGATCTCATACATTC 1001
 QY 321 HisTyrHisAlaValGluAlaArgAspAlaIleLeuProValIleGlyGluTyrTyrIle 340
 DB 1002 CATATCATGCAAAAGCAAGCAAGGATGATCAAGCAGAGTGTGGCGGACTACTATTA 1061
 QY 341 IleAspArgThrProIlePheValIleMetTyrTrpGluAlaValGluCysIleTyrIle 360
 DB 1062 ATCGACGAGCTCCAAATTTTCAAGCAATGTATAGAGGCTTAAGAAATGATCATCAATC 1121
 QY 361 GluProAspGluAspSerGluHisIleValIlePheTyrTyrHisIleMet 377
 DB 1122 GAGCCCGATGAGATGAGGACCAAGAGTGTGTTCTGTATCCACAGATG 1172
 RESULT 2
 ID AAT95688 standard; DNA; 1128 BP.
 AC AAT95688;
 DT 25-MAR-2003 (revised)
 DT 20-APR-1998 (first entry)
 XX
 DE Crepis alpina delta 12 acetylase encoding DNA.
 XX
 KW Crepis alpina delta 12 acetylase; plant; yeast; acetylenic compound;
 XX fatty acid; coating; plastic; lubricant; oilseed; ss.
 OS Crepis alpina.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1128
 FT /*tag= a
 FT /product= "Crepis alpina delta 12 acetylase"
 XX
 PN W09737033-A1.

PD 09-OCT-1997.
 XX 14-FEB-1997; 97WO-SE000247.
 XX 29-MAR-1996; 96SE-00001236.
 XX (BAFO/) BAFOR M.
 PA (BANNA/) BANNA A.
 PA (DAHL/) DAHLQVIST A.
 PA (GUMM/) GUMMSON P.
 PA (LEEM/) LEE M.
 PA (LENN/) LENNAN M.
 PA (SJOE/) SJOEDAHN S.
 PA (STYM/) STYMAN S.
 XX Bafor M, Banas A, Dahlqvist A, Gummeson P, Lee M, Lenman M,
 PI Sjoedahl S, Stymne S;
 XX WPI; 1997-503117/46.
 DR P-PSDB; AAW36793.
 XX New acetylase used for production of crepenylic acid from linoleic acid -
 PT derived from Crepis alpina; used for production of acetylenic fatty acids
 PT suited for the production of coatings, plastics and lubricants.
 XX Claim 7; Page 21; 33pp; English.
 XX This DNA encodes the Crepis alpina delta 12 acetylase. This is used in
 CC the production of acetylenic compounds. The process comprises treating
 CC C18 fatty acids having a double bond at position delta 12 with an
 CC acetylase to form 12-ynolic acids. The acetylenic compounds can be
 CC produced by organisms such as oilseed plants, yeast and fungi which are
 CC transformed with this acetylase DNA. These organisms can accumulate
 CC these acetylenic compounds which are chemical feedstocks, particularly
 CC for coatings, plasticisers and lubricants. The process enables the
 CC production of these acetylenic compounds from a renewable resource with
 CC high purity and at reasonable cost. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 CC Sequence 1128 BP; 270 A; 308 C; 237 G; 313 T; 0 U; 0 Other;
 XX SQ
 Alignment Scores:
 Pred. No: 1.18e-167 Length: 1128
 Score: 1635.00 Matches: 289
 Percent Similarity: 87.50% Conservative: 40
 Best Local Similarity: 76.86% Mismatches: 45
 Query Match: 79.92% Indels: 2
 DB: Gaps: 1
 US-10-069-772-2 (1-377) x AAT95688 (1-1128)
 QY 1 MetGlyValIaGlyGlyArgMetSerAspProSerGluGlyValAsnIleLeuGluArgVal 20
 DB 1 ATGGGTGGCGGTGGCCGT-----GTCGACCTTCGCAAAACCCCTCATGGAACGTGTC 54
 QY 21 ProValAspProPheThrLeuSerAspLeuValValIleProThrHisCysPhe 40
 DB 55 TCAATTATCAACCTTCACCGTAGATGATCTCAAGCAAGAAATCCCTCCCATTCGCTTC 114
 QY 41 GluArgSerValIleArgSerSerTyTyValValHisAspLeuIleValIleTyVal 60
 DB 115 AAGCATCTGTAATCCGTTCTTACTACATAGTCCAGATGATGATATATGCGCTACATC 174
 QY 61 PheTyTyLeuIleAsnThrTyTyIleProLeuIleProThrProLeuAlaTyTyLeuAla 80
 DB 175 TTCTACTCTCTGCGCAAAATATATTCGATTCCTCCCTGCTTACGCTTACCTGCTGCT 234
 QY 81 TrpProValTyTyTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGlyHis 100
 DB 235 TGGCCCTTACTGCTTCTGTCAGATGATCTCTCAACGCGCTTATGGGTATGCTGCTAC 294
 QY 101 GluCysGlyHisHisAlaPheSerAspTyGlnLeuIleAspPheIleValGlyPheVal 120

DB 295 GAATGCGGTGACCAATGCCCTTCAGCGACTACCAATGCGGTGACGACACTGTCGCTTCATC 354
 QY 121 LeuHisSerAlaLeuLeuThrProTyPheSerTrpTySerHisArgAsnHis 140
 DB 355 CTCACCTGCTTCTTCATGACCCCGTATTTCTCTCGGAATACAGCCACCGAACCAT 414
 QY 141 AlaAsnThrAsnSerIleAspAsnAspGluValTyTyIleProTyArgLysSerIleVal 160
 DB 415 GCCAAACAAATTCGCTTGAACAGATGATGATATGATATGATATGATATGATATGATATG 474
 QY 161 LysIleTySerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPheArg 180
 DB 475 GCGCTTACTATTAAGTTCTTCAACACCCGCTGCGCATGATATGATATGATATGATATG 534
 QY 181 LeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSerGlyLysTyGlyArg 200
 DB 535 TTCACTGAGCTTCTCTTACTCTTTCACAAATTTTTCGGCAGATGATGAAAGG 594
 QY 201 PheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGlnVal 220
 DB 595 TTTCGCAACCATTTGACACCCCATGATGATGATTTTCAAGAAGCGGATTCAGGTC 654
 QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyAlaIleLysLeuValAlaVal 240
 DB 655 TTGCTATCGATCTTGGGCTTCTGCTGCTTACGAGTAAACTTGGCGGTGACAGCG 714
 QY 241 LysGlyAlaAlaValTrpValIleAsnMetTyTyAlaIleProValLeuGlyValSerValPhe 260
 DB 715 AAAGCGCGCTGCTGGTACGATGATGATGATGATGATGATGATGATGATGATGATGAT 774
 QY 261 PheValLeuIleThrTyTyLeuHisHisThrHisLeuSerLeuProHisTyTyAspSerThr 280
 DB 775 TTTCATATCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 834
 QY 281 GluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPheLeuAsn 300
 DB 835 GAATGGAACCTGCTGAGGCGCTTGTGTCAACATGATGATGATGATGATGATGATGAT 894
 QY 301 ArgValPheHisAspValThrHisThrHisValLeuHisIleLeuSerTyTyIlePro 320
 DB 895 AGTGTCTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 954
 QY 321 HisTyTyHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyTyLys 340
 DB 955 CACTATCATGAGAGAGAGAGAGAGATGATCAACAGCTTGGGAGACTTTATATAG 1014
 QY 341 IleAspArgThrProIlePheLysValMetTyTyArgGluAlaLysGlyIleTyTyIle 360
 DB 1015 ATCGATAGACTCCAAATTCGAAAGCAATGATGAGAGGCGCAAGATGATGATGATGAT 1074
 QY 361 GluProAspGluAspSerGluHisLysGlyValPheTrpTyTyHisLys 376
 DB 1075 GAGCTGAAAGAGTAGAGAGTCCAGAGGTGATATATGATGATGATGATGATGATGAT 1122
 RESULT 3
 ID AAV63102 standard; cDNA; 1312 BP.
 AC AAV63102;
 XX 02-FEB-1999 (first entry)
 DE Crepis sp. delta-12-epoxygenase cDNA clone Crepx.
 XX Fatty acid epoxygenase; Crepx; delta-12-epoxygenase;
 KM mixed function monooxygenase; epoxygenated fatty acid; transgenic plant;
 KM vegetable oil; oilseed; ss.
 XX Crepis sp.
 OS
 XX Key Location/Qualifiers
 FH 26.1150
 FT CDS /*tag= a

XX MO9846762-A1.
 XX 22-OCT-1998.
 XX
 PR 09-APR-1998; 98MO-AU000246.
 XX
 PR 15-APR-1997; 97AU-00006223.
 PR 15-APR-1997; 97AU-00006226.
 PR 16-APR-1997; 97US-0043706P.
 PR 20-JUN-1997; 97US-0050403P.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (STYM/) STYMNE S.
 PI Stymne S, Green A, Singh S, Lenman M;
 XX
 DR MPI: 1998-568734/48.
 DR P-PSDB; AAM79743.
 XX
 PT New isolated fatty acid epoxxygenase gene - used particularly for
 PT transforming plants for producing modified oils for use in, e.g.
 PT coatings, resins, glues, plastics, surfactants or lubricants.
 XX
 PS Claim 16; Page 84-86; 150pp; English.
 XX
 CC This cDNA clone, designated Crepx, codes for a novel epoxxygenase (see
 CC AAM79743) of a Crepis sp. (not Crepis palaestina) that has a high
 CC verholnic acid content. The Crepx gene shows a high degree of homology to
 CC the novel Cpa12 delta-12-epoxxygenase gene (see AAV63101) of C.
 CC palaestina. Crepx cDNA was isolated from a Crepis sp. cDNA library using
 CC a Crepis alpha acetylase partial gene sequence (see AAV63104) as
 CC probe. The invention relates generally to novel genetic sequences (see
 CC AAV63101-03) encoding fatty acid epoxxygenases (see AAV79742-44),
 CC especially delta-12-epoxxygenases or mixed function monooxygenases. These
 CC provide the means by which fatty acid metabolism can be manipulated in
 CC e.g. yeast, mould, bacteria, insects, birds, mammals and plants
 CC (especially oilseed plants such as flax), in particular to convert
 CC unsaturated fatty acids to epoxxygenated fatty acids. The invention
 CC extends to genetically modified oil-accumulating organisms and to the
 CC oils derived from them. These oils can be used in production of coatings,
 CC resins, glues, plastics, surfactants or lubricants
 CC
 XX
 SQ Sequence 1312 BP; 347 A; 301 C; 263 G; 399 T; 0 U; 2 Other;
 Alignment Scores:
 Pred. No.: 7,79e-163 Length: 1312
 Score: 1592.50 Matches: 285
 Percent Similarity: 86.24% Conservative: 41
 Best Local Similarity: 75.40% Mismatches: 47
 Query Match: 77.80% Indels: 5
 Gaps: 3
 DB: 2
 US-10-069-772-2 (1-377) x AAV63102 (1-1312)
 QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyValSerLeuLeuGluArgVal 20
 Db 26 ATGGGTGCGCGCGCGCGT-----GATCGACATCGCAAAAGTCGTCATCGAAGCGTTC 79
 QY 21 ProValAspPro---ProPheThrLeuSerAspLeuValSerLeuLeuProThrHisGly 39
 Db 80 TCAGTGTGATCCAGTAACCTCTCACTGAGTATTTGAAGCAAGCAATCCCTCCACATTGC 139
 QY 40 PheGluArgSerValIleArgSerSerValValValValIleAspLeuIleValAlaVal 59
 Db 140 TTCACGCACTGTCATCGTTCATCTTAATGATGTTGTCAGATCTCATATATGCTTAC 199
 QY 60 ValPheValLeuAlaSerThrValLeuProLeuLeuProThrProLeuAlaValLeu 79
 Db 200 ATCTTCTATCTTCTGCAACACATATATCCCTATATCCCTCATCCCTGAGCTACTTA 259
 QY 80 AlaTrpProValLeuValLeuPheGluAlaSerLeuLeuValLeuValLeuValLeu 99

Db 260 GCTTGGCGGCTTACGTGTTCTGCAAGCTAGCTCTCACTGGGTTATGATCTCGGC 319
 QY 100 HisGluCysGlyHisIleAlaPheSerAspTyrGluLeuIleAspAspIleValGlyPhe 119
 Db 320 CATGATGTGGTCCATGCTGCTTATGACATCAATGAGTTCAGCACTGTTGGGCTTC 379
 QY 120 ValLeuHisSerAlaLeuLeuThrProTyrPheSerTrpValSerHisArgAsnHis 139
 Db 380 ATCATCATTTCAATTTCTCTCCACCCCGTATTTCTTGGAAATACAGTCAACCGGAAATCAC 439
 QY 140 HisAlaSerThrAsnSerLeuAspAsnAspGluValTyrIleProValArgValSerVal 159
 Db 440 CATTCACACACAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 499
 QY 160 ValValIleTyrSerValLeuLeuAsnAsnProGluValPheThrLeuValPhe 179
 Db 500 CTCAAGCGTATCTATTAACCTTAAACCAACCCAGCTGTCAGCTGTTGTTGTTATTC 559
 QY 180 ArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrLeuLeuSerGlyValValTyrGly 199
 Db 560 ATGTTCACCCCTAGGATTTCTTAACTTGAACAATATTTCCGCAAGAAATACGAT 619
 QY 200 ArgPheAlaSerHisPheAspProMetSerProIlePheAsnAspArgValArgValGln 219
 Db 620 AGGTTTGCACCACTTCGACCCCATGATGATGATGATGATGATGATGATGATGATGATGAT 679
 QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleValLeuValAla 239
 Db 680 GTTCTTCCTTGGATCTTGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 739
 QY 240 AlaValGlyValAlaValPheValIleAsnMetTyrAlaLeuProValLeuGlyValSerVal 259
 Db 740 AATTAAGAGAGCTGCTGGTGGTGGCTGATGATGATGATGATGATGATGATGATGATGAT 799
 QY 260 PhePheValLeuIleThrTyrLeuHisIleThrIleSerLeuPheProHisTyrAspSer 279
 Db 800 TTTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 859
 QY 280 ThrGluTrpAsnTrpIleValGlyValLeuSerThrIleAspArgAspPheLeu 299
 Db 860 ACTGAATGAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 919
 QY 300 AsnArgValPheHisAspValThrHisThrIleValLeuHisIleLeuIleSerTyrIle 319
 Db 920 AATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979
 QY 320 ProHisTyrHisAlaValGlyAlaArgAspAlaIleValSerProValLeuGlyGluTyr 339
 Db 980 CCACACTATCTATGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1039
 QY 340 LysIleAspArgThrProIlePheValAlaMetTyrAlaValGlyValGlyValTyr 359
 Db 1040 ATGATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
 QY 360 IleGluProAspGluAspSerGluHisValGlyValPheTyrPheTyrHisValMet 377
 Db 1100 ATTCAGGCT-----GATAGCAAGCTCAAGGTGTATATGATGATCAATAATG 1147
 Db
 RESULT 4
 ID AAV63101 standard; cDNA; 1358 BP.
 XX AAV63101;
 AC
 DT 02-FEB-1999 (first entry)
 XX
 DE Crepis palaestina delta-12-epoxxygenase cDNA clone Cpa12.
 XX
 KW Fatty acid epoxxygenase; Cpa12 gene; mixed function monooxygenase;
 KW delta-12-epoxxygenase; epoxxygenated fatty acid; transgenic plant;
 KW vegetable oil; oilseed; se.
 OS Crepis palaestina.

XX	Key	Location/Qualifiers
FH	CDS	30..1154
FT		/tag= a
XX		
XX	MO9846762-A1.	
PN		
PD	22-OCT-1998.	
XX		
PF	09-APR-1998;	98WO-AU000246.
XX		
PR	15-APR-1997;	97AU-00006223.
PR	15-APR-1997;	97AU-00006226.
PR	16-APR-1997;	97US-0043706P.
PR	20-JUN-1997;	97US-0050403P.
XX		
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.	
PA	(STYM/) STYME S.	
XX		
PI	Stymne S, Green A, Singh S, Lennan M,	
DR	WPI, 1998-568734/48.	
DR	P-PsDB; AA079742.	
XX		
PT	New isolated fatty acid epoxigenase gene - used particularly for	
PT	transforming plants for producing modified oils for use in, e.g.	
PT	coatings, resins, glues, plastics, surfactants or lubricants.	
XX		
ES	Claim 15; Page 78-81; 150pp; English.	
XX		
CC	This full-length cDNA clone, designated Cpai2, codes for a novel mixed	
CC	function monooxygenase (see AA079742) of Crepis palaestina that is	
CC	characterised as having delta-12-epoxygenase activity. It was isolated	
CC	from a C. palaestina cDNA library using a Crepis alba acetylase	
CC	partial gene sequence (see AA063104) as probe. The encoded protein	
CC	contains His-rich motifs (see AA079752-54) that are characteristic of	
CC	mixed function monooxygenases. The Cpai2 gene was shown to be highly	
CC	expressed in developing seeds, with no expression detectable in leaves.	
CC	The invention relates generally to novel genetic sequences (see AA063101-1-	
CC	03) encoding fatty acid epoxigenases (see AA079742-44), especially delta	
CC	12-epoxygenase or mixed function monooxygenases. These provide the means	
CC	by which fatty acid metabolism can be manipulated in e.g. yeast, mould,	
CC	bacteria, insects, birds, mammals and plants (especially oilseed plants	
CC	such as flax), in particular to convert unsaturated fatty acids to	
CC	epoxygenated fatty acids. The invention extends to genetically modified	
CC	oil-accumulating organisms and to the oils derived from them. These oils	
CC	can be used in production of coatings, resins, glues, plastics,	
CC	surfactants or lubricants	
XX		
SQ	Sequence 1358 BP; 358 A; 308 C; 278 G; 414 T; 0 U; 0 Other;	
XX		
Alignment Scores:		
Pred. No.:	1,73e-162	Length: 1358
Score:	1589.50	Matches: 285
Percent Similarity:	85.98%	Conservative: 40
Best Local Similarity:	75.40%	Mismatches: 48
Query Match:	77.65%	Indels: 5
DB:	2	Gaps: 3
US-10-069-772-2 (1-377) x AA063101 (1-1358)		
OY	1 MetGIyAlAGlGVlYArgMeSeSerAePProSeGlUGlYysAnlleuGIuArxVal	20
Dd	30 ANGGGTGCCCGCGGTCT-----GGTCGAACATCGAAABAAATCGGCATGCAACGTCTC	83
OY	21 ProValAePPro---ProPhetrlleuSerAePleuylalalePeorThriSeys	39
Dd	84 TCAGTGTATCCAGTAACCTTCTCATGAGATTGAACAACCAATCCCTCCCATTGC	143
OY	40 PheGIuArxSeVallleuSerSeryrTYValValHisAePleulleValAlAtyr	59
Dd	144 TTCGAGAGTTCGTATCCGCTCATCTTATAGTTGTTCMAAGTTCATTATATGCTTAC	203

OY	60	ValPheTYrTYrLeuAlaAsnThrTYrLerProLeuileProThrProLeuAlaTYrLeu	79
Db	204	ATCTTCACTTCTCTGGCCACACATATATCTCTACTCTCTACTAGCTAGCTACTTA	263
OY	80	AlaTrpProValTYrTYrPheTYrCysGlnAlaSerlleLeuthngilyLeuTrpValillegily	99
Db	264	GCTTGAGCCCGTTTACTGGTTCGTGACCACTAGCGTCACTGAGCTTATGATCGCGG	323
OY	100	HisGluCysGlyHisHisAlaPheSerzAspTYrGlnLeuileAspAspilleValGlythe	119
Db	324	CACGAAATGTGTCACCATGCTTTAGCACTACATATGTTTGACGACATCTGGGCTTC	383
OY	120	ValLeuHisSerzAlaLeuLeuThrProTYrPheSerzTrpTYrSerzHisArgAsnHis	139
Db	384	ATCTCCACCTCATTTCTCTCTACCCCGTATTTCTTGAAATTCAGTACCCGGAATAC	443
OY	140	HisAlaAsnThrAsnSerzLeuAspAsnAspGluValTYrilleProLYsArgLYsSerLYs	159
Db	444	CATTCCAAACAAGTTCGATTGATAGATAGATGAAGTTATCATTCGGAAGAAAGCAAGTCCAA	503
OY	160	VallylsileTYrSerzLYsLeuLeuAsnAsnProGlyArgValPheThrLeuValPhe	179
Db	504	CTCGGCGCTATCTATAAATTCTTTAACACACACCTGGCTGGCTGGTTGGTTGATTATC	563
OY	180	ArgLeuThrileGlyPheProLeuTYrLeuLeuThrAsnilleSerzilyLeuLYsPheLYs	199
Db	564	ATGTTGACCCCTAGAGATTTCTTTATACCTCTTGACAAATATTTCCGGGAAGAAATACAC	623
OY	200	ArgPheAlaAsnHisPheAspProMetSerProillePheAsnAspArgGluArgValGln	219
Db	624	AGGTTTGCCAAACCTTGACCCCAATAGTCCATTTTCAAGAAGCGGACGGTTTCAG	683
OY	220	ValleuLeuSerzAspPheGlyLeuLeuAlaValPheTYrAlaAlileLYsLeuLeuValAla	239
Db	684	GCTTCTCTTGCGAATCTGTGCTTCTTGCCGTGTTTATGGAATTAAGTTGCTGATACA	743
OY	240	AlaLYsGlyAlaAlaTrpValilleAsnMetTYrAlaAlileProValleuGlyValSerVal	259
Db	744	AATAAAGAGCGCTGGTGGTAGCGGTGCATGTATGAGAGTCCGGATTAAGGCGTATTAC	803
OY	260	PhePheValleuileThrTYrLeuHisHisThrHisleuSerLeuProHisTYrAspSer	279
Db	804	TTTTTCATGTGATCACTCTTGTGACCAACCACTCATGCTGCGCTCATTAATGATTTCA	863
OY	280	ThrGluTrpAsnTrpilleLYsGlyAlaLeuSerThrilleAspArgAspPheGlyPheLeu	299
Db	864	ACTGATGAACTGGATCAGAGGGGCGCTTGCAGCAATCGATAGGGAATTGGATTCTGTG	923
OY	300	AsnArgValPheHisAspValThrHisHisValleuHisHisleuilleserTYrille	319
Db	924	AATAGTGTTCATGATGATGTACACACTCATGTCAATGCTATTTGTTTTCATACACTT	983
OY	320	ProHisTYrHisAlaLYsGlyAlaArgAspAlaAlileLYsProValleuGlyGluTYrTYr	339
Db	984	CCACACTATCATGCAAGAGGACCAAGGATGCATCAAGCCAACTTGGGGACCTTTAT	1043
OY	340	LYsilleAspArgThrProillePheLYsAlaMetTYrArgGluAlaLYsGluCyselleTYr	359
Db	1044	ATGATTCGACAGAGATCTCCAAATTTTAAAGCAATGTGGAGAGGGGACAGGATGCATGAC	1109
OY	360	illeGluProAspGluAspSerzGlnHisLYsGlyValPheTYrTYrHisLYsMet	377
Db	1104	ATCGAGCT-----GATAGCAAGCTCAAAAGTGTATTATGTGATCATTAATATTTG	1151
RESULT 5			
ID	AAV72550		
XX	AAV72550	standard; cDNA; 1364 BP.	
AC	AAV72550;		
DT	27-AUG-2003	(revised)	
DT	10-FEB-1999	(first entry)	
XX			

DE Vernonia galamensis fatty acid epoxidising enzyme encoding cDNA.
XX
XX Vernonia galamensis; fatty acid desaturase; epoxidising enzyme;
KW expression; chimeric gene; recombinant enzyme; ss.
XX
XX Vernonia galamensis.
XX
FH Key Location/Qualifiers
FT CDS 103..1257
FT /tag=a
XX
XX US5646784-A.
XX
XX 08-DEC-1998.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX 11-JUN-1997; 97US-00872302.
XX
XX (DUPO) DU PONT DE NEMOURS & CO B I.
XX
XX Hitz WD;
XX
XX MPI, 1999-059065/05.
XX
XX P-PSDB; AAM83354.
XX
XX DNA encoding Vernonia galamensis fatty acid desaturase and fatty acid
PT epoxidising enzyme - used to alter levels of expression of the enzymes in
PT transformed host cells or to produce recombinant enzymes.
XX
XX Claim 6; Col 25-29; 21pp; English.
XX
XX The present sequence encodes Vernonia galamensis fatty acid epoxidising
CC enzyme. The present invention also describes: (i) Vernonia galamensis
CC fatty acid desaturase; (ii) chimeric genes comprising the fragments
CC linked to regulatory sequences; and (iii) transformed host cells
CC containing the chimeric genes. The DNA's from the present invention can
CC be used to alter levels of expression of the enzymes in transformed host
CC cells or to produce the recombinant enzymes by transformation of
CC microbial host cells. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 1364 BP; 391 A; 305 C; 280 G; 388 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 2.73e-161 Length: 1364
Score: 1578.50 Matches: 280
Percent Similarity: 87.16% Conservative: 39
Best Local Similarity: 76.50% Mismatches: 44
Query Match: 77.11% Indels: 3
DB: Gaps: 2

US-10-069-772-2 (1-377) x AAV72550 (1-1364)
QY 15 AsnIleuGluValProValASP---ProProPheThrLeuSerAspLeuValys 33
DB 157 AATATAAAGAGAGCGACCGGTTATAGCGGACCACTTCTGTTAAGCATTAAGAA 216
QY 34 AlaIleProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHis 53
DB 217 GCAATCCCTCCGCGATTCCTTCAGGATCGCATCCGTTATCTGTCAGTTCAG 276
QY 54 AspLeuIleValAlaTyTyValPheTyTyTyLeuAlaAsnThrTyIleProLeuIlePro 73
DB 277 GATTCATATTATACCTTCCTTTATACAGCGTCGCAACTCTTACATTCCTTCCT 336
QY 74 ThrProLeuAlaTyTyLeuAlaThrProValTyTyPheCysGlnAlaSerIleLeuThr 93
DB 337 CCTCTCTACCTTACTTACGATGCGCTGTTACTGTTTGCACATCTTCGATCTCACT 396
QY 94 GlyLeuTPValIleGlyHisGluCysGlyHisIleAlaPheSerAspTyTyGlnLeuIle 113
DB 397 GGTATTATGGGTCATTCGCGCATGAATGTGGCCATCATGCTTATAGAGACAGGGGTT 456

QY 114 AspAspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyPheSerTrpLys 133
DB 457 GATTAACACCGTTGATTCATCTTCATCTTCTTTCACACCTTACTTTCTTGAAA 516
QY 134 TySerHisArgAsnHisIleAlaAsnThrAsnSerLeuAspAspGluValTyTyIle 153
DB 517 TACAGCCATCGAAGACACCATCCACAGATTCACATCGAAGAAAGAGAGTTTACTT 576
QY 154 ProLysArgLysSerLysValLysIleTySer-----LysLeuLeuAsnProPro 171
DB 577 CCTAAGCCAGATCCCGACCTCAGAAATTAATTCATTCATTAATTCCTTGACAAACCCCT 636
QY 172 GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyLeuThr 191
DB 637 GGTCAATCTTCACTTTCATTCATGATGACCTTGAGCTTGGCTTCTTATACCTTGACC 696
QY 192 AsnIleSerGlyLysLysTyTyGlyArgPheAlaAsnHisPheAspProMetSerProIle 211
DB 697 AATATTCAGCGCAAGAAATACCAAGGTTTCCACACCATTTGATTCGTTAGCCCATC 756
QY 212 PheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaPhe 231
DB 757 TTCAGTGACGTTGAACGATCCAGTCGCTGATCGATGCGGTCTCATGCTGCTGTTT 816
QY 232 TyrAlaIleLysLeuLeuValAlaAlaLysGlyAlaIleAlaTPValIleAsnMetTyAla 251
DB 817 TACGGGCTTAAGTTTCTTGTAAGCAAAAGGTTGCGTTGGTTAATGCGATGACGA 876
QY 252 IleProValLeuGlyValSerValPhePheValLeuIleThrTyTyLeuHisIleHis 271
DB 877 GCCCAAGTGTTGGGCTGAATGCCCTCATATATATGATCATTTATTCACACACCAT 936
QY 272 LeuSerLeuProHisTyTyAspSerThrGluTrpAsnTrpIleLysGlyAlaLysSerThr 291
DB 937 CTGCTTCGCTCATTCATTCGATTCACCGAATGGAATCGAATGGAAGACCTTGACATCA 996
QY 292 IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisIleVal 311
DB 997 ATCGATAGAGATTCGCTCTGTAATAGGATGTTCCATGACGTCATCACAACACAGCTG 1056
QY 312 LeuHisIleLeuIleSerTyTyIleProHisTyTyHisAlaLysGluAlaArgAspAlaIle 331
DB 1057 TTGCATCATTTGTTCCGCTACATTCACATTCATGATGCAAGAGGCGAGGACGCAATA 1116
QY 332 LysProValLeuGlyGluTyTyTyLysIleAspArgThrProIlePheLysAlaMetTy 351
DB 1117 AAGCGGAGTTAGGGAGATACGATGATCGATGAGACTCCGTTTTCMAAGCAATGTGG 1176
QY 352 ArgGluAlaLysGluCysIleTyTyIleGluProAspGluAspSerGluHisLysGlyVal 371
DB 1177 AGAGAGGCGAAGAAATGATTCATTCAGGCGAGATGAGATGAAGTAAAGACACAAAGGTGA 1236
QY 372 PheTPTyHisLysMet 377
DB 1237 TATTGTTACATTAATAG 1254

RESULT 6
ADE40488
ID ADE40488 standard; DNA; 1398 BP.
XX
XX ADE40488;
XX
XX 29-JAN-2004 (first entry)
XX
XX P. granatum delta-12-desaturase PufAD12 DNA.
XX
XX desaturase; transgenic; plant; oil; triglyceride; unsaturated fatty acid;
KW food; animal feed; cosmetic; pharmaceutical; pomegranate; ds; gene;
KW delta-12-desaturase; PufAD12.
XX
XX Punica granatum.
OS
XX
XX Location/Qualifiers
FH Key

FT	CDS	94..1257	
FT		/*tag= a	
FT		/product= "delta-12-desaturase PufAD12"	
XX			
XX	DE10134660-A1.		
XX			
XX	06-FEB-2003.		
PD			
PD	20-JUL-2001; 2001DE-01034660.		
XX			
XX	20-JUL-2001; 2001DE-01034660.		
XX			
XX	(BADI) BASF PLANT SCI GMBH.		
XX			
XX	Feusener I, Hornung E, Pernsetich C;		
XX			
DR	WPI; 2003-722899/69.		
DR	P-PSDB; ADE40489.		
XX			
PT	New isolated nucleic acid encoding desaturase enzymes from pomegranate,		
PT	useful for recombinant production of unsaturated fatty acids, for e.g.		
PT	the production of food, animal feeds and pharmaceuticals.		
XX			
PS	Claim 11; SEQ ID NO 5; 38pp; German.		
XX			
CC	This invention describes a novel nucleic acid encoding a polypeptide with		
CC	desaturase activity. The products of the invention are used in the		
CC	construction of constructs, vectors, organisms and transgenic plants		
CC	containing the desaturase. The invention also describes methods for		
CC	preparing oils or triglycerides with increased content of unsaturated		
CC	fatty acids; oils, fats and fatty acid mixtures and a novel nucleic acid		
CC	encoding a protein able to convert a fatty acid to a more highly		
CC	unsaturated acid. The products of the invention are used to produce		
CC	transgenic plants (or other organisms) that produce oils and fats with		
CC	increased contents of unsaturated fatty acids, useful in preparation of		
CC	foods, animal feeds, cosmetics and pharmaceuticals and in homology		
CC	screening for isolation of genomic sequences. This sequence encodes a		
CC	fragment of the Punica granatum (pomegranate) delta-12-desaturase PufAD12		
CC	described in the disclosure of the invention.		
XX			
XX	Sequence 1398 BP; 311 A; 422 C; 370 G; 292 T; 0 U; 3 Other;		
Alignment Scores:			
Pred. No.:	4,35e-135	Length:	1398
Score:	1337.50	Matches:	230
Percent Similarity:	77.14%	Conservative:	67
Best local Similarity:	59.74%	Mismatches:	79
Query Match:	65.34%	Indels:	9
DB:	9	Gaps:	2
US-10-069-772-2 (1-377) x ADE40488 (1-1398)			
QY	1 MetGlyAlaGlyGlyArgMetSerAspProSer-----Glu 12		
Db	94 ATGGGAGCGCGGGAGAAATGACGGCTCCGCAACAACTGGGAGGCGAAGGAGACGAGAG		
QY	13 GilytSaenIleLengIuArgValPro---ValAspProProthThrIleuSerAspLeu 31		
Db	154 AGCCAGAAAGCCGGTCCAAAGGGTCCCTCCGCAACGCAACACATTCACTACACGAGATC 213		
QY	32 LysIlytSaIleIleProThrHisCySpheGluArgSerValIleArgSerSertyrYrVal 51		
Db	214 AAGAAAGGCCATCCCGCCACATTTGCTTCAAAAGCTCCCTCCTCAAGTCTTCTCTATGTC 273		
QY	52 ValHisAspLeuIleIleValAlaItyrValAlaPheTyrTyrIleuAlaSnhrTyrIleProLeu 71		
Db	274 CTCtATGACCTCACTTGTGGTGGCACTCTTATTAAGGTGCTACCACTTACATCGAGCC 333		
QY	72 IleProThrProLeuAlaItyrIleuAlaItyrProValItyrTyrPheCyGlnAlaSerIle 91		
Db	334 CTCGCGGGGCTCACTACGCTACGCGCGCTGCGCCGCTGTACTGGGCCCTGCAAGGGGTGCGTG 393		
QY	92 LeuthrGlyLeuItyrValIleGlyIleGluCyGlyHisIleAlaPheSerAspTyrGln 111		

Db	394	CTCAGCGGTTGTCGGTCTATAGCCACGAGTGCGGGACCAATGCGTTTAGCGACTACCAAG	453
Qy	112	LeuIleAspAspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSer	131
Db	454	TGGGTGACGACGTGTGTCGGCTGGGTACTGCACTACGACGCTCTCTGTTCCGTACTTCTCC	513
Qy	132	TrpIleuTyrSerHisArgAsnHisHisIleAlaAsnThrAsnSerLeuAsnAspAsnArgIleVal	151
Db	514	TGGAAAGTACAGCCACCGCGGACCACTCCAAACAGCGGCTCAGTAGAGGTGACGAGGTT	573
Qy	152	TyrIleProLysArgLysSerLysValIleTyrSerLysLeuLeuAsnAsnProPro	171
Db	574	TTCGTCGCCAAGCCCAAGTCCCAAGATGCCGTGGTTCCTCAAGTACCTGAACAACCGGCA	633
Qy	172	GlyArgValPheThrLeuValPheArgLeuThrLeuGlyPheProIleuTyrLeuLeuThr	191
Db	634	GCGCGAGTCATGACCGCTGATTTGTGACCTGACCTTGGGCTGGCCGTTGATCTTGAGCATTTG	693
Qy	192	AsnIleSerGlyLysLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIle	211
Db	694	AACGCTCTGTGGCTGGCCCTATGACAGGTTCCGTCTCCACTTTTGACCCGTAATGGCCGATC	753
Qy	212	PheAsnAspArgGlyArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPhe	231
Db	754	TACACCGAGGAGACCGTCTACAGATCTCACTTTGATGTAGGAGATCATGGCCGCCACG	813
Qy	232	TyrAlaIleLysLeuLeuValAlaAlaLysGlyAlaAlaIleTyrValIleAsnMetTyrAla	251
Db	814	TACACGCTGTACAAGATGACGACGACCCGCTGGCTGGTGGTTGTGTATATGGT	873
Qy	252	IleProValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHis	271
Db	874	GTCCCTCTCTGATGTGTAACGCACTCTGTGTCGACGATCACTTACCTCCAGCACACCCAC	933
Qy	272	LeuSerLeuProHisTyrAspSerThrGluTyrPasnThrIleLysGlyValLeuSerThr	291
Db	934	CCGGCCCTTCCCACTATGACTCGTCGGATGGACTGGCTCAAGGGGCACTGGCAACA	993
Qy	292	IleAspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisVal	311
Db	994	GCGACCGAGACTACGAGGATCTCCAAAGCTCTTCCAAACATACGACACGACGCAATGC	105
Qy	312	LeuHisHisLeuLeuSerTyrIleProHisTyrHisValAlaLysGluAlaArgPalaIle	331
Db	1054	GCCCAACCACTCTTCTCCACATGCGGACACTACACGCGATGAGGCTACCAAGCGATC	111
Qy	332	LysProValLeuGlyGluTyrTyrTyrIleAspArgThrProIlePheLysAlaMetTyr	351
Db	1114	AAGCGGAATACGGAGACTATCAACAGTTCCAGCGGACTCCGGTATACAAACGAGATGG	117
Qy	352	ArgGluAlaLysGluCysIleTyrIleGluProAspArgLysPheSerGluHisLysGlyVal	371
Db	1174	AGAGAGGCTTAGGAGATGCTGTACTGAGAGCCGACGACGCGGCCCAACAGTAAAGGGGTT	123
Qy	372	PheTyrTyrHisLys	376
Db	1234	TTCTGTGTAAGAAG	1248
RESULT 7			
AADD2380			
ID	AADD2380 standard; cDNA, 1422 BP.		
AC	AADD2380;		
XX	12-FEB-2002 (first entry)		
DT			
XX			
DE	Cotton oleoyl-PC delta12-desaturase (ghFAD2-2) protein cDNA.		
XX			
KM	Cotton: delta9-desaturase; fatty acid delta12-desaturase; palmitic acid;		
KM	linoleic acid; stearic acid; oleic acid; transgenic plant;		
XX	cotton seed oil; oleoyl-PC delta12-desaturase; FAD2-2; ss.		

OS	Gossypium hirsutum.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	98..1249
FT	/feature= a
XX	/product= "Cotton ghpAD2-2 protein"
PN	MO200179499-AI.
XX	
PD	25-OCT-2001.
XX	
PF	18-APR-2001; 2001WO-AU000436.
XX	
PR	18-APR-2000; 2000US-0198124P.
XX	
PA	(CSIR) COMMONWEALTH SCI & IND RES ORG.
XX	
P1	Green A, Singh S, Liu Q;
XX	
PI	WPI; 2001-602932/68.
DR	P-P8DB; AAEL13421.
XX	
PT	Modifying endogenous oil of cotton plants, to produce cotton seed oil
PT	with reduced palmitic acid and/or linoleic acid content, involves producing
PT	transgenic plants containing a fatty acid biosynthesis gene in a
PT	construct.
XX	
PS	Example 8; Fig 6; 201pp; English.
CC	The invention relates to a method for modifying the endogenous oil of a
CC	cotton plant, to produce cotton seed oil. The method comprises producing
CC	a transgenic cotton plant having a gene construct which includes a fatty
CC	acid biosynthesis gene operably linked to a promoter sequence capable of
CC	conferring expression of the delta9-desaturase (delta9 stearyl-ACP
CC	desaturase) gene, or fatty acid delta12-desaturase (oleoyl-PC delta12-
CC	desaturase) gene, in the seed of a cotton plant. The invention is useful
CC	for producing cotinseeded oil with reduced palmitic acid and/or linoleic acid
CC	content, and increased stearic acid and/or oleic acid content. The present
CC	sequence is cotton oleoyl-PC delta12-desaturase (ghpAD2-2) protein cDNA
CC	related to the invention
SQ	Sequence 1422 BP; 358 A; 335 C; 307 G; 422 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	1,56e-134 Length: 1422
Score:	1332.50 Matches: 230
Percent Similarity:	79.16% Conservative: 70
Best Local Similarity:	60.69% Mismatches: 74
Query Match:	65.10% Indels: 5
DB:	5 Gaps: 2
US-10-069-772-2 (1-377) x AMD2380 (1-1422)	
DY	1 MetGIYAAGLYVARGHWETSERASPProSerGIgLYLb-----AsnIle 16
Db	98 ATGGGTGTCGGAGGCAGAAATGTCTGCCAACAACAGTCAAAAAMACCGAATTCAACTCA 157
OY	17 LeugIUAryValPrOVAlasp---PropOpheThrLeuSerApLeuLySLyVAIlaIle 35
Db	158 CTGAAGCGAGTTCCATCTCAACAAAGCACCCCTTCACTGTGATGATAATCAAGAAGACCATC 217
OY	36 ProThrHisCyPhelGuArgerSeValIlleArgSerSerTyTrTyValValHisApLeu 55
Db	218 CCACACACACTGTTTCCAGGCGCTCCGTTTTAACGTCAATTCATCATATCCCTTAAGCACTT 277
OY	56 IlleValIArTyValPheTyTrTyLeuAlaSerThTyTrIleProLeuIleProThrPro 75
Db	278 AATATGGCCCTCTCTTTTAAACATGTGGCCACCAATTAATCTCCCTAACCTTCACAGGCT 337
OY	76 LeuAlaTyLeuAlaArPrProValTyTrTPheCyGlAlaSerIleLeuThrglyLeu 95
Db	338 CTCCTCAACGTGGCTTGACCTCTTTATTTGGCCATGCAAGGTTCATTTTGACCGAGCT 397

Oy		96	TTPVALLIGLYNHSGLUCYSGLYHISALAPHESEARPYRGINLEULILEASASP	115
Dd		398	TGGGTCAATGACCATGAAGTGGCCACCATGCTTCAGTAGTTATCAATGGCTTGACGAC	457
Oy		116	IIEVALGYHEVALLEUHISSERIALALEULEUTHPRORYPHESETRPLVETYSER	135
Dd		458	ACCGTGGCCATTACTCTCCACTCTTCTCTTAGTTCATATTTCTCTGGAAATATAGC	517
Oy		136	HISARGASNHIASHALASNTHIRXANSENLEUEARNANBPGIUVALLYRIEPROLYS	155
Dd		518	CACCGCGGTCAACCATYTCTAACCCGGTTCCTCTCGAAGAAGATGAGTTCGTYCCAG	577
Oy		156	ARGLYSERLYSERVALLEYRIEYRIERYLSERLYSEULEUANENANPROPQGIARYGVAlPhe	175
Dd		578	AAAAATCTGGTTTAAGAATGTGGGCCAAACACTTCACATTCACC GGCTTTCTG	637
Oy		176	ThIRLeuValPHeArgLeuthIRleuGlYPHeProLeuTYrLeuleuthIRAsnILeSerGIY	195
Dd		638	TCATATCACCATTCACATTCACCTTGTTGGCCGCTTACTAGCTTCAACGTTGCCGC	697
Oy		196	LYALRYETGLIYARPhEAlAsnHISPhEAAPROtESerPROIIePhEANBARG	215
Dd		698	CGCGCTTACACAKGGTTCCCTTGCCACATGACCCCTTACGGCCCCCAATTTTCGACCGG	757
Oy		216	GLUARVALGlnValLEuSERserPhEGlyLEuLEUALValPHeTYrAlaILElys	235
Dd		758	GAAAGACTCCAAMTCTAATCTCTACCGCGCGCTCGCTGTCGCTTACCGCTTAC	817
Oy		236	LEuLEuVALAlalAlaySGlYAlalATrPVAlIleasMeCTYrAlaleProValLeu	255
Dd		818	CGTCTCGTGTGGCCCAAAGGGTAGTGGTTATAGCGTTATAGGGGTGCCATTATTG	877
Oy		256	GLIYAlSERVALPHePhEVALleuILEThrTYrLeuHISHETHriSLeuSERLeuPro	275
Dd		878	GTGGTTAACCCCTCTTAGTAAATGATACGTAATTGGCAACACTCACCCATCTTTGCCG	937
Oy		276	HISDTRASPserThrcglTrUPAnTrPIeysglYAlaleSeThrIleASPARGASP	295
Dd		938	CACATATGATTCCTCGAGTGGACCTGAGANGAGAGAGCTTATACACTGTGGACAGAT	997
Oy		296	PHeGLYPHeLEuANARGValPHeHISABVALThriSThriSHALeuiSHISLeu	315
Dd		998	TATGGATTTTAAACAAGSTTTTCCATAACATPAACGCACTCATGTGGCTCATATTG	105
Oy		316	ILesETyrILeProHISethriSHALySGlUALarGARPALIleYSProVALLeu	335
Dd		1058	TTTTTCACATGGCTCATATCATGCTCANTGGTGCACCAAGGGGATPAAGCCCATATTG	111
Oy		336	GLIYGLUTYrTYrILySLeASPARgThrPROIIePhELySAlameCTYrARGGluAlalyS	355
Dd		1118	GGGAATACATCAAGTTCATGGATGGAGTCTGTATAAAGCGATATGAGGAGGCCAAG	117
Oy		356	GLICYerILETyRIleGluPROASPGluASerSerGIuHISLySGIYVALPHeTYr	374
Dd		1178	GAGTGTCTCTACGTTGAAACCAATAGGGCCACAAAGATTAAGGTGTGTTTGTTT	1234
RESULT 8				
AAl69486	ID	AAl69486	standard; cDNA; 1411 BP.	
AC XX		AAl69486;		
XX DT		08-MAR-2002	(first entry)	
XX DE		C. officinalis	Cofad2 cDNA.	
XX KM		Cofad2;	linoleic acid; conjugated fatty acid; plant; cosmetic;	
XX KW		pharmaceutical;	lubricant; ss.	
XX OS		Calendula officinalis.		
XX FT	Key	Location/Qualifiers		
		CD5	89..1240	

```
FT      /*tag= a
FT      /product= "Cofad2"
XX      MO200185968-A2.
XX      15-NOV-2001.
XX      09-MAY-2001; 2001WO-IB001059.
XX      09-MAY-2000; 2000US-0203027P.
XX      (BIOR-) BIORIGINAL FOOD & SCI CORP.
XX      Qiu X;
XX      WPI; 2002-089796/12.
XX      P-PSDB; AMG80695.
XX      Nucleic acids which encode a conjugase and its related enzyme a delta
XX      desaturase to be used for the large scale production of conjugated
XX      linoleic acid and linolenic acid in plants.
XX      Claim 3; Fig 1; 49pp; English.
XX      This invention describes a novel polypeptide, Cofad2, capable of
XX      catalyzing the formation of two conjugated double bonds. The products of
XX      the invention can be used for the large scale production of conjugated
XX      linoleic acids. The composition may be used for cosmetic or
XX      pharmaceutical purposes. The conjugated linoleic acids may be used for
XX      coating, painting or cold weather ester-type lubricant purposes. There is
XX      not a natural source which is rich in conjugated linoleic acids and
XX      chemical processes result in a mixture of several isomers. Plant
XX      biotechnology is cost-effective and renewable with little side effects.
XX      This sequence encodes the Calendula officinalis Cofad2 protein
XX      SQ Sequence 1411 BP; 360 A; 374 C; 311 G; 366 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,466-133      Length:      1411
Score:          1323.50      Matches:      233
Percent Similarity: 76.32%      Conservative: 57
Best Local Similarity: 61.32%      Mismatches: 83
Query Match:      64.66%      Indels:      7
DB:              Gaps:      2

US-10-069-772-2 (1-377) x AAI69486 (1-1411)
QY      1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal 20
DB      89 ATGGGTGCGAGCGGTGCAATGCAGATCCCAACGCTGGCAACAAACGAGCCGAA 148
QY      21 ProValAsp-----ProProPheThrLeuSerAspLeuLysVal 34
DB      149 CCAATCCACCGGTCCACATGAAACACCCCATTCACATGAGACATCAGAAACCG 208
QY      35 IleProThrHisCysPheGluArgSerValIleArgSerSerTrpTrpValValHisAsp 54
DB      209 ATCCCACTCTATGTTTCAACCGATCGGTAATTCGTATTTTCATACGATCTTTTACAC 268
QY      55 LeuIleValAlaTrpValPheTrpTrpLeuAlaAsnThrTrpIleProLeuIleProThr 74
DB      269 CTCACAAATCGCGTCAATCTGTACATGACATGCAACAAATTCATCATCCTCCCTAGC 328
QY      75 ProLeuAlaTrpLeuAlaTrpProValTrpTrpPheCysGlnAlaSerIleLeuThrGly 94
DB      329 CCGCTCGCTACGTACGCGATGCGCTTACCTGGCCGCTCAAGGGGTGCTTAAACCGG 388
QY      95 LeuTrpValIleGlyHisGlyCysGlyHisIleAlaPheSerAspTrpGlnLeuIleAsp 114
DB      389 GTGTGGGTCAATAGCCACCAATGTGGCATCATGCTTTTACGACACCAATGGCTCAT 448
QY      115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTrpPheSerTrpLysTrp 134
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DB      449 GACACCGTGGTCTGCTTGCTGACTCGTTCCTACTCGTGCCCTTCTTCGTGAAATAT 508
QY      135 SerHisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnAspGluValTrpIlePro 154
DB      509 AGCCACCGTAGGACCACTGCAACACGGGCTCGATCGACACGATGAGTTTTCGTCCG 568
QY      155 LysArgLysSerLysValLysIleTrpSerLysLeuAsnAsnProProGlyArgVal 174
DB      569 AAGTTGAATATCGGCGTCCGGTCAACCGCCGCTACCTTAACCAACCAACCGCCGCAATC 628
QY      175 PheThrLeuValPheAlaGlyLeuThrLeuGlyPheProLeuTrpIleLeuThrAsnIleSer 194
DB      629 TTGACCTTACCTGTAACCTTAACCTCGTGGCTCTTATACCTTACGCTTCAAGCTTTCG 688
QY      195 GlyLysLysTrpGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214
DB      689 GGCGGTATCTAGACCGGTTGCGTCCATTTTCACCCGGAATAGCCGATTTACTCGAAG 748
QY      215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTrpAlaIle 234
DB      749 CGCGAACGGGCTCAAACTTTCATATCCGACGCGGAGATCTTACGCTTCTGCTACTC 808
QY      235 LysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTrpAlaIleProVal 254
DB      809 TTCCGACTCGCAATGACCAAGGCTCACGCGGTCTTACCAACGATGAGTGGCCGCTTA 868
QY      255 LeuGlyValSerValPhePheValLeuIleThrTrpLeuHisIleSerLeu 274
DB      869 CTGCTGTCACAGGTTTCTTATGTTGATTCATCTTACACACATCACCCTTCGCTC 928
QY      275 ProHisTrpAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArg 294
DB      929 CCGACATATGACTCAACGAAATGAGATGTTAGTGGGGCCCTCACACATGACCGCT 988
QY      295 AspPheGlyPheLeuAsnArgValPheHisAspValThrIleThrIleValLeuHisHis 314
DB      989 GATTACGGATCTTAAACAAAGTGTCTCATTAACCAACGACCTGAGTGGCCACCAT 1048
QY      315 LeuIleSerTrpIleProHisTrpHisAlaLysGlnAlaArgAspAlaIleLysProVal 334
DB      1049 TTGTTCTTACAAAGCTCATATTCATGCAATGAGACGACGAAAGTGAATCAACCGATT 1108
QY      335 LeuGlyGluTrpTrpLysIleAspArgThrProIlePheLysAlaMetTrpArgGluAla 354
DB      1109 TTGGCCATTTATTTACATTTGACGAGGACCTCGATTTTAAAGCGATATCGGAAACA 1168
QY      355 LysGluCysIleTrpIleGluProAspGluAspSerGluHisLysGlyValPheTrpTrp 374
DB      1169 AAGGAGTGCATTTATGTTGATTAAGATGAGAGAGGTGAAA--GATGGTGTATTATGGTAT 1225

RESULT 9
AAV84676
ID      AAV84676 standard; DNA; 1155 BP.
AC      AAV84676;
XX      04-MAR-1999 (first entry)
DE      Wild-type Fad2 gene F form coding sequence.
XX      Brassica, recombinant; microsomal; delta-12 fatty acid desaturase; oil;
XX      delta-15 fatty acid desaturase; seed; fatty acid; oleic acid; Fad3;
XX      erucic acid; canola; rapeseed; linolenic acid; oxidative; Fad2; ss.
XX      Brassica napus.
OS      Key
FH      CDS
FT      1. 1155
FT      /*tag= a
FT      /gene= "Fad2"
FT      /product= "Wild-type Fad2 F form"
XX      US5850026-A.
XX      PN
```

[illegible]

OY		136	HlsArgSerHisShiSaIAsnThrAspSerLeuAspAsnApGluValTyrLeuProlys	155			
Dd		421	CATGAAGCCCAACCATTCACAACACTGGCGCTCCTCGAAGAGAAGAAAGTTTGTCGCCAAG	480			
OY		156	ArgLysSerLysValLysIleTyrSerLysLeuAsnAsnProGlyArgValPhe	175			
Dd		481	AAGAAGTCAGACATCAAGGTGTACGGCAAGTAACCTCAAACCTTTGGAGCGAACCGTG	540			
OY		176	ThreValAlaPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSergLy	195			
Dd		541	ATGTTAACGGTTGACGTTCACTCTCGCGCGCGGTGTACTTAAGCCTTCAAGCTTCGGGA	600			
OY		196	LysLysTyr--GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp	214			
Dd		601	AGACCTTAGCAAGCGGCGGCTTCGCTTCGCATTTCACCCCAACGCTCCCATCTACACAGAC	660			
OY		215	ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle	234			
Dd		661	GCGGAGCGCTCCAGATATACATCATCTCGACGCTGACATCTTCGCGCGTCTGACAGTCTC	720			
OY		235	LysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrAlaIleProVal	254			
Dd		721	TTCGGTTAAGCGCGCGCGCACAGAGAGTGCGCTCGATGCTGCTTCAAGAGTCCCGCTT	780			
OY		255	LeuGlyLysSerValPhePheValLeuIleThrTyrLeuHisShiStrHisLeuSerLeu	274			
Dd		781	CTGATGTGATAGTGTTTCTCTGCTGTATCACTTACTTGACGACACAGCATCTTCCTG	840			
OY		275	ProHisTyrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArg	294			
Dd		841	CCTCAGTACGATTCGTCCGAGTGGGATTGCTTAGAGGGAGCTTTGGTACCGTTGACAGA	900			
OY		295	AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis	314			
Dd		901	GACTACGAAACTTGAACAAAGGCTTCCACATATTAACCGACAGCAGCGTGGCGCATAT	960			
OY		315	LeuIleSerTyrIleProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProVal	334			
Dd		961	CTGTTCTTCACGATGCGCGCATTTATCACCGCATGAGCTACCAGAGCGATTAAGCCGATA	1020			
OY		335	LeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGluAla	354			
Dd		1021	CTGGGAGAGTATTATCACTTCGATGGGACCGCGGCGTTAAGGGGATGTGAGGGAGGCG	1080			
OY		355	LysGluCysIleTyrIleGluProAspGluAspSergLysIleLysGlyValPheTrpTyr	374			
Dd		1081	AAGGAGTGTATCTAATGTGGAACCGGACAGCGCAAGGTGAGAAGAAAGGTGTTCTGTATC	1140			
OY		375	His 375				
Dd		1141	AAC 1143				
RESULT 10							
ID	AXX06619	standard; DNA; 1155 BP.					
XX	AXX06619;						
XX	DT	(first entry)					
DE	Brassicica wild-type Fad2-F gene coding sequence.						
XX							
KW	Fatty acid desaturase; FAD; Brassicaceae; Helianthus; mutation;						
XX	fatty acid; oleic acid; linoleic acid; Fad2 gene; ss.						
OS	Brassica napus.						
XX							
FH	Key	Location/Qualifiers					
FT	CDS	1..1155					
FT	/*tag=a						
XX	/product= "wild-type fatty acid desaturase"						
PJ	WO9856239-A1						

XX 17-DEC-1998.
 PD 11-JUN-1998; 98WO-US012332.
 PF 12-JUN-1997; 97US-00874109.
 PR (CRGI) CARGILL INC.
 PA Debonte LR, Zhegong F, Loh WH, Shorrosh BS;
 PI WPI: 1999-059929/05.
 XX P-PSDB; AAM94053.
 DR New isolated mutant fatty acid desaturase genes - obtained by mutation of
 PT Brassicaceae or Helianthus plants, used for producing plants or seeds
 XX having altered fatty acid compositions.
 PS Example; Page 73-75; 116pp; English.
 XX The invention relates to fatty acid desaturases (FAD) from Brassicaceae
 CC or Helianthus, where the FAD gene comprise at least one mutation in
 CC their sequences. The mutation is in a region encoding the His-Xaa-Xaa
 CC His motif of the delta-12 or delta-15 fatty acid desaturases. The
 CC invention also provides methods for producing the FAD mutant genes and
 CC gene products. The products can be used for producing plants and seeds
 CC which have altered fatty acid compositions, e.g. an elevated oleic acid
 CC content, a decreased, stabilised linoleic acid content, both elevated
 CC oleic acid and decreased, stabilised linoleic acid content or a
 CC decreased, stabilised level of alpha-linolenic acid and increased level
 CC of linoleic acid. The plants may be e.g. soybean, rapeseed, sunflower,
 CC safflower, castor bean or corn. The present sequence represents the DNA
 CC sequence of the coding region of the Brassica wild-type FAD2-F gene
 XX

SO Sequence 1155 BP; 246 A; 361 C; 275 G; 273 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No: 4,36e-133 Length: 1155
 Score: 1318.00 Matches: 233
 Percent Similarity: 77.17% Conservative: 61
 Best Local Similarity: 61.15% Mismatches: 81
 Query Match: 64.39% Indels: 6
 DB: 2 Gaps: 4

US-10-069-772-2 (1-377) x AAX06619 (1-1155)

QY 1 MetGlyValGlyValGlyMet-----SerAspProSerGluGlyLys-----AsnIle 16
 Db 1 ATGGGTGCAAGGTGAGAGATGCAAGTGTCTCTCCCTCCCAAGAGTGTGAAACGACACC 60
 QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuValAlaIle 35
 Db 61 ATCAAGCGCGTACCTCGGAGACACCGCCCTTCACTGCGAGAACTCAAGAAAGCAATC 120
 QY 36 ProThrHisCybPheGluArgSerValIleArgSerSerTyTyValValHisAspLeu 55
 Db 121 CCACCGCACTGTTCACAAAGCTGATCCCTGCTCTTCTCCTACCTCATGTCGGAACATC 180
 QY 56 IleValAlaTyValPheTyTyLeuAlaAsnThrTyTyrIleProLeuIleProThrPro 75
 Db 181 ATCATAGCT 240
 QY 76 LeuAlaTyValLeuAlaTyProValTyTyPheCybGlnAlaSerIleLeuThrGluLeu 95
 Db 241 CTCCTCTACTCTCGCTGCT 300
 QY 96 TyrValIleGlyHisGluCybGlyHisIleAlaPheSerAspTyTyrGlnLeuIleAspAsp 115
 Db 301 TGGGTCAATAGCCCAAGATGGGCGACACGCTTCAGCGCATACAGTGGCTTACGAC 360
 QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyPheSerTyTyrSer 135
 Db 361 ACCGTGGTCTCATCTTCACT 420

QY 136 HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgGluValTyTyrIleProLys 155
 Db 421 CATCGACGCCACCATTCACACACTGCTCTCCCTCGAGAGAGACGAAGTGTGTCCCAAG 480
 QY 156 ArgLysSerLysValIleTySerTyLeuLeuLeuAsnProProGlyArgValPhe 175
 Db 481 AAGAAGTCAGCAATCAATGATGAGGAGAGTCACTTCAACACCTTTGGGCGGACCGCTG 540
 QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyrLeuLeuThrAsnIleSerGly 195
 Db 541 ATGTTAACGTTCACTTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 QY 196 LysLysTyTy---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214
 Db 601 AGACCTTACGACGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
 QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyrAlaIle 234
 Db 661 CGCAGGCGTCCAGAAATACATCTCCGACGCTGCACTCCGCGCTGCTGCTGCTGCTGCTGCT 720
 QY 235 LysLeuLeuValAlaIleAlaLysGlyValAlaIleTyValIleAsnMetTyTyrAlaIleProVal 254
 Db 721 TTCGTTACCGCCGCGGCGAGGAGTGCCTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
 QY 255 LeuGlyValSerValPhePheValLeuIleThrTyLeuHisIleThrHisLysSerLeu 274
 Db 781 CTGATGTGCAATGTTCTCTCGTGTATCACTTACCTTACGACGACAGCATCTTCCCTG 840
 QY 275 ProHisTyArgSerThrGluTyTrpAsnTrpIleLysGlyAlaLysSerThrIleAspArg 294
 Db 841 CCTCACTACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
 QY 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisIleThrHisValLeuHis 314
 Db 901 GACTACGAAATCTTGAACAAGTGTTCACAAATTAACGACAGACAGCGGCGCATCAT 960
 QY 315 LeuIleSerTyTyrIleProHisTyTyrHisAlaLysGluAlaArgAspAlaIleTyProVal 334
 Db 961 CTGTTTCCACGAGGCGGCACTTATCAAGCATGAGACCTTCAAGCGGATTAACCGATA 1020
 QY 335 LeuGlyGluTyTyTyrLysIleAspArgThrProIlePheLysAlaMetTyTyrArgGluAla 354
 Db 1021 CTGGGAGAGATATATACATTCGATGAGCGCGGCTGTTAAGCGAGATGAGGAGGCGG 1080
 QY 355 LysGluGlySerIleTyTyrIleGluProAspGluAspSerGluHisGlyValPheThrTyTyr 374
 Db 1081 AAGGAGTAT 1140
 QY 375 His 375
 Db 1141 AAC 1143

RESULT 11
 AA251120 standard; DNA; 1155 BP.
 XX
 AC AA251120;
 XX
 DT 05-JUN-2000 (first entry)
 XX
 DE B. napus Delta-12 fatty acid desaturase-F (Fad2-F) wild type gene.
 XX
 KM Long chain monounsaturated fatty acid; erucic acid; oleic acid;
 KM delta-15 fatty acid desaturase; Fad3; linoleic acid; vegetable oil;
 KM industrial oil; lubricant; hydraulic oil; delta-12 fatty acid desaturase;
 KM Fad2; Fad2-F; rapeseed; de.
 XX
 OS Brassica napus.
 XX
 FH Location/Qualifiers
 FT 1..1155
 FT CDS /*tag= a

FT /product= "microsomal delta-12 desaturase"
 XX US6372965-B1.
 XX 16-APR-2002.
 XX 14-AUG-1998; 98US-00133962.
 XX 17-NOV-1992; 92US-00977339.
 XX 15-OCT-1993; 93WO-US009987.
 XX 20-JUN-1994; 94US-00262401.
 XX (DUPO) DU PONT DE NEMOURS & CO E. I.
 XX Lightner JE, Okuley JJ, Hitz W, Kinney AJ, Perez-Grau L;
 PI Yadav NS;
 XX WPI: 2002-392229/42.
 DR P-PSDB; ABB80028.
 XX
 PT New nucleic acid encoding delta-12 desaturase, delta-12 hydroxylase, or
 PT delta-12 fatty acid hydroxylase for creating transgenic plants and
 PT producing seed oil with altered levels of unsaturated fatty acids.
 XX
 PS Claim 1; Cql 71-74; 54pp; English.
 XX
 CC The invention relates to an isolated nucleic acid fragment encoding or
 CC comprising a sequence encoding a plant enzyme that is a delta-12
 CC desaturase, delta-12 hydroxylase, or delta-12 fatty acid hydroxylase.
 CC Chimeric genes comprising nucleic acids of the invention are used to
 CC create transgenic plants with altered levels of unsaturated fatty acids,
 CC and can modify plant lipid composition. Nucleic acids of the invention
 CC can be used as hybridization probes to isolate or amplify nucleotide
 CC sequences encoding other fatty acid desaturases or fatty acid desaturase-
 CC related enzymes. They can also be used in restriction fragment length
 CC polymorphism (RFLP) breeding to obtain altered levels of oleic acids in
 CC seed oil of oil producing plant species. They can also be used to produce
 CC seed oil containing altered levels of unsaturated fatty acids. Nucleic
 CC acids of the invention can combine the high oleate trait of transformed
 CC seeds with mutations for altered fatty acid compositions to obtain new
 CC fatty acid compositions and/or improved agronomy. A vegetable oil low in
 CC total saturates and high in monounsaturates would provide significant
 CC health benefits to consumers (reduced risk of coronary heart disease) as
 CC well as economic benefits to oil processors. The current sequence
 CC represents a rape microsomal delta-12 desaturase cDNA
 XX
 SQ Sequence 1423 BP; 320 A; 405 C; 333 G; 365 T; 0 U; 0 Other;
 Alignment Scores:
 Score: 7.53e-133 Length: 1423
 Percent Similarity: 1317.00 Matches: 234
 Best Local Similarity: 76.44% Conservative: 58
 Query Match: 61.26% Mismatches: 82
 DB: 64.34% Indels: 8
 Gaps: 4
 US-10-069-772-2 (1-377) x ABL58600 (1-1423)
 QY 1 MEGGVLVLAAGLVLAAGM-----SeraPProSerGIuGLyLyaAhn 15
 Db 129 ATGGGTCCAGGTGAGAGATGCAAGTCTCTCCCTCCCAAAAAGTGGAAACGACAAAC 188
 QY 16 ILeuGIuArgValProValAsp---ProPhePheThrLeuSerAspLeuValAsp 34
 Db 189 ATC---AAGCGCGTACCTCGGAGACACCGCCCTTCACTCGGAGAACTCAAGAAAGCA 245
 QY 35 ILeuProThriScyPheGIuArgSerValIleArgSerSerTYTYValValIleAsp 54
 Db 246 ATCCACCGCACTGTTCAAGCTCGATCCCTCGCTTCTCTCACTCATCTGGGAC 305
 QY 55 LeuIleValIleAlaTYrValPheTYrTYrLeuAlaIleAsnTYrIleProIleIleProThr 74
 Db 306 ATCATCATAGCTCTCTCTTACTAGTGGCAACCACTTACTTCCCTCTCCCTCAC 365

QY 75 ProLeuAlaTYrLeuAlaIleAlaTYrProValTYrTrpPheCysGlnAlaSerIleLeuThrGly 94
 Db 366 CCTCTCTCTTACTTCCGCTGGCGCTCTTACTAGGGCGCTGGCGGTGGCTCTTAACCGGC 425
 QY 95 LeuTrpValIleGlyIleGlyCysGlyIleIleAlaPheSerAspTYrGlnLeuIleAsp 114
 Db 426 GCTGGGTGATAGCCACAGATGGGGCCACCGCTTACCGCACTACAGTGGCTGGAC 485
 QY 115 AspIleValGlyPheValIleuHisSerAlaLeuLeuThrProTYrPheSerTrpIleTYr 134
 Db 486 GACACCGTGGCTTCACTTCT 545
 QY 135 SerHisArgAsnHisAlaIleAsnThrAsnSerLeuAspAsnAspGluValTYrIlePro 154
 Db 546 AGTCATGAGCGCCACATTCACACATCGGCTCCCTCGAGAGAGACGAAGTGTTCGCC 605
 QY 155 LysArgIleSerIleValIleTYrSerIleLysLeuAsnAsnProProGlyArgVal 174
 Db 606 AAGAAAGATCAGACATCAAGTGTACGGCAAGTACCTCAACACCTTTGGAGCGCAC 665
 QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTYrLeuLeuThrAsnIleSer 194
 Db 666 GTGATGTTAACGGTTCAGTTCACTTCGCGCTGCTTGTACTTACGCTTCAAGCTTCG 725
 QY 195 GlyLysIleTYr---GlyArgPheAlaAsnHisPheAspPromeSerProIlePheAsn 213
 Db 726 GGGAGACCTTACGACGGCGGCTTGCCTTGCATTCACCCCAACGCTCCCATCTACAC 785
 QY 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTYrAla 233
 Db 786 GACCGTAGCGCTCCAGATATACATCTCCGACCTGCGCATCTTCCGCTGCTACCGT 845
 QY 234 IleLysLeuLeuValAlaAlaIleGlyAlaAlaIleProValIleAsnMetTYrAlaIlePro 253
 Db 846 CTTCACCGCTACGCTGCTCCAGAGGTGCTCGATGCTCTCTTACGAGTTCCT 905
 QY 254 ValLeuIleSerValPhePheValIleuIleThrTYrLeuHisIleThrIleLeuSer 273
 Db 906 CTTCGATGTGCAACGGGCTTGTGTTGATCACTTACGACACACCATCTTCC 965
 QY 274 LeuProHisTYrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
 Db 966 CTGCGCTACATGACTGCTGAGTGGAGATGTGTGAGGGAGCTTGGCCACCGTTGAC 1025
 QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHis 313
 Db 1026 AGAGACTACGGATCTTGAACAGAGTCTTCCAAATATCAAGACACGACGTGGCGCAT 1085
 QY 314 HisLeuIleSerTYrIleProHisTYrHisAlaIleGluAlaArgAspAlaIleLysPro 333
 Db 1086 CACCTGTTTCGACACACCGCCGATTTATCAAGCATGAGAGTACGAAGCGATTAAGCG 1145
 QY 334 ValLeuGlyIleTYrTYrLysIleAspArgThrProIlePheIleAlaMetTYrArgGlu 353
 Db 1146 ATACTGGAGAGTATATCATGTTGATGAGACCGCGGTGTAAGCGATGTGAGGAG 1205
 QY 354 AlaIleGlyCysIleTYrIleGluProAspGluAspSerGluHisIleGlyValPheTrp 373
 Db 1206 GCGAAGAGAGTATCTATGTGGAACCGACACGCGAAGGTGAGAAAGGTGTTCGG 1265
 QY 374 TyrHis 375
 Db 1266 TACAAAC 1271
 RESULT 13
 ID AAX91076 standard; cDNA; 1464 BP.
 XX AAX91076;
 AC AAX91076;
 XX 15-NOV-1999 (first entry)
 DT XX

DE B. napus delta-12 fatty acid desaturase 2 (FAD2) D form encoding cDNA.
 KM Fatty acid; delta-12 desaturase; fatty acid desaturase; FAD; enzyme;
 KM linoleic acid; alpha-linolenic acid; mutant; nutritional value;
 XX genetic mapping; plant breeding; ss.
 OS Brassica napus.
 XX
 FH Key Location/Qualifiers
 FT CDS 130..1284
 FT /tag= a
 FT /product= "FAD2 D-form"
 XX
 EN EP945514-A1.
 XX
 PD 29-SEP-1999.
 XX
 PF 26-MAR-1998; 98EP-00302322.
 XX
 PR 26-MAR-1998; 98EP-00302322.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 PI Broglie RM, Miao G, Debonite LR, Reiter RS, Hitz WD;
 DR WPI; 1999-530050/45.
 DR P-PSDB; AAY27329.
 XX
 PT Altering fatty acid profiles in plant seeds, useful for changing
 PT nutritional value of seeds.
 XX
 PS Example; Page 19-21; 44pp; English.
 XX
 CC The invention relates to a method for altering the fatty acid composition
 CC in plant seeds and comprises transforming a plant with a nucleic acid
 CC construct (I) comprising a seed-specific regulatory sequence linked to
 CC either a mutant delta-12 or delta-15 fatty acid desaturase (FAD) gene
 CC encoding a protein with a mutation in a His-(Asp/Glu)-Cys-(Gly/Ala)-His
 CC amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15
 CC FAD. Expression of this construct in plants decreases the level of
 CC activity of these enzymes in the cells of the plant i.e. the construct
 CC acts as a dominant negative. The construct comprising a mutant delta-12
 CC gene is used to decrease the level of linoleic acid in the seeds of
 CC plants to (soybean, rapeseed, sunflower, oil palm, coconut palm, flax,
 CC castor and peanut) Similarly a construct comprising a mutant delta-15
 CC gene is used to decrease the levels of alpha-linolenic acid in the seeds
 CC of plants, especially Brassica canola. The new method may also be used to
 CC transform a plant with both (i) comprising DNA encoding mutant delta-12
 CC and (i) comprising DNA encoding mutant delta-15 FAD genes, to decrease
 CC the levels of both linoleic and alpha-linolenic acid simultaneously in
 CC their seeds. These methods alter the nutritional value of the seeds of
 CC plants which have been transformed. (I) may also be used as DNA
 CC diagnostic markers in plant genetic mapping and plant breeding programs.
 CC In addition (I) may be used to isolate other related FAD genes. The
 CC present sequence represents a Brassica napus cDNA which encodes the wild
 CC type D form of microsomal delta-12 fatty acid desaturase 2 (FAD2)
 XX
 SQ Sequence 1464 BP; 357 A; 407 C; 333 G; 367 T; 0 U; 0 Other;
 XX
 Alignment Scores:
 Pred. No.: 7.84e-133 Length: 1464
 Score: 1317.00 Matches: 234
 Percent Similarity: 76.44% Conservative: 58
 Best Local Similarity: 61.26% Mismatches: 82
 Query Match: 64.34% Indels: 8
 DB: 2 Gaps: 4
 US-10-069-772-2 (1-377) x AAY91076 (1-1464)
 QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLysAsn 15
 Db 130 ATGGGTGAGGTGAGGAATGCAAGTGTCTCTCCCTCCAAAGTAAGTGTGAAACGACAAAC 189

QY 16 IleLeuGluArgValProValAsp---ProProPheThrSerAspLeuLeuValAla 34
 Db 190 ATC---AAGCGCGATACCTCGGAGACACGCGCTTCACTGTCGAGATCAAGAAACCA 246
 QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
 Db 247 ATCCACCGCACTGTTTCAAAAGCTCGATCCCTGCTCTTCTCTACCTATCATCGGAGAC 306
 QY 55 LeuIleValAlaTyTyValPheTyTyLeuAlaAsnTyTyIleProLeuIleProThr 74
 Db 307 ATCATCAAGCGCTCGCTTCTATCTACCTCGCCACACATTCATTCCTCTCTCCCTAC 366
 QY 75 ProLeuAlaTyLeuAlaTrpProValTyTyTrpPheCysGluAlaSerIleLeuThrGly 94
 Db 367 CTTCTCTCTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
 QY 95 LeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyTyGluLeuIleAsp 114
 Db 427 GTCTGGGTCAATAGCCACAGATGGGGCCACACGCTTCAAGCATACCAATGGCTGGAC 486
 QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyTyPheSerTrpLysTy 134
 Db 487 GACACCGTCGCGCTCATCTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
 QY 135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAspAspGluValTyTyIlePro 154
 Db 547 AGTCATCAAGCGCCACCATTCACACCTGCTCTCTCGAGAGACAGAGATGTGTCTCCC 606
 QY 155 LysArgLysSerLysValLysIleTyTySerLysLeuAsnAsnProProGlyArgVal 174
 Db 607 AAGAAAGATGACAGCATCAATCAAGTGAAGCAAGTACCTCAACACCTTGGAGCGCAC 666
 QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSer 194
 Db 667 GTGATGTTCAGGCTTCAGTTCACCTCGCGCTTGTGATCTTCAAGCTTCAAGCTTCG 726
 QY 195 GlyLysLysTyTy---GlyArgPheAlaAsnHisAspPheAspProMetSerProIlePheAsn 213
 Db 727 GGGAGACCTTACGACGGGGCTTGCCTTGCATTCACCCCAAGCTCCCATCTACAC 786
 QY 214 AsparGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyAla 233
 Db 787 GACCGTAGCGCTCCAGATATATACATCCGACCGGTGCATCTCGCGTCTGTACCGGT 846
 QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyTyAlaIlePro 253
 Db 847 CTTCACCGCTACGCTGCTGCTCAAGAGTTCCTCGATGCTCTCTTACGAGTTCCT 906
 QY 254 ValLeuGlyValSerValPhePheValLeuIleThrTyTyLeuHisHisThrHisLeuSer 273
 Db 907 CTTCGATGTCAACGGGCTTCTTGTGTGATCACTTACCTTGCACGACACGACATCTTCC 966
 QY 274 LeuProHisTyTyAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
 Db 967 CTGCGTCACTATGACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1026
 QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisHisValLeuHis 313
 Db 1027 AGAGACTACGGAATCTTGAAACAGTCTTCCACATATCAACGACACGACAGCTGCGCAT 1086
 QY 314 HisLeuIleSerTyTyIleProHisTyTyHisAlaLysGluAlaArgAspAlaIleLysPro 333
 Db 1087 CACCTGTTCTGACACATCCCATATTCATCATCGATGAGAGCTACGAGCGCATTAAGCCG 1146
 QY 334 ValLeuGlyGluTyTyTyTyIleAspArgThrProIlePheLysAlaMetTyTyArgGlu 353
 Db 1147 ATACTGGGAGAGTATTAATCAATTCATGATGACGCGCGGTGAAGCGCATGTGGAGGAG 1206
 QY 354 AlaLysGluCysIleTyTyIleGluProAspGluAspSerGluHisLysGlyValPheTrp 373
 Db 1207 GCGAAGGAGTGTATCTATGTGAACCGGACAGGCAAGGTGAGAAAGAGTGTGTCTTGG 1266
 QY 374 TyrHis 375

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Db      1267 TACNAC 1272
RESULT 14
AAK91077
ID      AAK91077 standard; cDNA; 1155 BP.
XX
AC      AAK91077;
XX
DT      15-NOV-1999 (first entry)
XX
DE      B. napus mutant D-form of delta-12 FAD2 encoding cDNA.
XX
KM      Fatty acid; delta-12 desaturase; fatty acid desaturase; FAD; enzyme;
XX      linoleic acid; alpha-linolenic acid; mutant; nutritional value;
XX      genetic mapping; plant breeding; mutant; ss.
OS      Brassica napus.
OS      Synthetic.
XX
FH      Key
FT      CDS
FT      1. 1155
FT      /tag= a
FT      /product= "mutant FAD2 D-form"
FT      316
FT      /tag= b
FT      /note= "G to A transversion mutation of the D-form"
XX
XX      EP945514-NI.
XX
XX      29-SEP-1999.
XX
XX      26-MAR-1998; 98BP-00302322.
XX
XX      26-MAR-1998; 98BP-00302322.
XX
XX      26-MAR-1998; 98BP-00302322.
XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Brogile RM, Miao G, Debonte LR, Reiter RS, Hitz WD;
XX      WPI, 1999-530050/45.
XX      P-PSDB; AAY27330.
XX
XX
XX      Altering fatty acid profiles in plant seeds, useful for changing
XX      nutritional value of seeds.
XX
XX      Example 1; Page 23-25; 44pp; English.
XX
XX      The invention relates to a method for altering the fatty acid composition
XX      in plant seeds and comprises transforming a plant with a nucleic acid
XX      construct (I) comprising a seed-specific regulatory sequence linked to
XX      either a mutant delta-12 or delta-15 fatty acid desaturase (FAD) gene
XX      encoding a protein with a mutation in a His-(Asp/Glu)-Cys-(Gly/Ala)-His
XX      amino acid region. (I) encodes a mutant delta-12 or a mutant delta-15
XX      FAD. Expression of this construct in plants decreases the level of
XX      activity of these enzymes in the cells of the plant i.e. the construct
XX      acts as a dominant negative. The construct comprising a mutant delta-12
XX      gene is used to decrease the level of linoleic acid in the seeds of
XX      plants to (soybean, rapeseed, sunflower, oil palm, coconut palm, flax,
XX      castor and peanut) Similarly a construct comprising a mutant delta-15
XX      gene is used to decrease the levels of alpha-linolenic acid in the seeds
XX      of plants, especially Brassica canola. The new method may also be used to
XX      transform a plant with both (I) comprising DNA encoding mutant delta-12
XX      and (I) comprising DNA encoding mutant delta-15 FAD genes, to decrease
XX      the levels of both linoleic and alpha-linolenic acid simultaneously in
XX      their seeds. These methods alter the nutritional value of the seeds of
XX      plants which have been transformed. (I) may also be used as DNA
XX      diagnostic markers in plant genetic mapping and plant breeding programs.
XX      In addition (I) may be used to isolate other related FAD genes. The
XX      present sequence represents a Brassica napus cDNA which encodes the
XX      mutant D form of microsomal delta-12 fatty acid desaturase 2 (FAD2)
XX
XX      Sequence 1155 BP; 250 A; 357 C; 273 G; 275 T; 0 U; 0 Other;

```

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Alignment Scores:
Pred. No.: 1.52e-132 Length: 1155
Score: 1313.00 Matches: 233
Percent Similarity: 76.44% Conservative: 59
Best Local Similarity: 60.99% Mismatches: 82
Query Match: 64.14% Indels: 8
DB: 2 Gaps: 4

US-10-069-772-2 (1-377) x AAK91077 (1-1155)

QY      1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGlyGlyAsn 15
DB      1 ATGGGTGACGGGTGGAAGATGCAAGTCTCTCCCTCCAAAGAGTGAACCGACAAAC 60
QY      16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuIleuVal 34
DB      61 ATC--AAGCGGTACCCCTGCGAGACACCGCCCTTCACTGTGAGAACTCAAGAAAGCA 117
QY      35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTYrValValHisAsp 54
DB      118 ATCCACCGACGACTTTTCAACAGCTCCGATCCCTGCTTCTCTACCTGACGGGAC 177
QY      55 LeuIleValAlaTyValPheTyTYrLeuAlaAsnThrTYrIleProLeuIleProThr 74
DB      178 ATCATCATAGGCTCTGCTCTTCTACTACGTCGACACCACTTACTTCCCTCTCCCTCAC 237
QY      75 ProLeuAlaTYrLeuAlaIleProValTYrTYrPheCysGlnAlaSerIleLeuThrGly 94
DB      238 CCTCTCTCTTACTTGGCTGGCTGCTCTTACTGAGGCTGCGAGGCTGCTTACCGGC 297
QY      95 LeuTrpValIleGlyHisGluCysGlyHisHisIleAlaPheSerAspTYrGlyLeuIleAsp 114
DB      298 GTCTGGGTCAATGAGCCCAAGATGGCGCCACCAACCTTACGCACTACAGTGGTGAC 357
QY      115 AspIleValGlyPheValIleuHisSerAlaLeuLeuThrProTYrPheSerTrpIleTy 134
DB      358 GACACCGTCGCGCTCATCTTCCACTCTCTCTCTGCGCTTACTTCTCTCGAAGTAC 417
QY      135 SerHisArgAsnHisHisIleAlaAsnThrAsnSerLeuAspAsnArgIleValTYrIlePro 154
DB      418 AGTCATGACCGCCACCATTCACACATGCGCTCCCTCGAGAGACGAAGTGTGTGTCGCC 477
QY      155 LysArgLysSerLysValIleTYrSerLysLeuLeuAsnAsnProProGlyArgVal 174
DB      478 AAGAGAGATGACATCACTCAAGTGTACGCAAGTACTTCAACACCTTGGAGCGACC 537
QY      175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTYrLeuLeuThrAsnIleSer 194
DB      538 GTGATGTTTAACGGTTCAGTTCACTCTCGGCTTGCTTGTACTTACCTTCAAGCTTCG 597
QY      195 GlyLysLysTYr---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213
DB      598 GGGGACCTTACGACGGCGGCTTGTCCATTTTCCACCCCAACGCTCCCATCTACAC 657
QY      214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuAlaValPheTyVal 233
DB      658 GACCGGAGCGCTCTCCAGATTTTACATCTCCAGACGCTGACCTTCCGCTGCTGACGT 717
QY      234 IleLysLeuLeuValAlaAlaIleGlyAlaIleArgValIleAsnMetTYrAlaIlePro 253
DB      718 CTTCACCGCTACGGCTGCTGCTCAAGAGAGTTCCTCGATGCTGCTCTTACGAGATTCG 777
QY      254 ValLeuGlyValSerValPhePheValLeuIleThrTYrLeuHisHisThrHisLeuSer 273
DB      778 CTTCGTATGTGCAATGGGCTTCTTGTGTGTATCACTTATGACGACACCACTTCCTTC 837
QY      274 LeuProHisTYrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
DB      838 CTGCTCACTTATGACTGCTGTGATGGATTTGGAGGGAGCTTTGGCCACCGTTAC 897
QY      294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHis 313

```

DB 898 AGAGACTACGGAATCTTGAACAAGSTCTTCCACAATATCAGSAGACCCGACGTGGCGAT 957
QY 314 HisLeuIleSerTyrIleProHisIleTyrHisIleValuIleArgAspAlaIleLeuPro 333
DB 958 CACCTGTTCTGCACATGCCGATCATATCATGATGAGTAAGCAAGCGCATTAAGCCG 1017
QY 334 ValLeuGlyValTyrTyrTyrIleLeuSerArgThrProIlePheLeuAlaMetTyrArgGlu 353
DB 1018 ATACTGGAGAGATATATCATCTTCATGAGACGCGCGGTAAAGCCATGTGGAGGAG 1077
QY 354 AlaIleGlyCysIleTyrIleGluProAspGluAspSerGluHisIleGlyValPheTyr 373
DB 1078 CGAAGAGATGATATATGTGGAACCGACGAGGCAAGTGAAGAAGATGTGTCTTGG 1137
QY 374 TyrHis 375
DB 1138 TACAAC 1143
RESULT 15
AAT85848
ID AAT85848 standard; DNA; 1155 BP.
XX AAT85848;
AC AAT85848;
XX
XX
DT 17-OCT-2003 (revised)
DT 14-JAN-1998 (first entry)
XX
XX
DE Microsomal delta-12 fatty acid desaturase (F form) gene.
XX
XX
KW Delta-12 fatty acid desaturase; oleic acid; rapeseed oil; seed oil;
KW vegetable oil; canola; sunflower; Helianthus; ss.
XX
XX
OS Brassica napus; cv Westar.
XX
XX
FN WO9721340-A1.
XX
PD 19-JUN-1997.
XX
XX
PF 13-DEC-1996; 96WO-US020090.
XX
XX
PR 14-DEC-1995; 95US-00572027.
XX
XX
PA (CRGI) CARGILL INC.
XX
PI Debonte RL, Fan Z, Loh HT;
XX
XX
DR MPI; 1997-33248/30.
DR P-PSDB; AAM24997.
PT
PT Mutated Brassica or Helianthus delta-12 or -15 fatty acid desaturase
XX genes - and plants containing them, having altered fatty acid content of
XX seed oil, especially low saturates but high oleic acid content.
XX
PS Example 12; Page 71-72; 88pp; English.
XX
XX
CC This DNA sequence codes for canola microsomal delta-12 fatty acid
CC desaturase (FAD) F form (see AAM24997). Plants are claimed that contain a
CC mutation in the delta-12 FAD gene. A preferred mutation is in the region
CC encoding a conserved motif (see AAM24994) of delta-12 FADs. A T to A
CC transversion at nucleotide 515 of the canola delta-12 FAD gene (see
CC AAT85849) results in a Leu to His amino acid substitution that
CC inactivates the enzyme and alters the fatty acid composition of the seed
CC oil (see AAM24998). Mutant plants, preferably canola and sunflower, that
CC contain the mutation are obtained by conventional mutagenesis of plant
CC cells and plant regeneration. Further mutations may be introduced into
CC another conserved motif (see AAM24996) of delta-12 FAD and also into
CC delta-15 FAD. The mutant plants produce oils of low saturated fatty acid
CC content (maximum 5%, with not over 2% erucic acid), high oleic acid
CC content (at least 71%) and low linoleic acid content. The content of
CC palmitic acid may be high or low. The vegetable oils can be used in food
CC production and should help to reduce the incidence of coronary heart
CC disease and atherosclerosis. (Updated on 17-OCT-2003 to standardise OS
CC field)

XX
SQ Sequence 1155 BP; 249 A; 357 C; 274 G; 275 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.95e-132 Length: 1155
Score: 1312.00 Matches: 233
Percent Similarity: 76.44% Conservative: 59
Best Local Similarity: 60.99% Mismatches: 82
Query Match: 64.09% Indels: 8
DB: 2 Gaps: 4
US-10-069-772-2 (1-377) x AAT85848 (1-1155)
QY 1 MetGlyAlaGlyValArgMet-----SerAspProSerGluGlyLeuAsn 15
DB 1 ATGGGTGACGGTGAAGAAATGCAAGTGTCTCTCCCTCCAAAAGTGTGAACCGACAC 60
QY 16 IleLeuGlyArgValProValAsp---ProPheThrLeuSerAspLeuIleValAla 34
DB 61 ATC---AAGCCGTRACCTCGGACACACCGCCCTTCACTGTCGAGAACTCAAGAAACGA 117
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAsp 54
DB 118 ATCCACCGCACTGTTTCAAAAGCTCGATCCCTGCTCTTCTCTTACTCATCTGAGAC 177
QY 55 LeuIleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThr 74
DB 178 ATCATCATAGGCTCTCGCTTACTACTGCTCCACACCATTAATTCCCTCCCTCCCTAC 237
QY 75 ProLeuAlaTyrLeuAlaIleProValTyrTyrPheCysGluAlaSerIleLeuThrGly 94
DB 238 CCTCTCTCTACTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 297
QY 95 LeuTyrValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGluLeuIleAsp 114
DB 298 GTCTGGGTCAATAGCCCAAGATGAGGCGGCCACACGCTTCAAGCACTACAGAGCTTGAC 357
QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrTyr 134
DB 358 GACACCGTGGCTCTCATCTTCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
QY 135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAspAspAspGluValTyrIlePro 154
DB 418 AGTATCATGACCCCACTATTCACACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 477
QY 155 LysArgLysSerLysValIleValIleTyrSerLysLeuAsnAsnProProGlyArgVal 174
DB 478 AAGAAGAAAGTCAAGCATCAAGTGAAGCAAGTACCTCAACACCTTGGAGCGAC 537
QY 175 PheThrLeuValPheArgLeuThrIleGlyPheProLeuTyrLeuLeuThrAsnIleSer 194
DB 538 GTGATGTTAAGGTTCAAGTCACTCTCGCGCTTGTGTTAGCTTCAACCTCTCG 597
QY 195 GlyLysLysTyr---GlyArgPheAlaAsnHisAspAspPromeSerProIlePheAsn 213
DB 598 GGGAGACCTTACAGCGGCGCTGCTTCCATTTCCACCCCAAGCTTCCATCTTACAC 657
QY 214 AspArgGlyArgValGlnValIleLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233
DB 658 GACCGCGAGCTTCCAGATATATCATCTCCGACCGTGCATCTCGCGTCCGACAGGT 717
QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIlePro 253
DB 718 CTTCACCGCTACGCTGCTGCTCAAGAGTTCCTCGATGCTGCTTACGAGTTCG 777
QY 254 ValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisIleThrHisLeuSer 273
DB 778 CTTCGATTTGCAATAGGCTTTTGTGTTGATCTTTCAGCACTTGCAGCAACGATCTTCC 837
QY 274 LeuProHisTyrAspSerThrGluTyrPheAsnThrIleLysGlyAlaLeuSerThrIleAsp 293
DB 838 CTGCTCTACTATGACTGCTGATGAGGATGTTGAGGAGAGCTTGGCCACCGTTAC 897

```

Qy 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHis 313
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Db 898 AGAGACTACGGAATCTTGAAACAGGCTTCCACAATATCACGACACGACGTCGCGCAT 957
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 314 HisLeuIleSerTyrIleProHisTyrHisAlaIleGluAlaArgAspAlaIleLeuPro 333
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 958 CACCTGTTCTGACCATGCGCATTTATCATGCGATGGAAGCTACGAAAGCGATTAAGCCG 1017
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 334 ValLeuGlyGluTyrTyrIleAspArgThrProIlePheIleAlaMetTyrArgGlu 353
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1018 ATACTGGAGAGCTATTATCACTGCATGGACGCCGCTGTTAAGCGATGTGAGGAG 1077
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 354 AlaIleGlyGluCysIleTyrIleGluProAspGluAspSerGluHisIleGlyValPheTrp 373
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1078 GCGAAGGAGTGTATCTATGTGAACCGGACAGGCAAGGTGAAGAAGAGTGTGTTCTGG 1137
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Qy 374 TyrHis 375
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1138 TACAAC 1143
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

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Search completed: June 23, 2004, 15:58:02
 Job time : 389 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 15:43:26 ; Search time 77 Seconds
(without alignments)
2717.097 Million cell updates/sec

Title: US-10-069-772-2

Perfect score: 2047
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Issued Patents NA:*

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6: /cgnt_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
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2	1592.5	77.8	1312	4	US-09-059-769-3
3	1589.5	77.7	1358	4	US-09-059-769-1
4	1578.5	77.1	1364	2	US-08-872-302-3
5	1318	64.4	1155	4	US-09-354-231B-13
6	1318	64.4	1155	4	US-09-354-231B-13
7	1318	64.4	1155	4	US-09-128-602B-13
8	1318	64.4	1155	4	US-09-995-297-13
9	1317	64.3	1155	4	US-09-354-231B-9
10	1317	64.3	1155	4	US-09-128-602B-9
11	1317	64.3	1155	4	US-09-995-297-9
12	1317	64.3	1426	4	US-09-133-962A-3

13	1313	64.1	1155	4	US-09-354-231B-11	Sequence 11, Appli
14	1313	64.1	1155	4	US-09-128-602B-11	Sequence 11, Appli
15	1313	64.1	1155	4	US-09-995-297-11	Sequence 11, Appli
16	1312	64.1	1155	3	US-08-907-608-5	Sequence 5, Appli
17	1312	64.1	1155	4	US-09-354-231B-5	Sequence 5, Appli
18	1312	64.1	1155	4	US-09-128-602B-5	Sequence 5, Appli
19	1312	64.1	1155	4	US-09-482-287-5	Sequence 5, Appli
20	1312	64.1	1155	4	US-09-966-888-5	Sequence 5, Appli
21	1312	64.1	1155	4	US-09-995-297-5	Sequence 5, Appli
22	1311	64.0	1155	2	US-08-675-650B-5	Sequence 5, Appli
23	1311	64.0	1155	4	US-09-354-231B-15	Sequence 15, Appli
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25	1311	64.0	1155	4	US-09-995-297-15	Sequence 15, Appli
26	1310	64.0	1155	4	US-09-354-231B-17	Sequence 17, Appli
27	1310	64.0	1155	4	US-09-128-602B-17	Sequence 17, Appli
28	1310	64.0	1155	4	US-09-995-297-17	Sequence 17, Appli
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34	1305	63.8	1155	4	US-09-128-602B-7	Sequence 7, Appli
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40	1299	63.5	1155	4	US-09-128-602B-1	Sequence 1, Appli
41	1299	63.5	1155	4	US-09-482-287-1	Sequence 1, Appli
42	1299	63.5	1155	4	US-09-966-888-1	Sequence 1, Appli
43	1299	63.5	1155	4	US-09-995-297-1	Sequence 1, Appli
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45	1295	63.3	1155	4	US-09-128-602B-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-161-994A-1
Sequence 1, Application US/09161994A
Patent No. 6333448
GENERAL INFORMATION:
APPLICANT: BAFOR, Maureen
APPLICANT: BANAS, Antoni
APPLICANT: DAHLQVIST, Anders
APPLICANT: GUMBERSON, Per-Olov
APPLICANT: LEE, Michael
APPLICANT: SJODAL, Stefan
APPLICANT: STYRNE, Sten
APPLICANT: LEMMAN, Marit
TITLE OR INVENTION: NOVEL PLANT ENZYME AND USE THEREOF
FILE REFERENCE: BAFOR=1
CURRENT APPLICATION NUMBER: US/09/161.994A
CURRENT FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: 9601236.4
PRIOR FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1128
TYPE: DNA
ORGANISM: Crepis alpina
FEATURES:
NAME/KEY: CDS
LOCATION: (1)..(1125)
US-09-161-994A-1
Alignment Scores:
Pred. No.: 2.27e+195
Score: 1636.00
Percent Similarity: 87.50%
Best local Similarity: 76.86%
Query Match: 79.92%
Length: 1128
Matches: 289
Conservative: 40
Mismatch: 45
Indels: 2

DB: 4 Gaps: 1

US-10-069-772-2 (1-377) x US-09-161-994A-1 (1-1128)

QY 1 MetGlyAlaGlyArgMetSerAspProSerGluGlyValAsnIleLeuGluArgVal 20
 DB 1 ATGGGAGGGGATGGCGGT-----GCTGGACCTTGGCAAAACCCCTCAAGAGAGCTGTC 54

QY 21 ProValAspProPheThrLeuSerAspLeuGlyValAlaIleProThrHisCysPhe 40
 DB 55 TCAGTTGATTCACACCTTCACCGTGATGATCTCAAGACAGAAATCCCTCCCATTTGCTTC 114

QY 41 GluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAlaTyrVal 60
 DB 115 AAGGATCTGTAAATCCGTTCCCTTACTACATAGTCCACGATGCTATTAATGCCCTACATC 174

QY 61 PheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeuAla 80
 DB 175 TTCTACTCTCTTGGCGCAAAATACATTCGATTCCTCCCTGCCCCCTTACCTGCTGCT 234

QY 81 TrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGlyHis 100
 DB 235 TGGCCCTTACTGCTGTTGTGCAAGCTAGCATCCACCGGCTTATGGGTATGGGTAC 294

QY 101 GluCysGlyHisValPheSerAspTyrGlnLeuIleAspAspIleValGlyPheVal 120
 DB 295 GAATGCGGTGACACAGCTTCAGACATACCACTGGGCTTGAAGACACTGTGGCTTCAATC 354

QY 121 LeuHisSerAlaLeuLeuThrProTyrPheSerTyrIleTyrSerHisArgAsnHis 140
 DB 355 CTCACCTGTTTCTATGACCCCGATTTCTCTGGAAATACAGCCACCGGACCAACAT 414

QY 141 AlaAsnThrAsnSerLeuAspAspAspGluValTyrIleProTyrArgLysSerLysVal 160
 DB 415 GCCAACACAAATGCTTGACGACAGATGAAGTTTATCCCAAAAGACGACCAAGC 474

QY 161 LysIleTyrSerLysLeuLeuAsnAsnProProGlyArgValPheThrLeuValPheArg 180
 DB 475 GCGCTTACTTAAGATCTTCAACACCCACCTGGCGACGTGATTAATGTTCAATCAC 534

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QY 201 PheAlaAsnHisAspAspProMetSerProIlePheAsnAspGluArgValGlnVal 220
 DB 595 TTTCGCAACATTTGACCCCATGATGCGAATTTCAAAAGCGGAGCGGTTCAAGTC 654

QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAlaVal 240
 DB 655 TTGCTATCGGATCTTGGGCTTCTGCTGTGCTTACGAGATTAACTTGGCGGTACACG 714

QY 241 LysGlyAlaIleAlaTrpValIleAsnMetTyrAlaIleProValLeuGlyValSerValPhe 260
 DB 715 AAAGGCGCGCTGGGTACGTCGATTAAGGAATTCAGATTTAAGGGGTGTTATCTT 774

QY 261 PheValIleLeuIleThrTyrLeuHisHisIsthHisLeuSerLeuProHisTyrAspSerThr 280
 DB 775 TTTCGATATCATCACTACTTGTGACACACCATCTGTGGTCCCTATTATGATTCATCT 834

QY 281 GluTrpAsnTrpIleLysGlyValAlaLeuSerThrIleAspAspAspPheGlyPheLeuAsn 300
 DB 835 GAATGGAATCGCTGACAGGGGCTTTGTCAACAAATGAGGACCTTGGGTCTCTGAT 894

QY 301 ArgValPheHisAspValThrHisIsthHisValLeuHisHisIleLeuIleSerTyrIlePro 320
 DB 895 AGTGTCTCCATGATGTTTACACACTCACTGATGATCATCTTTTTCATACATTCCA 954

QY 321 HisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyrTyrLys 340
 DB 955 CACTATCATGCGAAGAGGACAAAGGATGCAATCAACACAGTCTTGGGACACTTATTAAG 1014

QY 341 IleAspArgThrProIlePheLysAlaMetTyrTrpGluAlaLysGluCysIleTyrIle 360

DB 1015 ATCGATAGACTCCCAATCTGAAAGCAATGTGAGAGGSCCAAGAAATGATCTTCATC 1074

QY 361 GluProAspGluAspSerGluHisLysGlyValPheTyrTyrHisLys 376
 DB 1075 GAGCTGAAAAGGATGAGGATCCAGGCTGTATATGCTGCAATTA 1122

RESULT 2

US-09-059-769-3
 ; Sequence 3, Application US/09059769
 ; Patent No. 6329518
 ; GENERAL INFORMATION:
 ; APPLICANT: Green, Allan
 ; APPLICANT: Singh, Surinder
 ; APPLICANT: Lemman, Marcit
 ; APPLICANT: Stymne, Sten
 ; TITLE OF INVENTION: Plant Fatty Acid Epoxxygenase Genes and Uses
 ; TITLE OF INVENTION: Therefor
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
 ; STREET: 5370 Manhattan Circle, Suite 201
 ; CITY: Boulder
 ; STATE: Colorado
 ; COUNTRY: US
 ; ZIP: 80303
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/059,769
 ; FILING DATE: April 14, 1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: AU P06223
 ; FILING DATE: 15-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: AU P06226
 ; FILING DATE: 15-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/043706
 ; FILING DATE: 16-APR-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/050403
 ; FILING DATE: 20-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Fetber, Donna M.
 ; REGISTRATION NUMBER: 33,878
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 499-8080
 ; TELEFAX: (303) 499-8089
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1312 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: *Crepis* sp.
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 26..1147
 ; US-09-059-769-3

Alignment Scores:

Pred. No.: 8,46e-190 Length: 1312
 Score: 1592.50 Matches: 285
 Percent Similarity: 86.24% Conservative: 41
 Best Local Similarity: 75.40% Mismatches: 47
 Query Match: 77.80% Indels: 5

DB: 4 Gaps: 3

US-10-069-772-2 (1-377) x US-09-059-769-3 (1-1312)

QY 1 MetGlyAGIAGIYARGMetSeraspProSerGluGlyValAsnIleLeuGluVal 20

DB 26 ATGGGTGCGGGGCGGT-----GGTGGACATCGGAAAGTGGTATGAGAAAGTGTTC 79

QY 21 ProPheThrLeuSerAspLeuValIleProThrHisCys 39

DB 80 TCAGTGTATCCAGTAACCTTCTCACTGAGTATTTGAAGCAAGCAATCCCTCCACATTTGC 139

QY 40 PheGluArgSerValIleArgSerSerTyTyValValHisAspLeuIleValAlaTy 59

DB 140 TTCGAGCATCTGTCATCCGTTCACTTATTAAGTTGTCAGGATCTATATTCCTTAC 199

QY 60 ValPheTyTyLeuAlaAsnThrTyTleProLeuIleProThrProLeuAlaTyLeu 79

DB 200 ATCTTCACTTCTGCGCAACATATCCCTATCTCCCTCATCTCTAGCCCTACTTA 259

QY 80 AlaTrpProValTyTyTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly 99

DB 260 GCTTGCGCGCTTACTGTTCTGTACAGTACGCTCTCACTGAGTTATGAGTCTCGGC 319

QY 100 HisGluCysGlyHisHisAlaPheSerAspTyGlnLeuIleAspAspIleValGlyPhe 119

DB 320 CATGATATGTGTACATCATGCTATGCAATACATGAGTGGAGCTTTC 379

QY 120 ValLeuHisSerAlaLeuLeuThrProTyTyPheSerTrpTySerHisArgAsnHis 139

DB 380 ATCATTCATTCATTTCTCTCAACCCGATATTTCTTGGAAATACAGTACCGGATAC 439

QY 140 HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyTleProTyArgLysSerLys 159

DB 440 CATTCACACACAAAGTTCATGATACATGATGATTTTCAATTCACAAAGCAAGTCCAA 499

QY 160 ValLysIleTySerTyLeuLeuAsnAsnProGlyArgValPheThrLeuValPhe 179

DB 500 CTCAGGCTATCTAATTAACCTTCTTACCAACCACTGTCAGCTGTGGTTTGGTTATC 559

QY 180 ArgLeuThrLeuGlyPheProLeuTyLeuLeuThrAsnIleSerGlyLysLysTyGly 199

DB 560 ATGTTCACCTTACGATTTCTTATACCTCTTGACAAATATTTTCGGGCAAGAAATACAT 619

QY 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGln 219

DB 620 AGGTTTGCACCACTTGCACCCAGTGAAGTCCAAATTTTCAAAAGCGTAGGGGTTTACG 679

QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTleAlaIleLeuLeuValAla 239

DB 680 GTCTTCCTTTGAGATCTTGTCTTCTGCTGTGTTTATGGAATTTAAAGTTGCTTACCA 739

QY 240 AlaLysGlyAlaAlaTrpValIleAsnMetTyTleAlaIleProValLeuGlyValSerVal 259

DB 740 AATAAAGAGCTGCTGGGTGCGTGCATGATGAGTTCGGGTCTAGGGGTATTTACC 799

QY 260 PhePheValLeuIleThrTyLeuHisHisThrHisLeuSerLeuProHisTyAspSer 279

DB 800 TTTTTCATGATGATCTCTTCTTACCAACCACTCATGCTGTGCTCCCTCATTTAGATTTCA 859

QY 280 ThrGluTrpAsnTrpIleLysGlyValLeuSerThrIleAspArgAspPheGlyPheLeu 299

DB 860 ACTGATATGAGTATGAGAGGGCTTTGTCAAGAACTGATGAGATCTTTGGTCTCTG 919

QY 300 AsnArgValPheHisAspValThrHisValLeuHisHisLeuIleSerTyTle 319

DB 920 AATAGTGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 979

QY 320 ProHisTyTleAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyTy 339

DB 980 CCACATCTATCTATGCAAGAAAGCAAGGATGATCAATCAACGATCTTGGGAGCTTTTAT 1039

QY 340 LysIleAspArgThrProIlePheValAlaMetTyTleArgGluAlaLysGlyCysIleTy 359

DB 1040 ATGATCGATAGACTCCCAATTTTAAAGCAATGAGAGAGGCGAGGAATGCAATGTAC 1099

QY 360 IleGluProAspGluAspSerGluHisIleGlyValPheTrpTyTyHisLysMet 377

DB 1100 ATCGAGCT-----GATGCAAGCTCAAGAGTGTATTGTGATCATTAATTC 1147

RESULT 3

US-09-059-769-1

Sequence 1, Application US/09059769

Patent No. 6329518

GENERAL INFORMATION:

APPLICANT: Green, Allan

APPLICANT: Singh, Surinder

APPLICANT: Lemman, Maric

APPLICANT: Stymne, Sten

TITLE OF INVENTION: Plant Fatty Acid Epoxigenase Genes and Uses

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Greenlee, Winner and Sullivan, P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

COUNTRY: US

ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/059,769

FILING DATE: April 14, 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P06223

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU P06226

FILING DATE: 15-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/043706

FILING DATE: 16-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/050403

FILING DATE: 20-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Feider, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1358 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

FEATURE:

NAME/KEY: CDS

LOCATION: 30..1151

US-09-059-769-1

Alignment Scores:

Pred. No.: 2,13e-189

Score: 1589.50

Percent Similarity: 85.98%

Best Local Similarity: 75.40%

Query Match: 77.65%

DB: 4

Length: 1358

Matches: 285

Conservative: 40

Mismatches: 48

Indels: 5

Gaps: 3

US-10-069-772-2 (1-377) x US-09-059-769-1 (1-1358)

QY 1 MetGlaIaGlyGlyArgMetSerProSerGluGlyValPheTyrHisLeuMet 20
 Db 30 ATGGGTGCGGGGCGT-----GGTGACATCGAAAAATCGTCAATGAAGCTGTC 83

QY 21 ProValaPro---ProPheThrLeuSerAspLeuValValIleProThrHisCys 39
 Db 84 TCAGTTGATCCAGTAACCTTCTCAGTGAATGAAGCAAGCAATCCCTCCCATGCG 143

QY 40 PheGluAysSerValIleArgSerSerTyrTyrValValHisAspLeuIleValaIaTyr 59
 Db 144 TTCAGAAATCTGTAATCGCTCATCTTAATGTTGTTCAAGATCTCAATTAATCCATC 203

QY 60 ValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrLeu 79
 Db 204 ATCTTCTAATCTCTTCCCAACATATATCCCTACTCTTCAATAGTCAAGCTCACTTA 263

QY 80 AlaTyrProValTyrTyrPheCysGluAlaSerIleLeuThrGlyLeuTyrValIleGly 99
 Db 264 GCTTGCGCCGTTTACTGTTCTGTCAAGCTACGCTCCATCGCTTATGATCTCGGC 323

QY 100 HisGluCysGlyHisHisAlaPheSerAspTyrGluLeuIleAspAspIleValGlyPhe 119
 Db 324 CACGATATGGTCACCATGCTTTAGCACTACACATGCTTTGACGACATCTGGGCTTC 383

QY 120 ValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrPheTyrSerHisArgAsnHis 139
 Db 384 ATCCCTCACTATTTCTCTCTCAACCCGATATTTCTTGGAATTCAGTCAACCGGATCAC 443

QY 140 HisAlaAsnThrAsnSerLeuAspAspAspGluValTyrIleProValArgLysSerLys 159
 Db 444 CATTCACACACAAATGATATATCAATGAAATTTACATCCGAAAGCAAGCAAGCAAA 503

QY 160 ValLysIleTyrSerLysLeuLeuAsnAsnProPheGlyArgValPheThrLeuValPhe 179
 Db 504 CTCGCGCGATCTATTAACCTTCTTAAACCAACCGCTGCGCTGTGGTTGATATTC 563

QY 180 ArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysLysTyrGly 199
 Db 564 ATGTTCAACCTTAGATTTCTTTATACCTTTGACAAATATTTCCGGCAAGAAATACGAC 623

QY 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAspAspArgGluArgValGln 219
 Db 624 AGGTTGGCAACCACTGCAACCCCATGAGTCCAAATTTCAAGAAAGTGAAGCGGTTTCAG 683

QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValaIa 239
 Db 684 GTCTTCTTTCGGATCTTGCTGCTCTTCCGCGTGTATTTAGAAATTAAGTTCTGTAGCA 743

QY 240 AlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValLeuGlyValSerVal 259
 Db 744 AATAAAGGAGCTGCTGGGTACCGCATGTATGAGATTCGGGTATTTAGGCTATTATACC 803

QY 260 PhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeuProHisTyrAspSer 279
 Db 804 TTTTTCGATGTGATCACTTCTTTCGACCAACCCATCAGTCTCCCTCATATATATCA 863

QY 280 ThrGluTyrAsnThrIleLeuGlyAlaLeuSerThrIleAspAspAspPheLeuPheLeu 299
 Db 864 ACTGATGAACTGATGATGAGGGGCTTGTGACAAATGATGAGGAGCTTGGATCTCGCG 923

QY 300 AsnAspValPheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyrIle 319
 Db 924 AATATGTTTTCATGATGATTTACACACTCATGTCATGATCATTTGTTTCAATACAT 983

QY 320 ProHisTyrHisAlaLysGluAlaArgAspAlaIleLysProValLeuGlyGluTyrTyr 339
 Db 984 CCACACTATCATGCAAAAGGAGGCAAGGATGCAATCAAGCCAACTTGGGCGACATTTAT 1043

QY 340 LysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGluCysIleTyr 359
 Db 1044 ATGATCGACAGGACTCCAAATTTTAAAGCAATGTGAGAGAGGAGGAGATGATGAC 1103

QY 360 IleGluProAspGluAspSerGluHisLysGlyValPheTyrTyrHisLeuMet 377
 Db 1104 ATCGAGCT-----GATAGCAAGCTCAAAAGTGTATATGATCAATAATG 1151

RESULT 4
 US-08-872-302-3
 / Sequence 3, Application US/08872302
 / Patent No. 5846784
 / GENERAL INFORMATION:
 / APPLICANT: Hitz, William D
 / TITLE OF INVENTION: Fatty Acid Modifying Enzymes From
 / TITLE OF INVENTION: Developing Seeds of Vernonia galamensis
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: E. I. duPont de Nemours and Co.
 / STREET: 1007 Market Street
 / CITY: Wilmington
 / STATE: Delaware
 / COUNTRY: USA
 / ZIP: 19898
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/872,302
 / FILING DATE:
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Majarian, William R
 / REGISTRATION NUMBER: P-41,173
 / REFERENCE/DOCKET NUMBER: BB-1084
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 302-992-4926
 / TELEFAX: 302-773-0164
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 1364 base pairs
 / TYPE: nucleic acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: cDNA
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: 103..1254
 / US-08-872-302-3

Alignment Scores:
 Pred. No.: 5.17e-188 Length: 1364
 Score: 1578.50 Matches: 280
 Percent Similarity: 87.16% Conservative: 39
 Best Local Similarity: 76.50% Mismatches: 44
 Query Match: 77.11% Indels: 3
 DB: 2 Gaps: 2

US-10-069-772-2 (1-377) x US-08-872-302-3 (1-1364)

QY 15 AsnIleLeuGluArgValProValaP---ProPheThrLeuSerAspLeuLys 33
 Db 157 AATATAACGAACGACCGGTTGATGCGGACCATTTCTGTAAAGGATCTAAAGAA 216

QY 34 AlaIleProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHis 53
 Db 217 GCATCCCTCCGATGCTTTCACAGGATCTGCATCCCTTCAATCGCTACGTTTCAG 276

QY 54 AspLeuIleValaIaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIlePro 73
 Db 277 GATCTCATTAATACCTTCTTTATACAGCGTCCGCAACTTATCATTCCTTCTCTCT 336

QY 74 ThrProLeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGluAlaSerIleLeuThr 93

Db	337	CTCTCTACCTTACTTAGCAGTGGCTGTATTACTGTTTGGCATCTTCGATCTCACT	396
Qy	94	GLYLEUTRPVALILEGLVHISGLUCYGLYHISGLAPHESEASPTRYGLILEU	113
Db	397	GGTTATATGGTCATTTGGCCATGAAATGTGGCCATCATGCTTATAGACATCCAGGGGT	456
Qy	114	ASPAPLILEVALGLPHEVALLEUHSERLALALEUHTHPRPTYPHSESTRPLVS	133
Db	457	GATACACCGGTGGATCATCTCCATTCCTTTCTTCTCACCTTACTTCTTCTTGGA	516
Qy	134	TYRSEHHSISARGASNHHSISALASANTHRANSEERLEUASPASAPSGLVALTYRILE	153
Db	517	TACAGCCATCGAAGACCATCGCAACGAAATTCATCTCGAAGAGAGAGGTTCACATT	576
Qy	154	PROLYBAHGLYSEERLYVALVALLERYSER-----LYSLEULEUASNPANPRO	171
Db	577	CTTAAGCCAAAGTCCCACTCCAGCAATTAATTCCTCAATTCAATTCTTGCAACACCCCT	636
Qy	172	GLYTRGVALPHEHTHLEUVALPHEARGLEUTHLEUGLYPHEPROLEUTHLEUHTHR	191
Db	637	GGTCGAATCTTCATTTTCTTCTTATCATGTTGACCTTGGGCTTCTTATACCTCTTGACC	696
Qy	192	ASNLIESERGLYLYSLYSERYTRCYVARGPHEALASNHHSIPHEASPPROMCESERPROILE	211
Db	697	AATATTTTCAAGCAAGAAATATCCAAAGTTTGGCAACCACTTTGATCCGTTAGGCCCATTC	756
Qy	212	PHENANAPARGLVARGVALGLNVALLEUUSERASRPHEGLYLEUENVALVALPHE	231
Db	757	TTTCAGTACGCGTGAACGAAATCCAGCGTCCGATCATGATGATGGCTCATGCTATGCTGT	816
Qy	232	TYRHALILELYBLEULEUVALALALALYSGLYALALATRPVALILEASMETRYRZLA	251
Db	817	TACGGGCTTAAGTTTCTTGAGCCGAAAAAGGCTTGGCTGGTAAATCGCATGTACGGA	876
Qy	252	ILEPROVALLEGLYVALSERVALPHEPHEVALLEUHTHRTYRLEUHSISHTHRHS	271
Db	877	GCCCCAGGCGTGGCGGTGATGCCCTTCAATAATAGATCACTTATCTCCACCAACCAT	936
Qy	272	LEUSERLEUPROHISTRYASPSESTRHGLUTRPAENTRPLEYSGLYVALALEUSERTHR	291
Db	937	CTGCTCTTGGCTCATTAATCGATTGCAACCGAATGGAATCGATCAAGAGACCTTGACTCA	996
Qy	292	ILEAPARGAPRPHIEGLYPHELEUASNAARGVALPHEHSIAPRVALTHHSISTHRISVAL	311
Db	997	ATCGATTAAGATTTTCGTCCTCGTAATAGGGGTTCATGACGTCACTCACACACACGTG	1056
Qy	312	LEUHSISISLEUHSISERYTRILEPROHISTRYHISALALYSGLVALARGAPRALILE	331
Db	1057	TTGCATCATTTGTTCCCGTACATTCCTCAATTTATCATGCAAGAGAGCGACGACCATTA	1116
Qy	332	LYSPROVALLEUGLYGLUTRYTRYRLYSILEAPARGTHRPROILEPHELYSALMETYR	351
Db	1117	AAGCCGCGTGTAGGGAGATATTCGATGATCATAGACCTCGGTTTACAAAGCAATGTGG	1176
Qy	352	ARGGLVALYVSGLVGYLLETTRYRILEGLUPROASRGLUWAPSEGLUHSILEYGLYVAL	371
Db	1177	AGAGAGGGAAGGATGCATCATCGACGACGATGAAGATGAAGAACACAAAGGTGTA	1236
Qy	372	PHETRPTRYHISLYSMET 377	
Db	1237	TATTGTACCATTAATATG 1254	
<p>RESULT 5 US-08-675-6508-1 : Sequence 1, Application US/086756508 : Patent No. 5850026 : GENERAL INFORMATION: : APPLICANT: DeBonte, L. et al. : TITLE OF INVENTION: CANOLA OIL HAVING INCREASED OLEIC ACID AND : TITLE OF INVENTION: DECREASED LINOLENIC ACID CONTENT : NUMBER OF SEQUENCES: 6 : CORRESPONDENCE ADDRESS: : ADDRESSEE: Fish & Richardson, P.C., P.A.</p>			

```

1 STREET: 60 South Sixth Street, Suite 3300
2 CITY: Minneapolis
3 STATE: MN
4 COUNTRY: USA
5 ZIP: 55402
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent In Release #1.0, Version #1.30
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/675,650B
12 FILING DATE: 03-JUL-1996
13 CLASSIFICATION: 800
14 ATTORNEY/AGENT INFORMATION:
15 NAME: Lundquist, Ronald C.
16 REGISTRATION NUMBER: 37, 875
17 REFERENCE/DOCKET NUMBER: 07148/042001
18 TELECOMMUNICATION INFORMATION:
19 TELEPHONE: 612/335-5070
20 TELEFAX: 612/288-9696
21 INFORMATION FOR SEQ ID NO: 1:
22 SEQUENCE CHARACTERISTICS:
23 LENGTH: 1155 base pairs
24 TYPE: nucleic acid
25 STRANDEDNESS: single
26 TOPOLOGY: linear
27 MOLECULE TYPE: DNA
28 HYPOTHEetical: NO
29 ANTI-SENSE: NO
30 ORIGINAL SOURCE:
31 ORGANISM: Brassica napus
32 FEATURES:
33 OTHER INFORMATION: wild type F form.
34 US-08-675-650B-1
35
36 Alignment Scores:
37 Pred.: 2.03e-155 Length: 1155
38 Score: 1318.00 Matches: 233
39 Percent Similarity: 77.17% Conservative: 61
40 Best Local Similarity: 61.15% Mismatches: 81
41 Query Match: 64.39% Indels: 6
42 DB: 2 Gaps: 4
43
44 US-10-069-772-2 (1-377) x US-08-675-650B-1 (1-1155)
45
46 Oy MetGIYAlagIyGlyAYArgMet-----SerAspProSergLugLyS-----Aenile 16
47 Db 1 ATGGGTGAAGTGAAGATGCAAGATGCTCTCCCTCCACAAAGAAGTCGTAACCGCACACC 60
48
49 Oy 17 LeungIarValProValasp---ProProPheThrLeuSerAspLeuIysAlaile 35
50 Db 61 ATCAAGCGCGTACCTGCAGACACCGGCCCTTCACTGCTGCGAAGACTCAAGAAAGCATC 120
51
52 Oy 36 ProTrnHisCyepneGluArGserVallleaGserSetrTyrrValVaIHaIsapleu 55
53 Db 121 CCACGCGCACTGTTCAAACGCTCGATCCCTCGCTCTTCTCTACCTCATCTGGGACATC 180
54
55 Oy 56 IleValAlaIarValPheTYrrTYrleuAlaentHYrrIleProleuIleProThpro 75
56 Db 181 ATCAAGCGCTCTGCTCTTCTACACGTCGCGCACCACTTACCTTCTCTCTCACCT 240
57
58 Oy 76 LeuAlaTyrLeuAlaTrpProValTYrrTrpPheCYsgInAlaSerIleleuthrgIyeu 95
59 Db 241 CTCtccTAcTTCcgcctcgcccttcctacTcAggGcGcTcGcCAAGGAtggGcTCTAACCGGcGTC 300
60
61 Oy 96 TrpValIIlegIyHIsGlnCYsgIyNIshIsalaPheSerAspTYrGlnleuIIeaPaAP 115
62 Db 301 TGGGTCAATAGCCCAAGAAATGCGGCCACACCGCTTCAGAGCACTACCAAGTGCGTTCAGCAG 360
63
64 Oy 116 IleValGlyPheValIleuHisSerIlaIeuIeuThrProTYrPheSerThrylvytyrser 135
65 Db 361 ACCGTCGGTCTCATCTTCACATCCCTTCCTCTGTCGCTTACTTCTCTCGAAGTACAG 420

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QY 136 HisArgAsnHisHisAlaAsnThrAsnSerLeuAspAspGluValTyrIleProlys 155
Db 421 CATGAGCCGACCAACATTCACACTGGCTCCCTCGAGAGACGAAAGTGTGTGCCCAAG 480
QY 156 ArgIysSerIysValIleTyrSerIysLeuLeuAsnAsnProGlyArgValPhe 175
Db 481 AAGAGTCAGACATCACTGAGACGCAAGTACCTCAACCAACCTTTGGAGCCGCTG 540
QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db 541 ATGTTAAGCGTTCACTCTCGGCTGGCGCTGTGCTTACCTTACGCTTCGCGGA 600
QY 196 LysIysTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214
Db 601 AGACCTTACGACGGGGCTTCGCTTCGCTTCATTCACCCCAACGCTCCATCACAACGAC 660
QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle 234
Db 661 CGCGAGCGCTTCGACATATACCTCCGACGCTGGCATCTCGCGCTGCTGACGGTCTC 720
QY 235 LysLeuLeuValAlaAlaIleGlyValAlaIleTyrValIleAsnMetTyrAlaIleProVal 254
Db 721 TTCGTTACGCCCGCCGCGAGAGTGGCTCGATGCTGCTTACGAGTCCCGCTT 780
QY 255 LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeu 274
Db 781 CTGATGTCAATGCTTCTCGTGTGATCACTTACCTTACGACACACCATCTCCCTG 840
QY 275 ProHisTyrAspSerThrGluTyrPheAsnTyrIleGlyAlaLeuSerThrIleAspArg 294
Db 841 CCTACTACGATTCCTCGAGTGGAGTGGTGGAGGAGGAGCTTTGGTACCGTTACGAGA 900
QY 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisValIleuHisHis 314
Db 901 GACTACGAAATCTTAAACAAGTCTTCCACATATATACGACACGACGTCGGCATCAT 960
QY 315 LeuIleSerTyrIleProHisTyrHisAlaIleGluAlaArgAspAlaIleIleAspProVal 334
Db 961 CTGTTCTCAGAGTCCGACATTCATCAGCGATGAGGATACCAAGCGATTAAGCGATA 1020
QY 335 LeuGlyGluTyrTyrIleValIleAspArgThrProIlePheValMetTyrArgGluAla 354
Db 1021 CTGGAGAGTATATACAGTTCGATGAGGACCGCGGTGAAGCCATGTCGAGGAGCG 1080
QY 355 LysGluCysIleTyrIleGluProAspGluAspSerGluHisIleGlyValPheTyrPyr 374
Db 1081 AAGGAGTATATATGTGAAACCGACGACGCAAGTGAAGAAGAAGTGTCTGCTAC 1140
QY 375 His 375
Db 1141 AAC 1143

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RESULT 6

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US-09-354-231B-13
; Sequence 13, Application US/09354231B
; Patent No. 6342658
; GENERAL INFORMATION:
; APPLICANT: Shorosh, Basil S.
; APPLICANT: DeBonte, Lorin R.
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063002
; CURRENT APPLICATION NUMBER: US/09/354,231B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (1) ... (1152)
US-09-354-231B-13
Alignment Scores:
Pred. No.: 2.03e-155 Length: 1155
Score: 1318.00 Matches: 233
Percent Similarity: 77.17% Conservative: 61
Best Local Similarity: 61.15% Mismatches: 81
Query Match: 64.39% Indels: 6
DB: 4 Gaps: 4
US-10-069-772-2 (1-377) x US-09-354-231B-13 (1-1155)
QY 1 MetGlyAlaGlyArgMet-----SerAspProSerGluGlyLys-----AsnIle 16
Db 1 ATGGGTGAGGTGGAGAAATCAAGTGTCTCTCCCTCCCAAGAAAGTGAACCAACGACAC 60
QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuValAlaIle 35
Db 61 ATCAAGCGCGTACCTCGGAGACACCGCTTCACTGCGAGAACTCAAGAAAGCAATC 120
QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu 55
Db 121 CAACGCACTTTTCAACAGCTCATCCCTGCTTCTCTCTACTCATCTGAGCATC 180
QY 56 IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75
Db 181 ATCATAGCTCTGCTCTTACTACGTGCGACCACTTACTTCCCTCTCCCTCACCT 240
QY 76 LeuAlaTyrLeuAlaIleProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95
Db 241 CTCTCTTACTTCCGCTGCTCTCTACTAGGCTGCGCAAGGAGTGGCTTAAACGGCGTC 300
QY 96 TrpValIleGlyHisIleGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAsp 115
Db 301 TGGGTATAGCCCAACAGATGGCGGACCAACCTTACGACGATACACAGTGTGACGAC 360
QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrIleSer 135
Db 361 ACCGTGGTCTCATCTTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 136 HisArgAsnHisHisAlaAsnThrAsnSerLeuAspAspGluValTyrIleProlys 155
Db 421 CATGAGCCGACCAACATTCACACTGGCTCCCTCGAGAGACGAAAGTGTGTGCCCAAG 480
QY 156 ArgIysSerIysValIleTyrSerIysLeuLeuAsnAsnProGlyArgValPhe 175
Db 481 AAGAGTCAGACATCACTGAGACGCAAGTACCTCAACCAACCTTTGGAGCCGCTG 540
QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db 541 ATGTTAAGCGTTCACTCTCGGCTGGCGCTGTGCTTACCTTACGCTTCGCGGA 600
QY 196 LysIysTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214
Db 601 AGACCTTACGACGGGGCTTCGCTTCGCTTCATTCACCCCAACGCTCCATCACAACGAC 660
QY 215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIle 234
Db 661 CGCGAGCGCTTCGACATATACCTCCGACGCTGGCATCTCGCGCTGCTGACGGTCTC 720
QY 235 LysLeuLeuValAlaAlaIleGlyValAlaIleTyrValIleAsnMetTyrAlaIleProVal 254
Db 721 TTCGTTACGCCCGCCGCGAGAGTGGCTCGATGCTGCTTACGAGTCCCGCTT 780
QY 255 LeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeu 274
Db 781 CTGATGTCAATGCTTCTCGTGTGATCACTTACCTTACGACACACCATCTCCCTG 840
QY 275 ProHisTyrAspSerThrGluTyrPheAsnTyrIleGlyAlaLeuSerThrIleAspArg 294
Db 841 CCTACTACGATTCCTCGAGTGGAGTGGTGGAGGAGGAGCTTTGGTACCGTTACGAGA 900

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Qy 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314
 Db 901 GACACGGAATCTTGAACAAGGTCTTCCACAATATTACGACACGCACTGGCGCATAT 960
 Qy 315 LeuIleSerTyrlleProHisIleTyrlleHisAlaLysGluAlaArgAspAlaIleLysProVal 334
 Db 961 CTGTTCTCCACAGTCCCATATTATCAACGATGAGAACCTACCAAGCGATTAAGCCGATTA 1020
 Qy 335 LeuGlyGluTyrlleTyrlleAlaAspArgThrProIlePheLysAlaMetTyrlleArgGluAla 354
 Db 1021 CTGGAGAGATATATCACTTGTGATGGACGCGGATGTTAAAGCATGTGAGGAGGCG 1080
 Qy 355 LysGluCysIleTyrlleGluProAspGluAspSerGluHisLysGlyValPheTrpTyrlle 374
 Db 1081 AAGAAGGTATCTATGTGTAACCGGACAGGCAAGGTGAGAAAGAGTGTCTCGTAC 1140
 Qy 375 His 375
 Db 1141 AAC 1143

RESULT 7

US-09-128-602B-13
 ; Sequence 13, Application US/09128602B
 ; Patent No. 6414223
 ; GENERAL INFORMATION:
 ; APPLICANT: Kodali, Dharna
 ; APPLICANT: Fan, Zhegong
 ; APPLICANT: Debonthe, Lorin R.
 ; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
 ; FILE REFERENCE: 07148-072001
 ; CURRENT APPLICATION NUMBER: US/09/128,602B
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FastSeq For Windows Version 4.0
 ; SEQ ID NO 13
 ; LENGTH: 1155
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 ; NAME/KEY: CDS
 ; LOCATION: (1) ... (1152)
 ; US-09-128-602B-13

Alignment Scores:

Pred. No.: 2,03e-155 Length: 1155
 Score: 1318.00 Matches: 233
 Percent Similarity: 77.17% Conservative: 61
 Best Local Similarity: 61.15% Mismatches: 81
 Query Match: 64.39% Indels: 6
 Gaps: 4

US-10-069-772-2 (1-377) x US-09-128-602B-13 (1-1155)

Qy 1 MecGlyAlaGlyValArgMet-----SerAspProSerGluGlyLys-----AsnIle 16
 Db 1 ATGGGTGAGGTGAGGAGATGCAAGTGTCTCTCCCTCCCAAGAACTGGAACCGACACC 60
 Qy 17 LeuGluArgValProValAsp---ProProPheThrLysSerAspLeuLysLysLysLys 35
 Db 61 ATCAAGGCGGTACCTCGGAGACACCGCCCTTCACTGCGAGAACTCAAGAAAGCATC 120
 Qy 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrlleValValHisAspLeu 55
 Db 121 CCACCGCAGCTTTCAACAGCTCATCCCTGCTTCTCTCTCACTCATCTGGGACATC 180
 Qy 115ValAlaTyrlleValPheTyrlleLeuAlaAsnHisThrIleProLeuIleProThrPro 75
 Db 181 ATCTAAGCTCTCTGCTTCTACTAGTCCGACACCTTACCTTCCCTCTCCCTACCCCT 240
 Qy 76 LeuAlaTyrlleAlaTyrlleProValTyrllePheCysGlnAlaSerIleLeuThrGlyLeu 95
 Db 1141 AAC 1143

Db 241 CTCTCTACTTGGCGCTCTCTACTGAGCCCTGCCAAGGAGTGCCTTAACCGGCGCTC 300
 Qy 96 TrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrlleLeuIleAspAsp 115
 Db 301 TGGGTATAGCCCAAGATGCGGCGGACCAAGCCTTACAGCATACCAAGTGGCTTACAGAC 360
 Qy 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrllePheSerTyrlleSer 135
 Db 361 ACCGTGGTCTCATCTTCCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
 Qy 136 HisArgAsnHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrlleProLys 155
 Db 421 CATGAGCGCACCACTTCCACACATGCGCTCTCTGACAGACAGAGTGTGTGTCCTCCAG 480
 Qy 156 ArgLysSerLysValLysIleTyrlleSerLysLeuAsnAsnProProGlyArgValPhe 175
 Db 481 AAGAATGACATCACTAGTGTGAGGAGTACCTTCAACACCTTTGGAGCGACCGTG 540
 Qy 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrlleLeuThrAsnIleSerGly 195
 Db 541 ATGTTAAGGTTCACTTCACTCTCGGCTGCGGCTTGTACTTACCTTCAAGCTTCCGGA 600
 Qy 196 LysLysTyrlle---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214
 Db 601 AGACCTTACAGACGCGGCTTGTCCATTTCCACCCCAAGCGCTCCCATCTTACACAC 660
 Qy 215 ArgGluArgValGluValLeuLeuSerAspPheGlyLeuAlaValPheTyrlleAla 234
 Db 661 CGCAGGCTCTCCAGATATACATCTCCGACCTGACATCTTCCGCTTGTCTACGCTTC 720
 Qy 235 LysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrlleAlaProVal 254
 Db 721 TTCCGTTAAGCGCGCGGAGAGAGTGGCTCGATGGTCTGCTTACAGAGTCCGCTT 780
 Qy 255 LeuGlyValSerValPhePheValLeuIleThrTyrlleHisHisThrHisLeuSerLeu 274
 Db 781 CTGATGTCAATGGTTCCTCGTGTGATCACTTATGTCAGCACACGCAATCTTCCCTG 840
 Qy 275 ProHisTyrlleAspSerThrGluTrpAsnTrpIleLysGlyAlaLysSerThrIleAspArg 294
 Db 841 CCTACCTACGATGTCGAGATGAGATGTTGAGGAGGCTTGGCTTACCGTTGACAGA 900
 Qy 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314
 Db 901 GACACGGAATCTTGAACAAGGTCTTCCACAATATTACGACACGCACTGGCGCATAT 960
 Qy 315 LeuIleSerTyrlleProHisIleTyrlleHisAlaLysGluAlaArgAspAlaIleLysProVal 334
 Db 961 CTGTTCTCCACAGTCCCATATTATCAACGATGAGAACCTACCAAGCGATTAAGCCGATTA 1020
 Qy 335 LeuGlyGluTyrlleTyrlleAlaAspArgThrProIlePheLysAlaMetTyrlleArgGluAla 354
 Db 1021 CTGGAGAGATATATCACTTGTGATGGACGCGGATGTTAAAGCATGTGAGGAGGCG 1080
 Qy 355 LysGluCysIleTyrlleGluProAspGluAspSerGluHisLysGlyValPheTrpTyrlle 374
 Db 1081 AAGAAGGTATCTATGTGTAACCGGACAGGCAAGGTGAGAAAGAGTGTCTCGTAC 1140
 Qy 375 His 375
 Db 1141 AAC 1143

RESULT 8

US-09-995-297-13
 ; Sequence 13, Application US/09995297
 ; Patent No. 6649782
 ; GENERAL INFORMATION:
 ; APPLICANT: Kodali, Dharna
 ; APPLICANT: Fan, Zhegong
 ; APPLICANT: Debonthe, Lorin R.
 ; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
 ; FILE REFERENCE: 07148-072002


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; CURRENT APPLICATION NUMBER: US/09/995,297
; CURRENT FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
; US-09-995-297-13

Alignment Scores:
Pred. No.: 2,036-155          length: 1155
Score: 1318.00              Matches: 233
Percent Similarity: 77.17%    Conservative: 61
Best Local Similarity: 61.15%  Mismatches: 81
Query Match: 64.39%          Indels: 6
DB: 4                        Gaps: 4

US-10-069-772-2 (1-377) x US-09-995-297-13 (1-1155)

QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLys-----AsnIle 16
DB 1 ATGGGTGAGGTGGAGAAATGCAAGTGTCTCTCCCTCCAGAAAGTCTGAACCGACACC 60
QY 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAla 35
DB 61 ATCAAGCCGCTACCTGGACACACCGCCCTTCACTGTGGAGAACTCAAGAAACCAATC 120
QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyTrpValValHisAspLeu 55
DB 121 CCAACGCACTGTTTCAAGCTCCATCCCTGCTCTTCTCTACTACTATCTGGAGACATC 180
QY 56 IleValAlaTyRValPheTyTrpLeuAlaAsnThrTyRleProLeuIleProThrPro 75
DB 181 ATCATAGCCTCTGCTCTACTAGCTGGACACCACTTACTCTCTCCCTCACCTCACCCT 240
QY 76 LeuAlaTyRLeuAlaTrpProValTyTrpPheCysGlnAlaSerIleLeuThrGlyLeu 95
DB 241 CTCCTCTACTCTGCTGCTGCTCTCTTCACTGGGCTCCCAAGGGTGGCTCTTACCGGCTC 300
QY 96 TrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyRGluleuIleAspAsp 115
DB 301 TGGGTCAATAGCCCAAGTGGCGGCCAACCGCTTCAAGGACTTACCAAGTGGCTTACGAC 360
QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyRPheserTyRlyser 135
DB 361 ACCGTGGGTCACTTCCACTCTTCCCTCCCTGCTTACTTCTTCCGGAAGTACAGT 420
QY 136 HisAlaGluHisHisAlaAsnThrAsnSerLeuAspAsnAspGluValTyRleProLys 155
DB 421 CATCGACCGCCACCATTCACACACTGCTCCCTCCGAGAGAGACGAAGTGTGTGCCCAAG 480
QY 156 ArgLysSerLysValIleTyRSerLysLeuAlaAsnProProGlyArgValAlaPhe 175
DB 481 AAGAAAGTCAAGATCAAGTGGTACCGCAAGTACTTCAACACCCCTTGGAGACCGCTG 540
QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyRLeuLeuThrAsnIleSerGly 195
DB 541 ATGTTAAGCGTTCAGTTCACCTCTCGGCTGGCCGTTGTACTTACCTTCAACGCTCGGGA 600
QY 196 LysLysTyR---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAsp 214
DB 601 AAGACCTTACGAGCGGGCTTCCCTTGGCCATTTCCACCCCAAGCTCCCATCTACACACAC 660
QY 215 ArgGluArgValGluValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyRAlaIle 234
DB 661 CGCGAGCGTCTCAAGATATACATCTCCGAGCTGGGATCTCTGCGGTCTGCTACGCTCTC 720

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QY 235 LysLeuLeuValAlaAlaLysGlyAlaAlaAlaTrpValIleLeuAsnMetTyRAlaIleProVal 254
DB 721 TTCCTTACGCCCGCCGCGACGAGAGTGGCTCGATGATCTCTCTTACGAGTCCCGCTT 780
QY 255 LeuGlyValSerValPhePheValLeuIleThrTyRLeuHisHisIleThrHisLeuSerLeu 274
DB 781 CTGATTTCAATAGTCTTCTCGTGTGTATCACTTACTTCTGACAGACACACCATCTCCCTG 840
QY 275 ProHisTyRAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArg 294
DB 841 COTCACTACGATTTGCTCCGAGTGGATGTGTGAGGGAGCTTGTGCTACCGCTTACAGAGA 900
QY 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisValLeuHisHis 314
DB 901 GACTACGGAATCTTGAAACAGGTCTTCCACATATTTACGACACCGACAGTGGCCGCTAT 960
QY 315 LeuIleSerTyRleProHisIleTyRHisAlaLysGluAlaArgAspAlaIleAspProVal 334
DB 961 CTGTTCTTCAAGATGCCCATTTATTCACCGCATGGAAGCTACCAAGCCATTAAGCCGATA 1020
QY 335 LeuGlyGluTyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyR 354
DB 1021 CTGGAGAGATATTATTCAGTTGATGAGACGCGCGGTGTTAAGCGATGTGAGGAGGCG 1080
QY 355 LysGluCysIleTyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRtyRty 374
DB 1081 AAGAGTGTATCTATTTGTGAACCGGACGGAAGGTGGAAGAAAGTGTCTGTGTAC 1140
QY 375 His 375
DB 1141 AAC 1143

RESULT 9
US-09-354-231B-9
; Sequence 9, Application US/09354231B
; Patent No. 6342658
; GENERAL INFORMATION:
; APPLICANT: Debonte, Lorin R.
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063002
; CURRENT APPLICATION NUMBER: US/09/354,231B
; CURRENT FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
; US-09-354-231B-9

Alignment Scores:
Pred. No.: 2,716-155          length: 1155
Score: 1317.00              Matches: 234
Percent Similarity: 76.44%    Conservative: 58
Best Local Similarity: 61.26%  Mismatches: 82
Query Match: 64.34%          Indels: 8
DB: 4                        Gaps: 4

US-10-069-772-2 (1-377) x US-09-354-231B-9 (1-1155)

QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLysAsn 15
DB 1 ATGGGTGAGGTGGAGAAATGCAAGTGTCTCTCCCTCCAAAAGTCTGAACCGACAAAC 60
QY 16 IleLeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAla 34
DB 61 ATC---AAGCGGTACCTTGGAGACACCGCCCTTCACTGTGAGAACTCAAGAAACGA 117

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QY 35 ILeProThriHisCySpheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
 Db 118 ATCCACCGGACGCTTTTCAAGCGCTCGATCCCTCTTCTCTTCTATCATCTGAGAC 177
 QY 55 LeuIleValAlaTyValPheTyTyIleuAlaAnthTyIleProLeuIleProThr 74
 Db 178 ATCATATAGGCTCTGCTCTTCTATCATCTGAGCGACCTTCTCTCTCTCTCTCTCAC 237
 QY 75 ProLeuAlaTyIleuAlaIleProValTyTyIlePheCyGlnAlaSerIleLeuThyGly 94
 Db 238 CCTCTCTCTCTCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 297
 QY 95 LeuTyPValIleGlyHisGluCyGlyHisIleAlaPheSerAspTyGlnLeuIleAsp 114
 Db 298 GTCGGGCTCATAGCCACGAGTGGGGCCACACGCTTCAAGGACTACAGTGGGTGAC 357
 QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThyProTyPheSerTyIleTyTy 134
 Db 358 GACACCGGCTCATCT 417
 QY 135 SerHisArgAsnHisIleAlaAsnThyAsnSerLeuAspAsnGluValTyIlePro 154
 Db 418 AGTCATGACGCGCACCATTCACACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 477
 QY 155 LysArgLysSerLysValIleValIleTySerLysLeuLeuAsnAsnProGlyArgVal 174
 Db 478 AAGAAGAGTACGACATCAAGTGTACGGCAAGTACCTCAACACCTTTGGAGCGACCC 537
 QY 175 PheThrLeuValPheArgLeuThyLeuGlyPheProLeuTyTyLeuLeuThyAsnIleSer 194
 Db 538 GTGATGTTAAGGTTACGTTCACTCTCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 597
 QY 195 GlyValLysTyTy---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213
 Db 598 GGGAGACCTTACGACGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
 QY 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyAla 233
 Db 658 GACCGTAGCGCTCTCCAGATATACATCTCCGACGCTGACATCTCTGCGTCTGTAACGT 717
 QY 234 IleLysLeuLeuValAlaAlaLysGlyValAlaIleValIleAsnMetTyAlaIlePro 253
 Db 718 CTCTACCGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
 QY 254 ValLeuGlyValSerValPhePheValLeuIleThyTyTyLeuHisIleThyHisLeuSer 273
 Db 778 CTCTGATGTTCACGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 837
 QY 274 LeuProHisTyAspSerThyGluTyPheAsnTyIleLysGlyAlaLeuSerThyIleAsp 293
 Db 838 CTGCTCATATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 897
 QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThyHisIleValLeuHis 313
 Db 898 AGAGACATACGGAATCTTGAACAAGTCTTCCACAATATCACGACACGAGTGGCGAT 957
 QY 314 HisLeuIleSerTyTyIleProHisTyTyHisAlaLysGlyValAlaArgAspAlaIleLysPro 333
 Db 958 CACCTGTTCTGACCATGCGCCATATCATGCGATGAGCTACGAGGCGATTAAGCGG 1017
 QY 334 ValLeuGlyGluTyTyTyTyIleAspArgThyProIlePheLysAlaMetTyArgGlu 353
 Db 1018 ATATCGGAGAGTATATCATCTGATGCGACGGCGGGTGAAGCATATGAGGGAG 1077
 QY 354 AlaLysGluCyTyTyTyTyIleGluProAspGluAspSerGluHisLysGlyValPheTyTy 373
 Db 1078 GCGAAGAGGTATCTATATGTCGACCGGACAGGACAGGTGAGAAAGAGTGTCTCG 1137
 QY 374 TyThiS 375
 Db 1138 TACAAAC 1143

RESULT 10
 US-09-128-602B-9
 ; Sequence: 9, Application US/09128602B
 ; Patent No. 6414223
 ; GENERAL INFORMATION:
 ; APPLICANT: Kodali, Dharm
 ; APPLICANT: Fan, Zhongong
 ; APPLICANT: Debouze, Lorin R.
 ; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
 ; FILE REFERENCE: 07148-072001
 ; CURRENT FILING DATE: 1998-08-03
 ; NUMBER OF SEQ ID NOS: 68
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 9
 ; LENGTH: 1155
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)...(1152)
 US-09-128-602B-9
 Alignment Scores:
 Pred. No.: 2,71e-155 Length: 1155
 Score: 1317.00 Matches: 234
 Percent Similarity: 76.44% Conservative: 58
 Best Local Similarity: 61.26% Mismatches: 82
 Query Match: 64.34% Indels: 8
 Gaps: 4
 US-10-069-772-2 (1-377) x US-09-128-602B-9 (1-1155)
 QY 1 MetGlyAlaGlyGlyAlaGMe-----SerAspProSerGluGlyLysAsn 15
 Db 1 ATGGGTGAGGTGAGAGATGCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
 QY 16 IleuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAla 34
 Db 61 ATC---AAGCGCGTACCTCGGAGACACCGGCTTCACTGTGCGAGAACTCAAGAAAGCA 117
 QY 35 ILeProThriHisCySpheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
 Db 118 ATCCACCGGACGCTTTTCAAGCGCTCGATCCCTCTTCTCTTCTATCATCTGAGAC 177
 QY 55 LeuIleValAlaTyValPheTyTyIleuAlaAnthTyIleProLeuIleProThr 74
 Db 178 ATCATATAGGCTCTGCTCTTCTATCATCTGAGCGACCTTCTCTCTCTCTCTCTCAC 237
 QY 75 ProLeuAlaTyIleuAlaIleProValTyTyIlePheCyGlnAlaSerIleLeuThyGly 94
 Db 238 CCTCTCTCTCTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 297
 QY 95 LeuTyPValIleGlyHisGluCyGlyHisIleAlaPheSerAspTyGlnLeuIleAsp 114
 Db 298 GTCGGGCTCATAGCCACGAGTGGGGCCACACGCTTCAAGGACTACAGTGGGTGAC 357
 QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThyProTyPheSerTyIleTyTy 134
 Db 358 GACACCGGCTCATCT 417
 QY 135 SerHisArgAsnHisIleAlaAsnThyAsnSerLeuAspAsnGluValTyIlePro 154
 Db 418 AGTCATGACGCGCACCATTCACACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 477
 QY 155 LysArgLysSerLysValIleValIleTySerLysLeuLeuAsnAsnProGlyArgVal 174
 Db 478 AAGAAGAGTACGACATCAAGTGTACGGCAAGTACCTCAACACCTTTGGAGCGACCC 537
 QY 175 PheThrLeuValPheArgLeuThyLeuGlyPheProLeuTyTyLeuLeuThyAsnIleSer 194
 Db 538 GTGATGTTAAGGTTACGTTCACTCTCGGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 597

QY 195 GlyIySlyrTYR---GlyArGpheAlaAenHisPheAepProMetSerProIlePheAen 213
Db 598 GGGAGACCTTACGAGCGCGCTTCCCTTCCACATTTCCACCCCAAGCGCTCCCATCTACAC 657
QY 214 ARAAGAGUAGValGlnValLeuLeuSerAepPheGlyLeuLeuAlaValPheTYrAla 233
Db 658 GACCGTAGCGCTCTCCAGATATACATCTCCAGCGCTGCGATCTCGCGCTGCTACCGAT 717
QY 234 IleuSLeuValAlaAlaIlysglyAlaValATrPValIleAenMetTYrAlaIlePro 253
Db 718 CTCTACCGCTACGCTGCTGCTCCAGAGATTCGCTGATGCTGCTGCTTACGAGATTCCT 777
QY 254 ValLeuGlyValSerValPhePheValLeuIleThTYrLeuHisHisThHisLeuSer 273
Db 778 CTTCGATTTGTCACGCGGTTCTTAACTTTGATGATCTTACCTTCACACACGATCTTCC 837
QY 274 LeuProHisTYrAepSerThGlnTrpAenTrpIleuSGLyAlaLeuSerThIleAep 293
Db 838 CTGCTCTACATGACTCGCTGCTGATGAGGAGTTGAGGAGCTTGGCCACCGCTTAC 897
QY 294 ArgAepPheGlyPheLeuAenArgValPheHisAepValThHisThHisValIleuHis 313
Db 898 AGAGACTACGGAATCTTGAACAAGGCTTCCACATATACAGGACACGCGATGGCGAT 957
QY 314 HisLeuIleSerTYrIleProHisIlysalIySGLyAlaArgAepAlaIleuSPro 333
Db 958 CACCGTTCTGACACATGCGCGATATATCATGCGATGACGATACGACGCGATTAAGCG 1017
QY 334 ValLeuGlyGlyTYrTYrIleuSLeuAepThTrpIlePheValAenMetTYrArgIleu 353
Db 1018 ATACGGGAGATATATATCATGAGGACCGGCTGTTAAAGCGATGGAGGAG 1077
QY 354 AlaIySGLyCysIleTYrIleuSLeuAepGlyAepSerGlnHisIlySGLyValPheTrp 373
Db 1078 GCGAAGAGATGATATATGATGACCGGACGAGCAAGGAGGAGAAAGGATGTTCTCG 1137
QY 374 TYrHis 375
Db 1138 TACAC 1143

RESULT 11
US-09-995-297-9
Sequence 9, Application US/09995297
Patent No. 6649782
GENERAL INFORMATION:
APPLICANT: Kodali, Dharna
APPLICANT: Pan, Zhegong
APPLICANT: DeBonte, Lorin R.
TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
FILE REFERENCE: 07148-072002
CURRENT APPLICATION NUMBER: US/09/995,297
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: US 09/128,602
PRIOR FILING DATE: 1998-08-03
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 1155
TYPE: DNA
ORGANISM: Brassica napus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1152)
US-09-995-297-9

Alignment Scores:
Pred. No.: 2,716-155
Score: 1317.00
Percent Similarity: 76.44%
Best Local Similarity: 61.25%
Query Match: 64.34%

Length: 1155
Matches: 234
Conservative: 58
Mismatch: 82
Indels: 8

DB: 4 Gaps: 4
US-10-069-772-2 (1-377) x US-09-995-297-9 (1-1155)
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QY 16 IleuGlyValGValProValAep---ProProPheThLeuSerAepLeuIlySAla 34
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QY 35 IleProThHisCysPheGlyAepSerValIleAepSerTYrTYrValIleHisAep 54
Db 118 ATCCACCGCACGTGTTAAAGCTGATACCTCGCTCTTCTCTTCTACTTCTATCTGAGAC 177
QY 55 LeuIleValAlaTYrValPheTYrTYrLeuAlaAenThTYrIleProLeuIleProTh 74
Db 178 ATCATCATAGCTCTCTGCTTCTTACGCTGCGACACTTACTTCTCTCTCTCTCAC 237
QY 75 ProLeuAlaTYrLeuAlaTrpProValTYrTrpPheCysGlnAlaSerIleuThrGly 94
Db 238 CTTCTCTCTACTTCTGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 297
QY 95 LeuTrpValIleGlyHisGlyCysGlyHisHisAlaPheSerAepTYrGlnLeuIleAep 114
Db 298 GTCTGGGTTCATAGCCCAAGAGTGGCGCACACGCTTACAGCTTACAGTGGCTGAC 357
QY 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThProTYrPheSerTrpIlyTYr 134
Db 358 GACACCGTGGCTCTATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
QY 135 SerHisArgAenHisHisAlaAenThHisSerLeuAepAenAepGlyValTYrIlePro 154
Db 418 AGTCATCAGCCGACCACTTCCAAACACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 477
QY 155 LysArgIySerIyValIyGlyIleTYrSerIySLeuAenAenProProGlyArgVal 174
Db 478 AAGAAGAAATGACATAGTGAAGTGAAGCAAGTCAACACCTTGGAGACACC 537
QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTYrLeuLeuThHisIleSer 194
Db 538 GTGATGTTAAGCGTTCAATTCATCTCGCGCTTGTGATCTTACGCTTCAACGCTCG 597
QY 195 GlyIySlyrTYR---GlyArGpheAlaAenHisPheAepProMetSerProIlePheAen 213
Db 598 GGGAGACCTTACGAGCGCGCTTCCCTGCGATTTCCACCCACGCTCCCATCTACAC 657
QY 214 ARAAGAGUAGValGlnValLeuLeuSerAepPheGlyLeuLeuAlaValPheTYrAla 233
Db 658 GACCGTAGCGCTCTCCAGATATACATCTCCAGCGCTGCGATCTCGCGCTGCTACCGAT 717
QY 234 IleuSLeuValAlaAlaIlysglyAlaValATrPValIleAenMetTYrAlaIlePro 253
Db 718 CTCTACCGCTACGCTGCTGCTCCAGAGATTCGCTGATGCTGCTGCTTACGAGATTCCT 777
QY 254 ValLeuGlyValSerValPhePheValLeuIleThTYrLeuHisHisThHisLeuSer 273
Db 778 CTTCGATTTGTCACGCGGTTCTTAACTTTGATGATCTTACCTTCACACACGATCTTCC 837
QY 274 LeuProHisTYrAepSerThGlnTrpAenTrpIleuSGLyAlaLeuSerThIleAep 293
Db 838 CTGCTCTACATGACTCGCTGCTGATGAGGAGTTGAGGAGCTTGGCCACCGCTTAC 897
QY 294 ArgAepPheGlyPheLeuAenArgValPheHisAepValThHisThHisValIleuHis 313
Db 898 AGAGACTACGGAATCTTGAACAAGGCTTCCACATATACAGGACACGCGATGGCGAT 957
QY 314 HisLeuIleSerTYrIleProHisIlysalIySGLyAlaArgAepAlaIleuSPro 333
Db 958 CACCGTTCTGACACATGCGCGATATATCATGCGATGACGATACGACGCGATTAAGCG 1017
QY 334 ValLeuGlyGlyTYrTYrIleuSLeuAepThTrpIlePheValAenMetTYrArgIleu 353

QY	354	AlatyvgluCyIleTyrIlegluProaspGluAaspSerGluHleIyvgIyValPheTyr	373
Db	1207	GGGAGGAGCTGATATTATGTGGAACTGGACAGGCAAGCTGAGCAAGAAAGGTGTCTTGG	1267
QY	374	TyrHis 375	
Db	1267	TACAACT 1272	
RESULT 13			
US-09-354-231B-11			
; Sequence 11, Application US/09354231B			
; Patent No. 6342658			
; GENERAL INFORMATION:			
; APPLICANT: DeBonte, Lorin R.			
; APPLICANT: Shorrosh, Basil S.			
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF			
; FILE REFERENCE: 07148-063002			
; CURRENT APPLICATION NUMBER: US/09/354.231B			
; CURRENT FILING DATE: 1999-07-16			
; PRIOR APPLICATION NUMBER: US 08/874,109			
; PRIOR FILING DATE: 1997-06-12			
; NUMBER OF SEQ ID NOS: 69			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 11			
; LENGTH: 1155			
; TYPE: DNA			
; ORGANISM: Brassica napus			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (1) ... (1152)			
US-09-354-231B-11			
Alignment Scores:			
Pred. No.: 8,62e-155 Length: 1155			
Score: 1313.00 Matches: 233			
Percent Similarity: 76.44% Conservative: 59			
Best Local Similarity: 60.99% Mismatches: 82			
Query Match: 64.14% Indels: 8			
DB: 4 Gaps: 4			
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QY	1	MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyIysAsn	15
Db	1	ATGGGTGACAGGGAAGAATGCAAGATGTCCTCCCTCCAAAGATGTGAACCGACAAC	60
QY	16	IleIeuGluArgValProValAsp---ProProPheThrIleuSerAspIeuIyIysAla	34
Db	61	ATC---AAGCGGTAACCTGCGACGACCGCCCTTCAGTGTGAGAACTCAAGAAAGCA	117
QY	35	IleProThrHisCyPheGluArgSerValIleArgSerSerTyrTyrValAlaHisAsp	54
Db	118	ATCCACCGCACTGTTTCAAGAGCTGCATCCCTGCTCTTCTACTACTATCTGGAGAC	177
QY	55	IeuIleValAlaTyrValPheTyrTyrIleuAlaAsnThrTyrIleProIeuIleProThr	74
Db	178	ATCATCATAGGCTCCTCGCTTCTACTACGTCGACCACTTACTTCCCTCCCTCAC	237
QY	75	ProIeuAlaTyrIleuAlaTyrProValTyrTyrPheCyGlnAlaSerIleIeuThrGly	94
Db	238	CCTCTCTCTACTTTCGCTTCGCTCTTCACTGGGCTGCGAAGGCTGGTCTTACCGAGC	297
QY	95	IeuThrValIleGlyHisGluCyGlyHisHisAlaPheSerAspTyrGlnIeuIleAsp	114
Db	298	GCTTGAGGTGATAGCCCAAGTCGGCCCAACAGCGCTTTCAGGCACTTACCAAGTGGCTGAGC	357
QY	115	AspIleValGlyPheValIeuHisSerAlaIeuIeuThrTyrTyrPheSerTyrIyAsp	134
Db	358	GACACCGTCGCGGCTCATCTTCCATCTCCCTCCCTGTCCTTACTTCTCCGGAAGTAC	417
QY	135	SerHisArgAsnHisAlaAsnThrAsnSerIleuAspAspGluValTyrIlePro	154

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Alignment Scores:

Pred. No.: 8,62e-155 Length: 1155
 Score: 1313.00 Matches: 233
 Percent Similarity: 76.44% Conservative: 59
 Best Local Similarity: 60.99% Mismatches: 82
 Query Match: 64.14% Indels: 8
 Gaps: 4

US-10-069-772-2 (1-377) x US-09-128-602B-11 (1-1155)

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QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLysAsn 15
Db 1 ATGGGTGACAGGTGGAAGAATGCAAGTGTCTCTCCCTCCCAAAAAGTGTGAACCGACAC 60
QY 16 IleuGluValValProValAsp---ProProPheThrLeuSerAspLeuLysAla 34
Db 61 ATC---AAGCGCGTACCTCGGAGACACCGCCCTTCACTGCGGAGAACCTAAGAAAGCA 117
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
Db 118 ATCCACCGGACCTTTTCAAGCTCAATCCCTGCTTTCTCTACCTCATCTGGGAC 177
QY 55 LeuIleValAlaTyValPheTyTyTyLeuAlaAsnThyTyIleProLeuIleProThr 74
Db 178 ATCATCATAGGCTCTGCTCTTACTACGTCGACCACTTACTTCCCTCTCTCCCTCAC 237
QY 75 ProLeuAlaTyTyLeuAlaTrpProValTyTyTrpPheCysGlnAlaSerIleLeuThyGly 94
Db 238 CCTCTCTCTACTCTTGGCTGGCTCTCTACTGAGGCTGCGGCTGCGCTTAACCGGC 297
QY 95 LeuTrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyTyGlnLeuIleAsp 114
Db 298 GTCTGGGTTCATAGGCCCAATGCGGCCACACCGCTTACGACGATACCATGCGCTGAC 357
QY 115 AspIleValGlyPheValIleuHisSerAlaLeuLeuThrProTyTyPheSerTyTyTy 134
Db 358 GACACCGCTCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
QY 135 SerHisArgAsnHisHisAlaAsnThrAsnSerLeuAsnAspAsnArgValTyIlePro 154
Db 418 AGTCATGAGCGCCACATCCACATCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 477
QY 155 LysArgGlySerLysValLysIleTySerLysLeuLeuAsnAsnProProGlyArgVal 174
Db 478 AAGAAGAAAGTCAGACATCAAGTGTACGGCAAGTACCTCAACACCTTTGGAGCACC 537
QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyLeuLeuThrAsnIleSer 194
Db 538 GTGATGTTAAGCGGTTCAGTTCACTCTGCGTGGCTTGTGACTTAGCCTTCAACGTCG 597
QY 195 GlyLysLysTyTy---GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213
Db 598 GGGAGACCTTACGACGCGGCTGCTTGCATTTTCCACCCCAACGCTCCCATCTACAC 657
QY 214 AspArgGluArgValGlnValIleuLeuSerAspPheGlyLeuAlaValPheTyAla 233
Db 658 GACCGTAGCGTCTTCAGATATACATCTCCGACGCTGACCTTCCGCGTGTGCTACGCT 717
QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaIleValIleAsnMetTyTyAlaIlePro 253
Db 718 CTTCACCGCTACGCTGCTGCTCAAGAGTTCCTCGATGCTCTGCTTCAAGAGTTCCT 777
QY 254 ValLeuGlyValSerValPhePheValIleuIleThyTyTyLeuHisHisLeuSer 273
Db 778 CTTCATGTTGCAACGGGTCTTGTATTTGATCTTCACTTTCGACGACACCATCTCTCC 837
QY 274 LeuProHisTyTyAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
Db 838 CTGCTCATCTATGCTGCTCTGAGTGGATGTGAGGGGACCTTTGGCCACCGTTGAC 897
QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThyHisHisValIleuHis 313
  
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Db 898 AGAGACTACGGAATCTTGAACAAAGTCTTCCAAATATCACGGACGACGTCGGCAT 957
QY 314 HisLeuIleSerTyTyIleProHisTyTyHisAlaLysGluAlaAspAlaIleLysPro 333
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QY 334 ValLeuGlyGluTyTyTyTyLysIleAspArgThrProIlePheLysAlaMetTyTyArgGlu 353
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QY 354 AlaLysGluCysIleTyTyIleGluProAspGluAspSerGluHisLysGlyValPheThr 373
Db 1078 GCGAAGAGGTATCTATCTATGTGAACCGGACAGCAAGGTGAAGAAAGGTGTCTGG 1137
QY 374 TyHis 375
Db 1138 TACAC 1143

RESULT 15
US-09-995-297-11
: Sequence 11, Application US/0995297
: Patent No. 6649782
: GENERAL INFORMATION:
: APPLICANT: Kodali, Dharma
: APPLICANT: Fan, Zhongong
: APPLICANT: Desbonte, Lorin R.
: TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
: TITLE OF INVENTION: FATTY ACID CONTENT
: FILE REFERENCE: 07148-072002
: CURRENT FILING DATE: US/09/995,297
: PRIOR APPLICATION NUMBER: 2001-11-27
: PRIOR FILING DATE: 1998-08-03
: NUMBER OF SEQ. ID NOS: 68
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11
: LENGTH: 1155
: TYPE: DNA
: ORGANISM: Brassica napus
: FEATURES:
: NAME/KEY: CDS
: LOCATION: (1)...(1152)
US-09-995-297-11

Alignment Scores:
Pred. No.: 8,62e-155 Length: 1155
Score: 1313.00 Matches: 233
Percent Similarity: 76.44% Conservative: 59
Best Local Similarity: 60.99% Mismatches: 82
Query Match: 64.14% Indels: 8
Gaps: 4

US-10-069-772-2 (1-377) x US-09-995-297-11 (1-1155)

QY 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLysAsn 15
Db 1 ATGGGTGACAGGTGGAAGAATGCAAGTGTCTCTCCCTCCCAAAAAGTGTGAACCGACAC 60
QY 16 IleuGluValValProValAsp---ProProPheThrLeuSerAspLeuLysAla 34
Db 61 ATC---AAGCGCGTACCTCGGAGACACCGCCCTTCACTGCGGAGAACCTAAGAAAGCA 117
QY 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyValValHisAsp 54
Db 118 ATCCACCGGACCTTTTCAAGCTCAATCCCTGCTTTCTCTACCTCATCTGGGAC 177
QY 55 LeuIleValAlaTyValPheTyTyTyLeuAlaAsnThyTyIleProLeuIleProThr 74
Db 178 ATCATCATAGGCTCTGCTCTTACTACGTCGACCACTTACTTCCCTCTCTCCCTCAC 237
QY 75 ProLeuAlaTyTyLeuAlaTrpProValTyTyTrpPheCysGlnAlaSerIleLeuThyGly 94
Db 238 CCTCTCTCTACTCTTGGCTGGCTCTCTACTGAGGCTGCGGCTGCGCTTAACCGGC 297
  
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QY 95 LeuTrpValIleGlyHisGluCysGlyHisHisIleAlaPheSerAspTyrGlnLeuIleAsp 114
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Db 418 AGTCATGACGCGCACCATTCACACACTGGCTCCCTCGAGAGACGAGAGTGTTCCTCC 477
QY 155 LysArgLysSerLysValLysIleTyrSerLysLeuLeuAsnAsnProProGlyArgVal 174
Db 478 AAGAAGAGTCAAGATCAAGTACGCGCAAGTACCTCAACACCTTGGGACGCAAC 537
QY 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSer 194
Db 538 GTGATGTTAACGGTTCAGTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 597
QY 195 GlyLysLysTyr--GlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsn 213
Db 598 GGGAGACCTTACGAGCGGGGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 657
QY 214 AspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAla 233
Db 658 GACCGTGAAGCGCTCAGATATACATCTCCGACGCTGCGATCTCCGCTGCTGCTGCTG 717
QY 234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIlePro 253
Db 718 CTCTACCGCTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 777
QY 254 ValLeuGlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSer 273
Db 778 CTCTGATTTGTCACGCGGCTTCTAGTTGATCACTTACTTACAGACACGCTGCTGCTG 837
QY 274 LeuProHisTyrAspSerThrGluTyrAsnThrIleLysGlyAlaLeuSerThrIleAsp 293
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QY 294 ArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHis 313
Db 898 AAGAGCTACGGATCTTGAACAAGGCTTCCACAATATCACGACACGACGCTGCGCAT 957
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Db 958 CACCGTTCCTGACGATGCGCATTATCATGCGATGGAAGCTACGAGCGGATTAAGCG 1017
QY 334 ValLeuGlyGluTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGlu 353
Db 1018 ATACTGGGAGATATATCATAGTTCAGTGGAGCGCGGTGTTAAGCGATGCGAGGAG 1077
QY 354 AlaLysGluCysIleTyrIleGluProAspArgLysAspSerGluHisLysGlyValPheTyr 373
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QY 374 TyrHis 375
Db 1138 TACAAC 1143

Search completed: June 23, 2004, 17:34:48
Job time : 93 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 16:53:33 ; Search time 402 Seconds
(without alignments)
4296.196 Million cell updates/sec

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Perfect score: 2047
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Searched: 3017426 seqs, 229054650 residues
Total number of hits satisfying chosen parameters: 6034852

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1716.5	83.9	1199	9	US-09-981-124-19	Sequence 19, Appl
2	1592.5	77.8	1309	9	US-09-981-124-3	Sequence 3, Appl
3	1589.5	77.7	1358	9	US-09-981-124-1	Sequence 1, Appl
4	1356.5	66.3	1586	13	US-10-425-114-14778	Sequence 14778, A
5	1356.5	66.3	2931	13	US-10-424-599-123945	Sequence 123945, A
6	1356.5	66.3	6220	15	US-10-465-800-3	Sequence 3, Appl
7	1356.5	66.3	6220	15	US-10-176-149-3	Sequence 3, Appl
8	1346.5	65.8	1457	13	US-10-425-114-12782	Sequence 12782, A
9	1332.5	65.1	1422	9	US-09-837-751-5	Sequence 5, Appl
10	1323.5	64.7	1411	9	US-09-852-399-3	Sequence 3, Appl
11	1318	64.4	1155	9	US-09-995-287-13	Sequence 13, Appl
12	1318	64.4	1155	10	US-09-771-904-13	Sequence 13, Appl
13	1318	64.4	1155	17	US-10-715-100-13	Sequence 13, Appl
14	1317	64.3	1155	9	US-09-995-297-9	Sequence 9, Appl
15	1317	64.3	1155	10	US-09-771-904-9	Sequence 9, Appl
16	1317	64.3	1155	17	US-10-715-100-9	Sequence 9, Appl
17	1315	64.2	1156	16	US-10-330-775-3	Sequence 3, Appl
18	1313	64.1	1155	9	US-09-995-287-11	Sequence 11, Appl
19	1313	64.1	1155	10	US-09-771-904-11	Sequence 11, Appl
20	1313	64.1	1155	16	US-10-330-775-5	Sequence 5, Appl
21	1313	64.1	1155	17	US-10-715-100-11	Sequence 11, Appl
22	1312	64.1	1155	9	US-09-995-287-5	Sequence 5, Appl
23	1312	64.1	1155	10	US-09-771-904-5	Sequence 5, Appl
24	1312	64.1	1155	16	US-10-435-521-5	Sequence 5, Appl
25	1312	64.1	1155	17	US-10-715-100-5	Sequence 9, Appl
26	1311	64.0	1155	9	US-09-995-297-15	Sequence 15, Appl
27	1311	64.0	1155	10	US-09-771-904-15	Sequence 15, Appl
28	1311	64.0	1155	17	US-10-715-100-15	Sequence 15, Appl
29	1310	64.0	1155	9	US-09-995-287-17	Sequence 17, Appl
30	1310	64.0	1155	10	US-09-771-904-17	Sequence 17, Appl
31	1310	64.0	1155	17	US-10-715-100-17	Sequence 17, Appl
32	1308	63.9	1155	16	US-10-435-521-3	Sequence 3, Appl
33	1305	63.8	1155	9	US-09-995-297-7	Sequence 7, Appl
34	1305	63.8	1155	10	US-09-771-904-7	Sequence 7, Appl
35	1305	63.8	1155	17	US-10-715-100-7	Sequence 7, Appl
36	1299	63.5	1155	9	US-09-995-297-1	Sequence 1, Appl
37	1299	63.5	1155	10	US-09-771-904-1	Sequence 1, Appl
38	1299	63.5	1155	16	US-10-435-521-1	Sequence 1, Appl
39	1299	63.5	1155	17	US-10-715-100-1	Sequence 1, Appl
40	1296.5	63.3	1411	9	US-09-837-751-3	Sequence 3, Appl
41	1295	63.3	1155	9	US-09-995-297-3	Sequence 3, Appl
42	1295	63.3	1155	10	US-10-715-100-3	Sequence 3, Appl
43	1295	63.3	1155	17	US-10-715-100-3	Sequence 3, Appl
44	1283.5	62.7	1724	13	US-10-425-114-25066	Sequence 25066, A
45	1283.5	62.7	1729	13	US-10-425-114-21414	Sequence 21414, A

ALIGNMENTS

RESULT 1
US-09-981-124-19
; Sequence 19, Application US/09981124
; Patent No. US20020166144A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lemman, Maric
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
; FILE REFERENCE: 26-98A
; CURRENT APPLICATION NUMBER: US/09/981, 124
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/043706
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: AU P06223
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 60/050403


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340 LysIleAspArgThrProIlePheIleValMetTyrArgIleValMetGluCysIleTyr 359
1037 ATGATCGATGATGAGCTCCATTTTAAAGCATGTGAGAGAGGCGGAGATGATGATAC 1096
360 IlegIuProAspGluAspSerGluHisIleGlyValPheTyrHisIleMet 377
1097 ATCGAGCCT-----GATAGCAAGCTCAAGGTTGTTATGTTGATCAATAATTG 1144

RESULT 3
US-09-981-124-1
; Sequence 1, Application US/09981124
; Patent No. US20020166144A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Lemman, Maric
; APPLICANT: Styenne, Sten
; TITLE OF INVENTION: FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN MOD
; TITLE OF INVENTION: FATTY ACID METABOLISM
; FILE REFERENCE: 26-98A
; CURRENT APPLICATION NUMBER: US/09/981,124
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: US 09/059769
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/043706
; PRIOR FILING DATE: 1997-04-16
; PRIOR APPLICATION NUMBER: AU P06223
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: AU P06226
; PRIOR FILING DATE: 1997-04-15
; PRIOR APPLICATION NUMBER: US 60/050403
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1358
; TYPE: DNA
; ORGANISM: Crepis palaestina
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (30)..(1151)
; OTHER INFORMATION:
US-09-981-124-1

Alignment Scores:
Pred. No.: 1,65e-181 Length: 1358
Score: 1589.50 Matches: 285
Percent Similarity: 85.98% Conservative: 40
Best Local Similarity: 75.40% Mismatches: 48
Query Match: 77.65% Indels: 5
DB: 9 Gaps: 3

US-10-069-772-2 (1-377) x US-09-981-124-1 (1-1358)
QY 1 MetGlyAlaGlyValArgMetSerAspProSerGluGlyIleAsnIleLeuGluArgVal 20
DB 30 ATGGATGCGCGGCGTCT-----GGTCGACATCGGAAAAATGCGTATGAGAACTGTC 83
QY 21 ProValAspPro---ProPheThrIleuSerAspLeuValysAlaIleProThrHisCys 39
DB 84 TCAGTTGATCCAGTAACCTTCTCAGTGAATGGAAGCAAGCAATCCCTCCCATTTGC 143
QY 40 PheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeuIleValAlaTyr 59
DB 144 TTCGAGAGATCGTATACCGCTCATCTTACTATGTTGTTCAAGATCTCATTAATGGCTAC 203
QY 60 ValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrProLeuAlaTyrIleu 79
DB 204 ATCTTCTACTTCTCTGCGCAACATATATCCCTACTCTTCTACTAGCTAGCTTACTTA 263
QY 80 AlaTrpProValTyrTrpPheCysGlnAlaSerIleLeuThrGlyLeuTrpValIleGly 99
DB 264 GCTTGGCCGTTTACTCGGTTTCTGTCAAGCTAGGCTCTCACTGCTTATGATGATCCTGCG 323

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QY 100 HisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAspIleValGlyPhe 119
DB 324 CACGAAATGGTGCACCATGCTTTAGCAACTACATGATGTTGACGACATGTTGGGCTTC 383
QY 120 ValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrPheSerHisArgAsnHis 139
DB 384 ATCTCCCACTATTTCTCTCTCACTCCCGATTTCTTGGAATTCAGTCCCGGATATAC 443
QY 140 HisAlaAsnThrAsnSerLeuAspAsnAspGluValTyrIleProTyrArgLysSerLys 159
DB 444 CATTCACACACAGTTCATGATGATACATGATGATGATGATGATGATGATGATGATGAT 503
QY 160 ValLysIleTyrSerLysLeuLeuAsnAsnProTyrArgValPheThrLeuValPhe 179
DB 504 CTCGGCGCTATCTAATCACTTCTTACACACCACTGGCTGGCTGGCTGGCTGGCTGGCT 563
QY 180 ArgLeuThrLeuGlyPheProLeuTyrIleLeuThrAsnIleSerGlyLysLeuTyrGly 199
DB 564 ATGTTACACCTTACGATTTCTTTATACCTTTGACAAATATTTCCGGCAGAAATACGAC 623
QY 200 ArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGluArgValGln 219
DB 624 AGCTTGGCAACCACTTGCACCCCATGATCCAAATTTCAAAAGACGTGAGCGGTTTCAG 683
QY 220 ValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAla 239
DB 684 GCTTCCTTTGGGATCTTGCTCTTCTGCGGTTTATGGAATTAAGATTGCTGTACACA 743
QY 240 AlaLysGlyAlaIleTyrValIleAsnMetTyrAlaIleProValLeuGlyValSerVal 259
DB 744 AATAAGAGAGCTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 803
QY 260 PhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeuProHisTyrAspSer 279
DB 804 TTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863
QY 280 ThrGluTyrAsnTyrIleLysGlyAlaLeuSerThrIleAspArgAspPheGlyPheLeu 299
DB 864 ACTGAATGGAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 923
QY 300 AsnArgValPheHisAspValThrHisThrHisValLeuHisHisLeuIleSerTyrIle 319
DB 924 AATAGTGTGTTTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 983
QY 320 ProHisTyrHisAlaLysGlyAlaArgAspAlaIleLysProValLeuGlyValTyrTyr 339
DB 984 CCACATTCATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1043
QY 340 LysIleAspArgThrProIlePheLysAlaMetTyrArgGluAlaLysGluCysIleTyr 359
DB 1044 ATGATCGACAGGACTCCATTTTAAAGCAATGTAAGAGGAGGAGGAGGAGGAGGAGGAG 1103
QY 360 IleGluProAspGluAspSerGluHisLysGlyValPheTyrTyrHisLysMet 377
DB 1104 ATCGAGCT-----GATAGCAAGCTCAAGGTGTTTATGTTGATCATTAATG 1151

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RESULT 4

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US-10-425-114-14778
; Sequence 14778, Application US/10425114.
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28

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; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 14778
; LENGTH: 1586
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3028-001-B9_FLI
US-10-425-114-14778

Alignment Scores:
Pred. No.: 3,24e-153 Length: 1586
Score: 1356.50 Matches: 237
Percent Similarity: 78.42% Conservative: 61
Best Local Similarity: 62.37% Mismatches: 77
Query Match: 66.27% Indels: 5
DB: 13 Gaps: 2

US-10-069-772-2 (1-377) x US-10-425-114-14778 (1-1586)
QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLys-----AsnIle 16
DB 74 ATGGGGGGGGGGTGGCGGAATGATGTTCTCTGCCACAGAGATCAGAGTTGACCT 133
QY 17 LeuGluArgValProValAsp---ProPheThrLeuSerAspLeuLysValAlaIle 35
DB 134 TTGAAGCGGGTCCATTTGAAAACTTCATTTAGTCTCAGCCAAATCAAGAGGTCAIT 193
QY 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValValHisAspLeu 55
DB 194 CCACCTACCTGTTTCCAGCGTTCTGTTTCCGCTCATCTCTCATGTTGTTTACGACCTC 253
QY 56 IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75
DB 254 ACCATAGGCTCTGCGCTATATGTTATGTTCCACCATTCATTCACCTCTCCAGCCCT 313
QY 76 LeuAlaTyrLeuAlaIleTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95
DB 314 CTCTCTTCTTGGGATGCGCAATCTACCTGCGCTGCGCAAGGTTGATCTTACGAGATT 373
QY 96 TrpValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyrGlnLeuIleAspAsp 115
DB 374 TGGGTCATGGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 433
QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrPheSerTyrLysTyrSer 135
DB 434 ATTGTGGCTTGTGCTCTCCATCCGCTGCTCTAGTCCATCTTTTCAATGAAATACAGC 493
QY 136 HisArgAsnHisHisAlaAsnThrAsnSerLeuAsnAspGluValTyrIleProLys 155
DB 494 CATGCGCGTCACTCCAACTGCTGCTCTTGAAGCGGAGTGAAGTATGTTGCAAG 553
QY 156 ArgLysSerLysValLysIleTyrSerLysLeuAsnAsnProProGlyArgValPhe 175
DB 554 CAGAAATCTGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 613
QY 176 ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrIleLeuThrAsnIleSerGly 195
DB 614 ACTCTGTGTCACCTCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 673
QY 196 LysLysTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
DB 674 AGGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 733
QY 216 GluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLys 235
DB 734 GATGATCTCAAAATATATATATATATATATATATATATATATATATATATATATATAT 793
QY 236 LeuLeuValAlaAlaLysGlyAlaAlaIleTyrValIleAsnMetTyrAlaIleProValLeu 255
DB 794 CGCTTGGCAGGCAAAAGCACTTGGCGGAGTGTGTTTATGAGTTCCATGCTGA 853
QY 256 GlyValSerValPhePheValLeuIleThrTyrLeuHisHisThrHisLeuSerLeuPro 275

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Db	1413	CTCTCTTCTTGGGATGGCCAACTCTACAGGCGTGTCCAAAGTTGATCTTACAGAACTT	1414
Qy	96	TTTValIIeGIYhiIsGLuCYsGLIYhiIsaIaIaPheSerIarPYrGLInLeuIIeAsp	115
Db	1413	TGGGTATATGGCCAAAGATGTGGCCACCATTCATTCAGTACTCCAAATCTTGATAT	135
Qy	116	IIeValGIyPheValLeuIIeSerIaIeLeuThrPProIYrPheSerTriIySTyrSer	135
Db	1353	ATGTGTGGCCCTGTCTCTCCACTCGGAGTCTCTTACGCCATCTTTTACATGAAATACAGC	129
Qy	136	HIaTgAenIIshIsaIaenThraSerIeuaSphaenAaPGLIValTYrIIeProIys	155
Db	1293	CATGGCCGTCACTCCAAACACATCGTTCTCTTACGCCAAATGAAATTTGTGCCAAAG	123
Qy	156	ArGIySerIySValIySIIeTYrSerIySLeuIeuaenAaProIcGIYArGIyA	175
Db	1233	CAGAAAGTCTGTATCAAGTGTACTCTTAATATACCTTAACATCTCCAGGACAGATCTC	117
Qy	176	ThIeUaIaPheAaGLeUThLeuGLIyPheProLeuTYrLeuLeuThraIIeSerIy	195
Db	1173	ACTCTGTGTACACCTCTACCTTGATGGCCCTGTGACTTGGCTTAAGATTTCTGAA	114

[illegible]

1473 CTCCTCTTCTTGGCATGGCCAACTTACTGAGGCTGTCCAAAGTTGCATCTTAAGCAAGT 1414

QY .96 TTPVALLIGLVIHSGLVCGSLVIHSHIALPHESERAPTYRGINLEUILEAPAP 115

Db 1413 TGGGTTCATATGCCCATGATGTGGCCACCATTCAATTCAGTGACTTCCAGTTCTTGATAT 135

QY 116 ILEVALGIPHEVALLEUHSERIALDEULEUHPROTPRPHESERTPLYSERTSER 135

Db 1353 ATGTGTGGCTGTGCTTCCTCACTCGAGTCTCTTAAGTCCCATATCTTTTCAAGAAATACAGC 129

QY 136 HISARGANSHISIALAENTHASNSESERLEUASBPANBPGLVATYRIEPROLYS 155

Db 1293 CATGCCGCTACCACTCCACACTCGTTCTCTTGAGCGGATGAAAGTATTTGTGCCAAG 123

QY 156 ARGLYSERLYSVALYSLIETYSERLYSLEUENANBPPOPGIYARGVALPHE 175

Db 1233 CAGAAGTCTCTTATCAAGTGTACTCTTAAATACCTTAACATCTCCAGCAGAGTCTTC 117

QY 176 THRLEUVALPHEAAGLEUTHLEUGLYPHERPROLEUPTYLEULEUTHASNLISERTLY 195

Db 1173 ACTCTGTGCTGCACCCCTCACCTTGGTGGCTGTGACTTGCTTAAAGTTTCTGCA 1114

QY 196 LYSLSYTYRGLYATGPHEALIASHISAPHEAPROMETSERPROILEPHEASBPARG 215

Db 1113 AGGCTTATGATAGATTGCTTGCTGCCATATACCAATGTGCTCCATTACTGTATGCT 105

QY 216 GLUARGVALGINVALLEULEUSERAPBPHEGLYLEULEUALAVAI PHETYRALALIELYS 235

Db 1053 GAAGCACTTCAAAATATATATATGATGATGACAGATGCAAGNACTTGCAATGAGCTTTC 994

QY 236 LEULEUVALIAIALYVGLYVALAATRPVALLIEAENMETYRALALIEPROVALLEU 255

Db 993 CGCTTTCGCATGCGAAAGAGACTTGCTCGGTGGTGTGTGTATGAGAGTTCCATTTGCTA 934

QY 256 GLYVALSERVALPHEPHEVALLEUILETHRTYRLEUHSISHTPRHISLEUSERLEUPRO 275

Db 933 GTGCTTCAAGGATTTTGTGTATATATTCATTCTTGCGACATCTCACTCCGCTGATGCCA 874

QY 276 HISYTPASPERTHRTGUTPRASNTPLIELYSGLYALALEUSERTHRIEAPARGAP 295

Db 873 CATTAACCTTCTCGATGGAGTGGTGTGAGAGAGCTTTAGCAACAGTGGATGAGAT 814

QY 296 PHEGLYPHELEUANAARGVALPHEHISAPRYALHTRHISTPRHISVALLEUHSISLEU 315

Db 813 TATGAAATCCCGAACAAGGCTTCCAAATATTTACAGACACTCATGTGACATCACTTG 754

QY 316 ILESERTYRIEPROHSIYTHISALYLSGLIUALARGAERAPALIELYSPROVALLEU 335

Db 753 TTCTTCACAACTCCATTCATTAACGAAATGAGGCTTACAAAGCAATTAACCCATTTTG 694

QY 336 GLYGLUTYTYRLYSILEASBPARGTHRTPROILEPHELYSALAMETTYRARGIUALYLS 355

Db 693 CGAAGATATATCGTTGATGAGACTCCATTTTGCAAGGCAAGTGTGAGAGAGCAAGA 634

QY 356 GLUCYALILEYRIEGLUPROASBPGLUASBPGRGLUHSISLYSGLYVALPHESTPTYRHIS 375

Db 633 GAGGTATATTATGTGAGCCAGATCAAAATGACGAGCAAGAGGTGATTTTGTATCAAC 574

RESULT 6

US-10-465-800-3

/ Sequence 3, Application US/10465800

/ Publication No. US20040029283A1

/ GENERAL INFORMATION:

/ APPLICANT: Eli Lilly, JoAnne

/ TITLE OF INVENTION: Intron Double Stranded RNA Constructs and Uses Thereof

/ FILE REFERENCE: 16517.266

/ CURRENT APPLICATION NUMBER: US/10/465, 800

/ CURRENT FILING DATE: 2003-06-20

/ PRIOR APPLICATION NUMBER: US 60/390,186

/ PRIOR FILING DATE: 2002-06-21

/ NUMBER OF SEQ ID NOS: 55

/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 3


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Qy      96  TrpValIleGlyHisGluCysGlyHisIleAspSerAspTyrGlnLeuIleAspAsp 115
Db      5034 TGGGTCAATTGGCCATGAGTGTGGCCACCATTCATTCAGTACCTACAGTCTTGATGAT 5093
Qy      116  IleValGlyPheValIleuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer 135
Db      5094 ATTGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 5153
Qy      136  HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgIleValTyrIleProLys 155
Db      5154 CATGGCTGCTACCATCCACATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 5213
Qy      156  ArgLysSerLysValLysIleTyrSerLysLeuLeuAsnProProGlyArgValPhe 175
Db      5214 CAGAAAGCTCTGTACAGTGTACCTTAATACCTTAATACCTTAATACCTTAATACCTTAAT 5273
Qy      176  ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db      5274 ACTGTCTGTCTACCCCTCACCTTGGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 5333
Qy      196  LysLeuTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
Db      5334 AGGCTTATGATATATATATATATATATATATATATATATATATATATATATATATAT 5393
Qy      216  GluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLys 235
Db      5394 GAACGACTTCAAAATATATATATATATATATATATATATATATATATATATATATATAT 5453
Qy      236  LeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValIle 255
Db      5454 CGCTTGTCCATGAGCAAAAGAGCTTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 5513
Qy      256  GlyAlaSerValPhePheValLeuIleThrTyrLeuHisIleSerHisLeuSerLeuPro 275
Db      5514 GTGGTCAATGAGATTTGGTGTGTATATATATATATATATATATATATATATATATAT 5573
Qy      276  HisTyrAspSerThrGlnTyrAsnTyrIleLysGlyAlaLeuSerThrIleAspArgAsp 295
Db      5574 CATACACTTCTCTGAGTGGAGCTGTGTGAGAGAGCTTTAGCAACAGTGTATGAGAT 5633
Qy      296  PheGlyPheLeuAsnArgValPheHisAspValThrHisIleValIleHisIleLeu 315
Db      5634 TATGAGATCTCGAACAAGCTTCTCATATATATATATATATATATATATATATATATAT 5693
Qy      316  IleSerTyrIleProHisIleAlaLysGlnAlaAspAlaIleLysProValIleu 335
Db      5694 TTCTCCCAATGACCATATATATATATATATATATATATATATATATATATATATAT 5753
Qy      336  GlyLysTyrTyrLysIleAspArgThrProIlePheLysAlaMetTyrArgGlyAlaLys 355
Db      5754 GGAAGATATATCGCTTGTATGAGATCTATTTGTCAAGGCAATGTGTGAGAGAGCAAGA 5813
Qy      356  GluCysIleTyrIleGlnProAspGlnAspSerGlnHisLysGlyValPheTyrThrHis 375
Db      5814 GAGGTATTTATGTGAGAGCAAGATCAAGTACCGAGACAAAGGTATTTGTGTACAC 5873

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RESULT 8

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US-10-425-114-12782
; Sequence 12782, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128

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; SEQ ID NO 12782
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701211444_F11
US-10-425-114-12782

Alignment Scores:
Pred. No.: 4,58e-152 Length: 1457
Score: 1346.50 Matches: 236
Percent Similarity: 78.16% Conservative: 61
Best Local Similarity: 62.11% Mismatches: 78
Query Match: 65.78% Indels: 5
DB: 13 Gaps: 2

US-10-069-772-2 (1-377) x US-10-425-114-12782 (1-1457)
Qy      1  MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLys-----AsnIle 16
Db      30  ATGGGGGGGGGTGGCCGAACGATGCTTCTCCCAACAGAGTCAAGAGTTGACCT 89
Qy      17  LeuGluArgValProValAsp--ProProPheThrLeuSerAspLeuLysAlaIle 35
Db      90  TTGAAGCGGGGTGCCATTTGAAACCTCCATTTAGTCTCAAGCCAAATCAAGAGTCAAT 149
Qy      36  ProThrHisCysPheGluArgSerValIleArgSerSerTyrTyrValAlaHisAspLeu 55
Db      150  CCACCTCACTGTTCACAGCGTTCTGTTTCCGCTCATTTCTCTAAGTGTGTAGACCTC 209
Qy      56  IleValAlaTyrValPheTyrTyrLeuAlaAsnThrTyrIleProLeuIleProThrPro 75
Db      210  ACGATAGCTTCTGCTCTATATATATATATATATATATATATATATATATATATATATAT 269
Qy      76  LeuAlaTyrLeuAlaTyrProValTyrTyrPheCysGlnAlaSerIleLeuThrGlyLeu 95
Db      270  CTCTCTTCTTGGCATGGATGCCATCTAGTGGCTGTCCAGAGTGTGCATCTTACCTGAGTT 329
Qy      96  TrpValIleGlyHisGluCysGlyHisIleAspSerAspTyrGlnLeuIleAspAsp 115
Db      330  TGGGTCAATTGGCCATGAGTGTGGCCACATGATGATGATGATGATGATGATGATGATGAT 389
Qy      116  IleValGlyPheValIleuHisSerAlaLeuLeuThrProTyrPheSerTrpLysTyrSer 135
Db      390  ATTGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 449
Qy      136  HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgIleValTyrIleProLys 155
Db      450  CATGGCTGCTACCATCCACATCCATCCATCCATCCATCCATCCATCCATCCATCCATCC 509
Qy      156  ArgLysSerLysValLysIleTyrSerLysLeuLeuAsnProProGlyArgValPhe 175
Db      510  CAGAAAGCTCTGTATCAAGTGTACTTAATAACCTTAACATCTTCCAGGAGAGTCTTC 569
Qy      176  ThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGly 195
Db      570  ACTGTCTGTCTACCCCTCACCTTGGTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGG 629
Qy      196  LysLeuTyrGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
Db      630  AGGCTTATGATATATATATATATATATATATATATATATATATATATATATATATAT 689
Qy      216  GluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLys 235
Db      690  GAACGACTTCAAAATATATATATATATATATATATATATATATATATATATATATATAT 749
Qy      236  LeuLeuValAlaAlaLysGlyAlaAlaTyrValIleAsnMetTyrAlaIleProValIle 255
Db      750  CGTCTTGCATGAGCAAAAGAGCTTGGTGGTGTGTGTATATATATATATATATATATATAT 809
Qy      256  GlyAlaSerValPhePheValLeuIleThrTyrLeuHisIleSerHisLeuSerLeuPro 275
Db      810  GTGGTCAATGATTTTGTGTATATATATATATATATATATATATATATATATATATATAT 869

```


QY 276 HistyrApsSerThrGluTrpAsnTrpIleuysGlyAlaLeuSerThrIleAspArgAsp 295
Db 870 CATTAACATCTCTGAGTGGGAGCTGTGAGAGAGAGCTTTAGCAACAGTGAATGAGAT 929
QY 296 PheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHisIleu 315
Db 930 TATGGAATCTGAACAGCTCTCCATATATTTACAGACACTGATGACCATCTTG 989
QY 316 IleSerTrpIleProHisTrpHisIleAlaLysGluAlaArgAspAlaIleAspValLeu 335
Db 990 TTCTCCAAATGCCCAATATATATGATGAGCTTACAAAGGCAATAAACCATTTTG 1049
QY 336 GlyGluTrpTrpLysIleAspArgThrProIlePheValIleMetTrpArgGluAlaLys 355
Db 1050 GGAGAGTATATCCGCTTGTGATGAGACTCATTTGTCAAGGCAATGTGAGAGAGCAAGA 1109
QY 356 GluCysIleTrpIleGluProAspGluAspSerGluHisLysGlyValPheTrpTrpHis 375
Db 1110 GAGGTATTTATGTGAGCCAGATCAAGTACCGAGCAAGAGTGTATTTGTGATACAC 1169

RESULT 9
US-09-837-751-5
; Sequence 5, Application US/09837751
; Patent No. US2002010412A1
; GENERAL INFORMATION:
; APPLICANT: Green, Allan
; APPLICANT: Singh, Surinder
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: Method of Modifying the Content of Cottonseed Oil
; FILE REFERENCE: 45-00
; CURRENT APPLICATION NUMBER: US/09/837,751
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: US 60/198,124
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1422
; TYPE: DNA
; ORGANISM: *Gossypium* sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (98)..(1246)
; US-09-837-751-5

Alignment Scores:
Pred. No.: 2,176-150 Length: 1422
Score: 1332.50 Matches: 230
Percent Similarity: 79.16% Conservative: 70
Best Local Similarity: 60.69% Mismatches: 74
Query Match: 65.10% Indels: 5
Gaps: 2

US-10-069-772-2 (1-377) x US-09-837-751-5 (1-1422)

QY 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLys-----AsnIle 16
Db 98 ATGGGTGCTGAGGAGGAGATGTGCTTCCAAAGTCCAAAACCCGAATTGCAATCA 157
QY 17 LeuGluArgValProValAsp---ProProPheTrpLeuSerAspLeuLysValIle 35
Db 158 CTGAAGCGAGTTCCTACTCAAGCCACCTTCACTGTGAGTGAAGTCAAGAAACCCATC 217
QY 36 ProThrHisCysPheGluAspSerValIleArgSerSerTrpTrpValValHisAspLeu 55
Db 218 CCACCACTGTTTCCAGGCTCCGCTTTTACGCTCATTTCTCATCTCTTACACATTT 277
QY 56 IleValAlaTrpValPheTrpTrpLeuAlaAsnTrpTrpIleProLeuIleProThrPro 75
Db 278 ATATTGGGCTCTCTTTTACATGATGAGGACCAATTAATCTCTTACACTTCTCAGGCT 337
QY 76 LeuAlaTrpLeuAlaTrpProValTrpTrpPheCysGlnAlaSerIleLeuThrLysLeu 95

Db 338 CTCTCCAACTGGCTGGCTCTTTATTTGGCCATGCAAGGTGATTTTACCGGCTT 397
QY 96 TrpValIleGlyHisGluCysGlyHisIleAlaPheSerAspTrpGluLeuIleAspAsp 115
Db 398 TGGGTATAGCCCATATGATGAGGCAACATGCTCTTCAAGTATATCAATGAGCTTGACAGC 457
QY 116 IleValGlyPheValLeuHisSerAlaLeuLeuThrProTrpPheSerTrpLysSer 135
Db 458 ACCGTGGCTTATCTTCCACTCTCTCTTCAATATTTCTTGTGAATAATATAGC 517
QY 136 HisArgAsnHisIleAlaAsnThrAsnSerLeuAspAsnArgValTrpIleProLys 155
Db 518 CACCGGCTCAACATTTCTTACACCGGTTCCCTCCAAAGGATGAAGTCTTGCCAG 577
QY 156 ArgLysSerLysValLysIleTrpSerLysLeuLeuAsnAsnProProGlyArgValPhe 175
Db 578 AAAAATCTGGTTTAAATGATGGGCGCAACATTCACCAATCCACCGGCTGGTTCTG 637
QY 176 ThrLeuValPheValGluThrLeuGlyPheProLeuTrpLeuLeuThrAsnIleSerGly 195
Db 638 TCAATCAACCATTCACATTAACCTTGTGGCGGCTTTAATTAGCTTCAACGTTGCCGGC 697
QY 196 LysLysTrpGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArg 215
Db 698 CGGCTTACGACAGGCTTGTGCTGCATATACCTTACCGGCCCATTTTCCGACCGG 757
QY 216 GluArgValGluValLeuLeuSerAspPheGlyLeuLeuAlaValPheTrpAlaIleLys 235
Db 758 GAAAGACTCCAAATCTAATATCTGAGCGCGGCTGCTGCTGCTATGCGCTTAC 817
QY 236 LeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTrpAlaIleProValLeu 255
Db 818 CGTTCGCTGGTGGCCAAAGGGTGTGGTGTGTATACGGTTTATGGGGTCCATATATG 877
QY 256 GlyValSerValPhePheValLeuIleThrTrpLeuHisIleSerHisLeuSerLeuPro 275
Db 878 GTGGTTAACGCTTCTTATGATATGATACGATTTTGCACACATCCATCTTTGGCG 937
QY 276 HistyrApsSerThrGluTrpAsnTrpIleuysGlyAlaLeuSerThrIleAspArgAsp 295
Db 938 CACTATGATCTCTCGAGTGGAGCTGATGAGAGGAGCTTATCACTGAGACAGAGAT 997
QY 296 PheGlyPheLeuAsnArgValPheHisAspValThrHisValLeuHisIleu 315
Db 998 TATGGGATTTTAAACAGTTCCTCATTAACCAACCACTCATGTGCTCATCATTTG 1057
QY 316 IleSerTrpIleProHisTrpHisIleAlaLysGluAlaArgAspAlaIleAspValLeu 335
Db 1058 TTTTGCACAAATGCTCATATATATGCTGAGTGGCCACCAAGGCAATAAACCATATTG 1117
QY 336 GlyGluTrpTrpLysIleAspArgThrProIlePheValIleMetTrpArgGluAlaLys 355
Db 1118 GGGGAATCTATCACTGATGAGGATGCTGTCTATTAAGCGCATATGAGAGGAGCGAAG 1177
QY 356 GluCysIleTrpIleGluProAspGluAspSerGluHisLysGlyValPheTrpTrp 374
Db 1178 GAGGTCTCTTACGTTGAACAGATGAGGCGCAAGTAAGTGTGTGTGTTT 1234

RESULT 10
US-09-852-399-3
; Sequence 3, Application US/09852399
; Patent No. US2002045232A1
; GENERAL INFORMATION:
; APPLICANT: Olu, Xiao
; TITLE OF INVENTION: PRODUCTION OF CONJUGATED LINOLEIC ACID AND
; TITLE OF INVENTION: LINOENIC ACIDS IN PLANTS
; FILE REFERENCE: BNZ-002
; CURRENT APPLICATION NUMBER: US/09/852,399
; CURRENT FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: USN 60/203,027
; PRIOR FILING DATE: 2000-05-09
; NUMBER OF SEQ ID NOS: 4


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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1411
; TYPE: DNA
; ORGANISM: Calendula officinalis
; FEATURES:
;   NAME/KEY: CDS
;   LOCATION: (89) ... (1237)
US-09-852-399-3

Alignment Scores:
Pred. No.:      2,63e-149      Length:      1411
Score:          1323.50        Matches:      233
Percent Similarity: 76.32%      Conservative: 57
Best Local Similarity: 61.32%    Mismatches: 83
Query Match:    64.66%         Indels:       7
DB:              9             Gaps:         2

US-10-069-772-2 (1-377) x US-09-852-399-3 (1-1411)
Qy 1 MetGlyAlaGlyGlyArgMetSerAspProSerGluGlyLysAsnIleLeuGluArgVal 20
Db 89 ATGGGTGAGCGCGGTCCGATCGAATCGAATCCCAACGCTGGCAACAAACGAGCCGAA 148
Qy 21 ProValAsp-----ProProPheThrLeuSerAspLeuLysVala 34
Db 149 CCAATCCAAACGGGTCCCAATGAAACACCCCATTCACAGTTGAGACATGACAGAAACCG 208
Qy 35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyTyTyValValHisAsp 54
Db 209 ATCCCACTCTATTGTTTCAACCGATCGGTAAATCGTATTTTCAATAGCTCTTTTACGAC 268
Qy 55 LeuIleValAlaTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 74
Db 269 CTCACATCGGTCATCTTGTACATCTTGTACATCTTGTACATCTTGTACATCTTGTACAT 328
Qy 75 ProLeuAlaTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 94
Db 329 CCGCTCGCTACGTCATGCGTCCGCTTACGCGCTTACGCGCTTACGCGCTTACGCGG 388
Qy 95 LeuThrValIleGlyHisGluCysGlyHisIleAsnIleAsnIleAsnIleAsnIleAsn 114
Db 389 GTGTGGGTCATAGCCGACGAAATGCGCATCATGCTTTTACGACACCAATGCGTCGAT 448
Qy 115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyTyPheSerTyTyTyTy 134
Db 449 GACACCGTGGGTCTCGTCTTGTACATCTTGTACATCTTGTACATCTTGTACATCTTGT 508
Qy 135 SerHisArgAsnHisHisIleAsnThrAsnSerLeuAspAsnAspGluValTyTyTyTy 154
Db 509 AGCCACCGTACGACCACTCGAACACGCGGCTCGATCGACGACGATGAGTTTTCGTCG 568
Qy 155 LysArgLysSerLysValLysIleTySerLysLeuAsnAsnProProGlyArgVal 174
Db 569 AAGTTGAATCGGCGGTCCGCTCAACCGCGGTAACCTTAACCAACCAACCGGCGCATC 628
Qy 175 PheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyTyTyTyTyTyTyTyTyTy 194
Db 629 TTGACCTTACTCTGTAACCTTAACCTTACCTGCTTCTTACTTACTTACTTACTTACTT 688
Qy 195 GlyLysLysTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 214
Db 689 GGCCTGTAATCGACCGGTCGCGTTCGATTCGACCGGATGACCGGATGACCGGATGAC 748
Qy 215 ArgGluArgValGlnValLeuSerAspPheGlyLeuLeuAlaValPheTyTyTyTy 234
Db 749 CGCAACGCGGTCAAACTTCAATCCGACCGCGGATCTTAAGCCGATCTTGTGATCTC 808
Qy 235 LysLeuLeuValAlaAlaLysGlyValAlaAlaTyTyTyTyTyTyTyTyTyTyTyTyTy 254
Db 809 TTCGCACTCGAAGACCAAGGCGTCAACGCGTCTTCAACATGATGAGGCGCGCTTA 868
Qy 255 LeuGlyValSerValPhePheValLeuIleThrTyTyTyTyTyTyTyTyTyTyTyTyTy 274

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Db 869 CTCGTGTCACGCGTTCTTACGTCTTATGATTCATTCCTTACACACACTCCTTCGCTC 928
Qy 275 ProHisTyArgSerThrGluTrpAsnTrpIleLeuGlyAlaLeuSerThrIleAspArg 294
Db 929 CCGCACTTACGCTACACGGAATGAGATGGATGGATGGATGGATGGATGGATGGATGGAT 988
Qy 295 AspPheGlyPheLeuAsnArgValPheHisAspValThrHisIleValLeuHisHis 314
Db 989 GATTACGGGATCTTAAACAAAGTGTCCATTAACCAACCAACCAACCAACCAACCAAC 1048
Qy 315 LeuIleSerTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 334
Db 1049 TTGTTCTTCAACGCTTACATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1108
Qy 335 LeuGluGlyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 354
Db 1109 TTGGGCGATTATTTATCAGTTTACGCGGACCTCGATTTTAAAGCGGATATCGGAAACA 1168
Qy 355 LysGluCysIleTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 374
Db 1169 AAGGATGACATTTATGTTGATGAAGATGAGGAGTGAAGAA---GATGGTGTATTGAT 1225

RESULT 11
US-09-995-297-13
; Sequence 13, Application US/09995297
; Patent No. US20020092038A1
; GENERAL INFORMATION:
;   APPLICANT: Kodali, Dharma
;   APPLICANT: Fan, Zhongong
;   TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
;   FILE REFERENCE: 07148-072002
;   CURRENT APPLICATION NUMBER: US/09/995,297
;   PRIOR FILING DATE: 1998-08-03
;   NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURES:
;   NAME/KEY: CDS
;   LOCATION: (1) ... (1152)
US-09-995-297-13

Alignment Scores:
Pred. No.:      8,77e-149      Length:      1155
Score:          1318.00        Matches:      233
Percent Similarity: 77.17%      Conservative: 61
Best Local Similarity: 61.15%    Mismatches: 81
Query Match:    64.39%         Indels:       6
DB:              9             Gaps:         4

US-10-069-772-2 (1-377) x US-09-995-297-13 (1-1155)
Qy 1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGluGlyLys-----AsnIle 16
Db 1 ATGGGTGACAGGTGGAAGAATGCAAGTGTCTTCTCCCAAGAGTGTGAACCGACACC 60
Qy 17 LeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysValAlaIle 35
Db 61 ATCAAGCGCTTACCTTCGAGACACCGCCCTTCACTGTGGAAGAACTCAAGAAAGCAATC 120
Qy 36 ProThrHisCysPheGluArgSerValIleArgSerSerTyTyTyTyTyTyTyTyTyTyTyTy 55
Db 121 CCACCGCATCTTTCAACACGCTGATCCCTGCTCTTCTTCTTCAATCTGATCGGACATC 180
Qy 56 IleValAlaTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTyTy 75

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Db      181 ATCATAGCCTCTGCTTCTACTAGTCGCGCAACCACTTACCTCCCTCTCCCTCACCT 240
Qy      76 LeuAlaTyLeuAlaTTPProValTyTTPheCysGlnaIAserIleLeuThiGlyLeu 95
Db      241 CTCCTCTACTCTCGCTGCGCTCTCTACTAGGCGCTGCCAAGAGGTGGTCTCTACCGGCGTC 300
Qy      96 TTPValIleGlyNleGlyNleGlyNleGlyNleGlyNleGlyNleGlyNleGlyNle 115
Db      301 TGGGCAATAGCCCAAGAGTGGCGGCGCAACCGCTTACAGCACTACAGTGGCTTACAGC 360
Qy      116 IleValGlyPheValLeuHisSerAlaLeuLeuThiProTyTPheSerTTPLeuTySer 135
Db      361 ACCGTGGTCTCATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Qy      136 HisArgAenhiShiSalAasnThiAsnSerLeuAspAspGlyValTyTTPheProlys 155
Db      421 CATGAGCCCAACCATTCACACAGCTGGCTCCCTCGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      156 ArgIysSerIysValIysIleTySerIysLeuLeuAsnProProGlyArgValPhe 175
Db      481 AAGAAGTCAGACATCATGTGTACGCGCAAGTACCTCAACACCTTGGAGCGACCGTG 540
Qy      176 ThrLeuValPheArgLeuThiLeuGlyPheProLeuTyTTPheLeuThiAsnIleSerGly 195
Db      541 ATGTTAACGCTTCACTTCTCTGCGCTGCGCTGCGCTGCGCTTACCTTCAAGCTCGGGA 600
Qy      196 LysIysTyTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214
Db      601 AGACCTTACGACGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy      215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyAlaIle 234
Db      661 CGCGAGCTCTCCCAATATACATCTCCGACGCTGACATCTCGCGCTGCTGACGCTGCTC 720
Qy      235 LysLeuLeuValAlaAlaIysGlyAlaValTTPValIleAsnMetTyAlaIleAspLeu 254
Db      721 TTCCTTACGCGCGCGCGCGAGAGTGGCTGCTGCTGCTGCTGCTTACAGAGTCCGCTT 780
Qy      255 LeuGlyValSerValPhePheValLeuIleThiTyTTPheLeuHisSerThiIleLeuSerLeu 274
Db      781 CTGATGTGCATATGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Qy      275 ProHisTyTyrAspSerThiGlyTTPAsnTTPIleTyGlyAlaLeuSerThiIleAspArg 294
Db      841 CCTCACTACGATTCCTCCGAGTGGAGTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
Qy      295 AspPheGlyPheLeuAsnArgValPheHisAspValTTPHisSerThiValLeuHisHis 314
Db      901 GACTACGGAATCTTGAACAGGCTTCCCAATATTTACGACACGCGAGCGCGCATCT 960
Qy      315 LeuIleSerTyTTPheProHisSerValAlaIysGlyAlaArgAspAlaIleTySerProVal 334
Db      961 CTGTTCTCAGATCCCGCATTTATACCGGAGTGAAGTACCAAGCGCATTAAGCGATA 1020
Qy      335 LeuGlyGlyTyTTPheProHisSerValAlaIysGlyAlaArgAspAlaIleTySerProVal 354
Db      1021 CTGGAGAGGATATATCACTTCACTGAGAGCGCGGTGGTGAAGCGCATGAGGAGGAGCG 1080
Qy      355 LysGlyGlyValIleTyTTPheProHisSerValAlaIysGlyAlaArgAspAlaIleTySerProVal 374
Db      1081 AAGGAGTATCTATGTGAGACCGGACGCGAGGAGTGAAGAGAGAGTGTGCTGGTAC 1140
Qy      375 His 375
Db      1141 AAC 1143

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; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: PATRY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063003
; CURRENT APPLICATION NUMBER: US/09/771,904
; CURRENT FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 08/874,109
; PRIOR FILING DATE: 1997-06-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-09-771-904-13

Alignment Scores:
Pred. No.: 8,77e-149 Length: 1155
Score: 1318.00 Matches: 233
Percent Similarity: 77.17% Conservative: 61
Best Local Similarity: 61.15% Mismatches: 81
Query Match: 64.39% Indels: 6
Gaps: 4

US-10-069-772-2 (1-377) x US-09-771-904-13 (1-1155)
Qy      1 MetGlyAlaGlyGlyArgMet-----SerAspProSerGlyGlyS-----AsnIle 16
Db      1 ATGGGTGAGAGTGGAGAGATTCAGATGTCTCTCTCTCTCAAGAGTCTGAACGACAC 60
Qy      17 LeuGluArgValProValAsp--ProProTherThiLeuSerAspPheLeuValAlaIle 35
Db      61 ATCAAGCGCGTACCTCGAGACACACCGGCTTCACTGTGAGAGAACTCAAGAAAGCAATC 120
Qy      36 ProThiHisCysPheGluArgSerValIleArgSerSerTyTTPValIleHisAspLeu 55
Db      121 CCACCGCACTGTTCACACGCTGATCCCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Qy      56 IleValAlaTyValPheTyTTPheLeuAlaAsnThiTyTTPheProLeuIleProThiPro 75
Db      181 ATCATAGCCTCTGCTTCTACTAGTCGCGCAACCACTTACCTCCCTCTCTCCCTCACCT 240
Qy      76 LeuAlaTyLeuAlaTTPProValTyTTPheCysGlnaIAserIleLeuThiGlyLeu 95
Db      241 CTCCTCTACTCTCGCTGCGCTCTCTACTAGGCGCTGCCAAGAGGTGGTCTCTACCGGCGTC 300
Qy      96 TTPValIleGlyNleGlyNleGlyNleGlyNleGlyNleGlyNleGlyNleGlyNle 115
Db      301 TGGGCAATAGCCCAAGAGTGGCGGCGCAACCGCTTACAGCACTACAGTGGCTTACAGC 360
Qy      116 IleValGlyPheValLeuHisSerAlaLeuLeuThiProTyTPheSerTTPLeuTySer 135
Db      361 ACCGTGGTCTCATCTTCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
Qy      136 HisArgAenhiShiSalAasnThiAsnSerLeuAspAspGlyValTyTTPheProlys 155
Db      421 CATGAGCCCAACCATTCACACAGCTGGCTCCCTCGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      156 ArgIysSerIysValIysIleTySerIysLeuLeuAsnProProGlyArgValPhe 175
Db      481 AAGAAGTCAGACATCATGTGTACGCGCAAGTACCTCAACACCTTGGAGCGACCGTG 540
Qy      176 ThrLeuValPheArgLeuThiLeuGlyPheProLeuTyTTPheLeuThiAsnIleSerGly 195
Db      541 ATGTTAACGCTTCACTTCTCTGCGCTGCGCTGCGCTGCGCTTACCTTCAAGCTCGGGA 600
Qy      196 LysIysTyTyr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsnAsp 214
Db      601 AGACCTTACGACGCGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Qy      215 ArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyAlaIle 234

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[illegible]

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RESULT 13
US-10-715-100-13
; Sequence 13, Application US/10715100
; Publication No. US20040083503A1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharmu
; APPLICANT: Pan, Zhengong
; APPLICANT: Debonte, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; TITLE OF INVENTION: FATTY ACID CONTENT
; FILE REFERENCE: 07148-072002
; CURRENT APPLICATION NUMBER: US/10/715,100
; PRIOR FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: US/09/995,297
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; PRIOR FILING DATE: 1998-08-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13
;
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
; US-10-715-100-13

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Alignment Scores: 8.77e-149 Length: 1155
Pred. No.:

Percent Similarity:	77.17%	Conservative:	6
Best Local Similarity:	61.15%	Mismatches:	8
Query Match:	64.39%	Indels:	6
DB:	17	Gaps:	4

US-10-069-772-2 (1-377) x US-10-715-100-13 (1-1155)

[illegible]

QY 355 LysGluCysIleTyrIleGluProAspGluAspSerGluHisLysGlyValPheTyr 374

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Db      1081 AAGAGGTATCTATGTGGAACCGGACGAGGTGGAAGAAAGGTGTCTGTGATC 1140
Qy      375 His 375
Db      1141 AAC 1143

RESULT 14
US-09-995-297-9
; Sequence 9, Application US/09995297
; Patent No. US20020092038A1
; GENERAL INFORMATION:
; APPLICANT: Kodali, Dharma
; APPLICANT: Fan, Zhegong
; APPLICANT: Debonte, Lorin R.
; TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TOTAL MONOUNSATURATED
; FILE REFERENCE: 07148-072002
; CURRENT APPLICATION NUMBER: US/09/995,297
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 09/128,602
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)
US-09-995-297-9

Alignment Scores:
Pred. No.:      1,166-148      Length:      1,155
Score:          1317.00      Matches:      234
Percent Similarity: 76.44%      Conservative: 58
Best Local Similarity: 61.26%      Mismatches: 82
Query Match:      64.34%      Indels:      8
DB:               9          Gaps:      4

US-10-069-772-2 (1-377) x US-09-995-297-9 (1-1155)
Qy      1 MetGlyAlaGlyIArgMet-----SerAspProSerGluGlyLysAsn 15
Db      1 ATGGGTGACGGTGAAGATCAAGTGTCTCTCCCTCCCAAAAGTCTGAAACCGACAA 60
Qy      16 IleLeuGluArgValProValAsp---ProProPheThrLeuSerAspLeuLysVala 34
Db      61 ATC--AAGCGGTACCTCGCGAGACACCGCCCTTCACTGCGAGAACTCAAGAAAGCA 117
Qy      35 IleProThrHisCysPheGluArgSerValIleArgSerSerTyrrValValHisAsp 54
Db      118 ATCCACCGGACAGTGTTCAAAGCTCGATCCCTGCTCTTCTCTACTATCATCGGAGC 177
Qy      55 LeuIleValAlaTyrrValPheTyrrTyrrLeuAlaAsnThrTyrrIleProLeuIleProThr 74
Db      178 ATCATCATAGGCTCTGCTTCTACTACGTCGACACACTTACTTCTCTCTCTCTCAC 237
Qy      75 ProLeuAlaTyrrLeuAlaTrpProValTyrrTrpPheCysGlnAlaSerIleLeuThrGly 94
Db      238 CCTCTCTCTACTTGGCTGCGCTCTTACTAGGCTGCGCTCCAGGCGTGGCTTAACCGGC 297
Qy      95 LeuTrpValIleGlyHisGluCysGlyHisIleHisAlaPheSerAspTyrrGlnLeuIleAsp 114
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Qy      115 AspIleValGlyPheValLeuHisSerAlaLeuLeuThrProTyrrPheSerTrpIleTyrr 134
Db      358 GACACCGTGGCGCTCATCTTCCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 417
Qy      135 SerHisArgAsnHisIleAlaAsnThrAsnSerIleuAspAsnGlnValTyrrIlePro 154

```

```

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Qy      195 GlyLysLysTyrr---GlyArgPheAlaAsnHisPheAspPrometSerProIlePheAsn 213
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Qy      234 IleLysLeuLeuValAlaAlaLysGlyAlaAlaTrpValIleAsnMetTyrrAlaIlePro 253
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Qy      274 LeuProHisTyrrAspSerThrGluTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
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Qy      314 HisLeuIleSerTyrrIleProHisIleTyrrHisAlaLysGluAlaAspAlaIleLysPro 333
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Qy      354 AlaLysGluCysIleTyrrIleGluProAspGluAspSerGluHisLysGlyValPheThr 373
Db      1078 GCGAAGAGTGTATCTATGTGAAACCGGACGAGGAGGTGAAAGAAAGTGTCTTGG 1137
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; Publication No. US2003013379A1
; GENERAL INFORMATION:
; APPLICANT: Debonte, Lorin R.
; APPLICANT: Fan, Zhegong
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
; FILE REFERENCE: 07148-063003
; CURRENT APPLICATION NUMBER: US/09/771,904
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: US 08/874,109
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Brassica napus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1152)

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US-09-771-904-9

Alignment Scores:

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US-10-069-772-2 (1-377) x US-09-771-904-9 (1-1155)

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 QY 55 LeuIleValAlaTyrrValPheTyrrLeuAlaAsnThrTyrrIleProLeuIleProThr 74
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 Db 298 GTCTGGGTCATAGCCCAAGGCGGCGGCAACAGCCTTCAAGGACTACCAAGGCTGAGC 357
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 Db 478 AAGAAAGATGACACATCAAGGTACGCAAGTACCTTCAACACCTTGGGAGCAGCACC 537
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 QY 274 LeuProHisTyrrAspSerThrGlyTrpAsnTrpIleLysGlyAlaLeuSerThrIleAsp 293
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Search completed: June 23, 2004, 18:36:31
 Job time : 428 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 23, 2004, 15:39:21 ; Search time 2371 Seconds
(without alignments)
4748.225 Million cell updates/sec

Title: US-10-069-772-2
Perfect score: 2047
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Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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12: gb_est3:*
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14: gb_est5:*
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27: em_gss_vrt1:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1283.5	62.7	1856	11 AY104050	AY104050 Zea mays
2	1195	58.4	1807	12 B1683572	B1683572 RocheFord
3	1117	54.6	691	13 BQ994479	BQ994479 OGF7F12.Y
4	1102.5	53.9	989	14 CK269848	CK269848 EST715926
5	1087.5	53.1	973	14 CK262936	CK262936 EST709014
6	1078.5	52.7	725	13 BQ866257	BQ866257 OGF7H15.Y
7	1049.5	51.3	1794	12 B1683576	B1683576 EST 01 B7
8	1048	51.2	918	14 CK269030	CK269030 EST715108
9	1010	49.3	900	29 CG442730	CG442730 OGVH809TV
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14	955	46.7	963	14 CK270183	CK270183 EST716261
15	950	46.4	1080	13 BU238570	BU238570 DB01.13f0
16	941	46.0	948	14 CK278983	CK278983 EST725061
17	937	45.8	763	13 BQ853589	BQ853589 OGB20018
18	937	45.8	784	12 B1925058	B1925058 EST544947
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22	924.5	45.2	975	29 CG304699	CG304699 OGB3263TV
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27	906	44.3	753	13 BQ857435	BQ857435 OGB7104.Y
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35	874	42.7	905	14 CB349164	CB349164 CAB2SG000
36	870	42.5	856	14 CK278793	CK278793 EST724871
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39	862.5	42.1	837	14 CK276272	CK276272 EST722350
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ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE
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Email: ttruchef@uic.edu
Seq primer: M13 reverse.
Location/Qualifiers
source

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ORIGIN

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US-10-069-772-2 (1-377) x B1683572 (1-1807)

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RESULT 3

BO994479

LOCUS

DEFINITION

Q67F12.79.ab1 OG_ERGHJ lettuce serriola Lactuca sativa cdna clone

Q67F12, mRNA sequence.

ACCESSION

BO994479

VERSION

BO994479.1 GI:22414014

KEYWORDS

EST.

SOURCE

ORGANISM

Lactuca sativa

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asterids; campanulids; Asterales; Asteraceae; Cichorioideae;

Cichorieae; Lactuca.

1 (bases 1 to 691)

REFERENCE

AUTHORS

Kozik, A., Michelmore, R. W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, U.,

Ellison, P., Kolman, J., Slabaugh, M. S., Livingston, K., Zhou, Y.,

Lai, Z., Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compositae.ucdavis.edu/

Unpublished (2002)

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Asmunden Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]

belongs to contig OG_Contig2502, see http://cgdb.ucdavis.edu/

for details.

Plate: Q677 row, F column: 12.

FEATURES

source

Location/Qualifiers

1. .691

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/lab_host="E. coli"

/clone_lib="OG_ERGHJ lettuce serriola"

/note="Vector: pBRCDNA5flab; The library was constructed

from 10 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cspdb.ucdavis.edu/TAAG_T15US6-germinating_seeds
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Qy 76 LeuAlaTyLeuAlaATPProValTyTTrpPheCyGlnAlaSerIleLeuThrglyLeu 95
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Qy 216 GluArgValGlnValLeuLeuSerAspPheGlyLeuAlaValPheTyAlaIleLys 235
Db 685 GAGAGGCTACAGATCTTCTGATCTGATCTGAGTCTCGAGATTGTATCTGTAATC 744
Qy 236 LeuLeuValAlaAlaGlyAlaAlaATPValIleAsnMetTyAlaIleProValLeu 255
Db 745 CGTGTGCTTAGTAAAGTCTAGCTTGGCTAGGCTGACATCAAGGTACCCCTCTT 804
Qy 256 GlyIlySerValPhePheValLeuIleThrTyLeuHisIleThrasnLeuSerLeuPro 275
Db 805 GTCGTGAACGGCTTCTTCTCTATCACTTGAACGACACACCTCACTCATTCATTCCT 864
Qy 276 HisTyAspSerThrglyTrpAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAsp 295
Db 865 CACTACATTCACACCGATGGATGGCTTGAAGGAGCTTGGGACCTGTGACAGAGAC 924
Qy 296 PheGlyPheLeuAsnArgValPheHisAspValThrasnHisIleValLeuHisIleLeu 315
Db 925 TATGGGCTTTCTAAACAGTCTTCCACATCACTCACTCACTGATGTCACCATCTG 984

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```

RESULT 5
CK262936 973 bp mRNA linear EST 12-DEC-2003
LOCUS ESI709014 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION clone POABJ33 5' end, mRNA sequence.
ACCESSION CK262936
VERSION CK262936.1 GI:39819914
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 973)
Buell, C.R., Hart, A., Zismann, V., Karameycheva, S.A. and Baker, B.
REFERENCE
Generation of ESTs from abiotic stressed potato tissue
TITLE

```

JOURNAL COMMENT

Unpublished (2003)
Other ESTs: ESI709015
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@igr.org
Clones can be requested from TIGR via potato@igr.org
Seq primer: ATP TAG GTG ACA CTA TAG.

FEATURES

SOURCE

1..973
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POABJ33"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_id="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 14hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, 1d,
2d, and 4d). Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN

Alignment Scores:

Pred. No.: 1,33e-121 Length: 973
Score: 1087.50 Matches: 194
Percent Similarity: 77.22% Conservative: 50
Best Local Similarity: 61.39% Mismatches: 67
Query Match: 53.13% Indels: 6
DB: 14 Gaps: 2

US-10-069-772-2 (1-377) x CK262936 (1-973)

```

Qy 1 MetGlyAlaGlyGlyArgMetSerAspProSer-----GluGlyLysAsnIle 16
Db 25 ATGGAGAGCTGGTGGCGATGTCTGCTCAAAAGCGACGATGAAGTAAGAAGATCT 84
Qy 17 LeuGluArgValProValAsp---ProProPheThrasnSerAspLeuLysAlaIle 35
Db 85 CTTCAAAAGGTACCAACCTCAACGCCCTTTCACAGTGTGATATCAAAAGCTATTC 144
Qy 36 ProThriHisCySphegluArgSerValIleArgSerSerTyTyValValHisAspLeu 55
Db 145 CCACCTCACTGCTTCAAAAGGCTCTCACTGCTCACTTCTCTATGTTGATGATACCTC 203
Qy 56 IleValAlaTyValPheTyTyLeuAlaAsnThyTyIleProLeuIleProThrPro 75
Db 204 ATACTCGTTCATCATGTACTACTACCTCAACACTTCTTCCACCTCTTCCATCCCA 263
Qy 76 LeuAlaTyLeuAlaATPProValTyTTrpPheCyGlnAlaSerIleLeuThrglyLeu 95
Db 264 TATTGCTCATTTGCGCTTATTTTATCTGATTTTCCAGGGTGTGTTGACCTGTATT 323

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QY 96 TTPVALLIEGLYHISGLUCYGLYHISHSIALAPSESERAPTYRGLINLEULEAPASP 115
DB 324 TGGGTTAATGCCACGAATGTGGCCATCAAGCTTTCAGATTACCAATGGGTTATATAC 383
QY 116 ILEVALIPHEVALLEUHSERALEULEUTHPROTYRPHSETRIPLETYSER 135
DB 384 ACCGTTGAGCTTATCTCTGCTGTCTGTGTGGCCGCTACTCTCTTGGAAATATAGT 443
QY 136 HISARGASNHISHIALASANTHRASNSERLEUASPASPGULVALTYRILEPROLYS 155
DB 444 CATGCGCCACCACTCCACAGCTGCTCCCGAGCGGATGAGAGTCTTTGTGCCAAG 503
QY 156 ARGVLSERYVALVLEIETERYSERLYLEULEUASANTPROGLYARVALPHE 175
DB 504 CCAAAATCTCAGCTCGATGTATTCCAAAGTTCGAATCCAAATCCACAGGCGGTCTTC 563
QY 176 THRLEUVALPHEARGLEUTHREUGLYPHEPROLEUPTYRLEULEUTHASNLIESERGLY 195
DB 584 TCACCTTACATCACTCTCACTCTGCTGGCCGTTGACTTTCCTTCAATATCTGAC 623
QY 196 LYSLYSTYRGLYARGPHEALASNHISPHASPPROMETSERPROILEPHEASNPARG 215
DB 624 AGACATACGACCGATTTGCACTGATGACCTTACCGCCCAATCAGACAAACGCT 683
QY 216 GLUATGVALLINVALLEUUSERSAPHEGLYLEULEUALVALPHETYRALLILEYS 235
DB 684 GAGAGGCTACAGATCTTCCTGTATGATGCTTCGAGATTGTATCTCTATAC 743
QY 236 LEULEUVALALALALYGLYALALATPVALILEASMETTYRALLILEPROVALLEU 255
DB 744 CATTATGCTTATGTAAGGCTTACCTTGCTGATGTCATGATGCTGATGCTGCTC 803
QY 256 GLYVALSERVALPHEPHEVALLEULEUTHRYTLEUHSISLETHRISLEUSERLEU 275
DB 804 GTCGGAACGCTTCTCTCTGTGATCACTTTCGACGACACACCACTCATGCGCA 863
QY 276 HISTYRASPSETRTHGLUTRPHANTRIPLEYSGLYALALEUSERTHRIEASPTARG 295
DB 864 CACTACGATTCACACGAGGAGGATGCTTAAGGAGGCTTTGGCAACCTGTGACAGAGC 923
QY 296 PHEGLYPHELEUASNPARGVALPHEHISAPVALTHRHISTHRISVAL 311
DB 924 TATGGGCTTCAACAGGCTTCCACACATCACCGACACCTACAGTG 971

RESULT 6
BQ866257
LOCUS OGCTH15.yg.ab1 OG ABCDI lettuce salinas Lactuca sativa cDNA clone
DEFINITION OGCTH15, mRNA sequence.
ACCESSION BQ866257
VERSION BQ866257.1 GI:22251722
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 725)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,
Ellison, P., Kolman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, J. and Bradford, K.
Lettuce and Sunflower ESTs from the Composite Genome Project
http://compgenomics.ucdavis.edu/
Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@catc.org [michelmore@vegmail.ucdavis.edu]

belongs to contig OG_CA_contig2502, see <http://cgpdb.ucdavis.edu/>
for details.
Plate: OGCT row: H column: 15.
FEATURES
source
1..725
location/Qualifiers
1..725
/organism="Lactuca sativa"
/mol_type="mRNA"
/cultivar="Salinas"
/db_xref="taxon:4236"
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/clone_lib="OG ABCDI lettuce salinas"
/note="Vector: pRCDSM5149. The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at <http://cgpdb.ucdavis.edu/>
TAG TISSUE=chemical induction
TAG LIB=OG ABCDI lettuce salinas
TAG_SEQ=GTGACCGGAG"

ORIGIN
Alignment Scores:
Pred. No.: 1,06e-120 Length: 725
Score: 1078.50 Matches: 200
Percent Similarity: 94.62% Conservative: 11
Best Local Similarity: 89.69% Mismatches: 11
Query Match: 52.69% Indels: 2
DB: 13 Gaps: 1

US-10-069-772-2 (1-377) x BQ866257 (1-725)

QY 1 METGLYALGLYGLYARGMET---SERASPSERGUGLYLYBASNLLEUGLYARG 19
DB 56 ATGGGTGACGAGGTGGCGATGTCAAGGATCATTTATGATGTAAGATTCGTGAACGT 115
QY 20 VALPROVALAPPROPPOPHETHRLEUSERSPLEUYSVALALILEPROTHIECYG 39
DB 116 GTCCCAAGT-GATCCACCGCTTTTCATTAAGTATTTAAAGAAAGGATCCCTGCCATTGC 174
QY 40 PHEGLUARGSERVALILEARGSERSETRTYRVALVALHISAPLEULEVALALATYR 59
DB 175 TTCAAGGATTCGTCATCCGCTTCACTTACATTTGTTGTCAGATCGATTGTCCTAC 234
QY 60 VALPHETYRTRYLEUALASANTHRTRYTLEPROLEU1LEPROTHPROLEUALATYRLEU 79
DB 235 GTTTTCTACTCTCTTGGCAAAATACATATATCTTTCTTCAGCTCCCTTGGCTACTTA 294
QY 80 ALATRPVALTYRTRYRPHCYEGLALASERILELEUTHRGYLEUTHVALILEGLY 99
DB 295 GCTTGGCCGGTTTATGTGTTTGTCAAGCAAGCATCTCCACAGGCTTATGGGTATCGGC 354
QY 100 HISGLUCYGLYHISHSIALAPSESERAPTYRGLINLEULEAPASPILEVALIGLYPHE 119
DB 355 CATGACACCGGTCACCATGCTTTCAGCAATACCAATGATGATGACATCTGCGCTTC 414
QY 120 VALLEUHSERALEULEUTHPROTYRPHSETRIPLETYSERHISARGASNHIS 139
DB 415 ATCTCCACATGAGCTCATGACACCTTATTTTCATGGAATATATAGCATCGAAATCAC 474
QY 140 HISALASANTHRASNSERLEUASPASNPGLVALTYRILEPROLYSARGVLSERYLS 159
DB 475 CATGCCAACCAAAATCTCCCTCGATTAAGATGAATTAATCTCTTAACGCAACTCTAAA 534
QY 160 VALVLSLEYTSELYSLEULEUASNPASNPBROGLYARVALPHEUTHLEUVALPHE 179
DB 535 GTCAAGTGATCTAATAACTTTTAACACACCACTGCTGACAGTTCATCTTTGGTTT 594
QY 180 ARGLEUTHREUGLYPHEPROLEUPTYRLEULEUTHASNLIESERGLYLYSTYRGLY 199

Db	595	AGGTTCACTTAGAGATTTCCTTTACTCTTAACTAATATTTCTGGCAGAAATACGGA	654
Qy	200	Argphea1aaenh1sphaeaspproweserProillepheamaasparGluarYalgin	219
Db	655	AGGTTTGCAACCACTTGTGATCCATGATGTCAAATTTTCACGACCGAGGAGATTACAG	714
Qy	220	Valleulen 222	
Db	715	GTTCGTGTTA 723	
RESULT 7			
LOCUS	BI683576/c	1794 bp	mRNA linear EST 31-DEC-2001
DEFINITION	EST 01 B73 LIBRARY Zea mays cDNA clone cmaas92 5', mRNA sequence.		
ACCESSION	BI683576		
VERSION	BI683576.1	GI:18021477	
KEYWORDS	EST.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	1 (bases 1 to 1794)		
TITLE	Mikkilineni V. and Rocheford T.		
JOURNAL	Genomic Organization of Fatty Acid-Desaturase-2 ESTs in Maize		
COMMENT	Unpublished (2001)		
	Contact: Dr. Torbert Rocheford		
	Torbert Rocheford		
	University of Illinois		
	1102, S. Goodwin Ave., Urbana, IL 61801, USA		
	Tel: (217) 333-9643		
	Fax: (217) 333-9817		
	Email: troche@uiuc.edu		
	Seq primer: M13 reverse.		
FEATURES	Location/Qualifiers		
Source	1..1794		
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	/clone_id="B73 LIBRARY"		
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ORIGIN			
Alignment Scores:			
Pred. No.:	1.52e-116	Length:	1794
Score:	1049.50	Matches:	209
Percent Similarity:	63.53%	Conservative:	61
Best Local Similarity:	49.18%	Mismatches:	88
Query Match:	51.27%	Indels:	67
DB:	12	Gaps:	9
US-10-069-772-2 (1-377) x BI683576 (1-1794)			
Qy	13	Glyysaani1eleuGluarYalProValasp---ProPropheThrlenuserapien	31
Db	1761	GGTGCGCGCGGATCGACGCGCGCGGATGAGAAAGCCCTCGTTACTCTGGTCAGATC	1700
Qy	32	Lyslysa1a1a1eProThrieCyasphedGluarGserVal1leargSerserYtyrYal	51
Db	1701	AAGAAGCGCATCCGCCACACCTGCTTGAAGCGCTCGGTGTCAAATCTTCGTACGTG	1644
Qy	52	ValHisaapLeu1leValAlaTyralPheTytyrLeuAlaenThTyrlleProleu	71
Db	1641	GTCCACGACCTGGTGATCGCGCGCGCTCTCTCTTCTCGCGCTGCACATACCGCGG	1582
Qy	72	IlleProthrrProleuAlaTyrlleuAlaTrpProValTytrPheCyGlnalaserile	91
Db	1581	CTCCAAAGCCCGCTCGCTAGCGCCCGCTGAGCTGATGATGATCGAGGGGTCGCG	1522

[illegible]

CK269030
 LOCUS CK269030 918 bp mRNA linear EST 12-DEC-2003
 DEFINITION EST15108 potato abiotic stress cDNA library Solanum tuberosum cDNA
 clone POACK42 5' end, mRNA sequence.
 ACCESSION CK269030
 VERSION CK269030.1 GI:39826008
 KEYWORDS EST.
 SOURCE Solanum tuberosum (potato)
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum.
 REFERENCE 1 (bases 1 to 918)
 Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
 TITLE Generation of ESTs from abiotic stressed potato tissue
 JOURNAL Unpublished (2003)
 COMMENT Other ESTs: EST15109
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potcdo-array@tigr.org
 Clones can be requested from TIGR via potcdo@tigr.org
 Seq primer: ATT TAG GTG ACA CTA TAG.
 FEATURES
 source Location/Qualifiers
 1..918
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 /mol_type="mRNA"
 /culturvar="Kennebec"
 /db_xref="taxon:4113"
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 /lab_host="DH10B-Tona"
 /clone_1fb="potato abiotic stress cDNA library"
 /note="Vector: pCMVSPORTC.1; Site 1: EcoRI; Site 2: NotI;
 supplier: Solanum tuberosum var. Kennebec plants were
 grown from cuttings on a 16hr light/8 hr dark cycle at 25
 C for 3-4 weeks. Abiotic stress conditions were applied to
 four separate sets of plants. Set 1 involved saturation of
 the soil with 150 mM NaCl and tissues were harvested at
 following application of the salt stress (leaves: 2hr,
 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, 1d,
 2d). Set 2 were grown under the standard conditions and then
 were water stressed by withdrawal of further watering
 applications. Drought stressed plants were harvested after
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
 and 5d). Set 3 were grown under the standard conditions
 and then were cold stressed by placement at 4 C. Cold
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d. Set 4 were grown under the standard conditions and
 then were heat stressed by placement at 35 C. Heat
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d and 4d and heat-stressed roots were harvested at 6 hr,
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and
 equal RNA from each tissue and stress was pooled to
 construct the cDNA library. RNA sample."

ORIGIN
 Alignment Scores:
 Pred. No.: 8.2e-117 length: 918
 Score: 1048.00 Matches: 185
 Percent Similarity: 76.72% Conservatave: 49
 Best Local Similarity: 60.66% Mismatches: 66
 Query Match: 51.20% Indels: 6
 DB: 14 Gaps: 2
 US-10-069-772-2 (1-377) x CK269030 (1-918)
 QY 2 gjalagjygljyargmetserasppro-----Serglucglylysahnlleu 17
 DB 3 GGAGCTGGGCTGCTATGCTCTCAATGGGAGAGTGAAGTA-AAAGAGATCTCTT 61
 QY 18 GUAAGVALProvalasp---ProProphetheThLeuseraspleuylalyalallepro 36

Db 62 CAAGAAGTACCAACCTCGAAGCCCCCTTTCACAGTGTGATATACAGAGGCTATCCCA 121
 QY 37 ThrHisCysPhegluaArgserValIleArgSerSerTyTyValValHisAspLeuIle 56
 Db 122 CCTGACTGCTTTCAAGGTCCTCATCGGCTCATCTTCCTATGTTGTATAGACTCTATA 181
 QY 57 ValAlaTyValPheTyTyTyLeuAlaAsnThTyTyIleProLeuIleProThProLeu 76
 Db 182 CTCGCTTCACAGTACTAGCTTGGTGAACCACTTACTTCCACCTTCCTCCATCCCAAT 241
 QY 77 AlaTyLeuAlaTyProValTyTyTyPheCysGlnAlaSerIleLeuThGlyLeuTyP 96
 Db 242 TGTACTAGTGGGCTGCTATTTACTGATTTGCCAGGCTTGTGTCATGCTGATTTGG 301
 QY 97 ValIleGlyHisGluCysGlyHisHisAlaPheSerAspTyTyGlnLeuIleAspAspIle 116
 Db 302 GTTATAGCCCAAGATGGCCATCAAGCTTTCAGTATTCATCAATGGGTGATGACACC 361
 QY 117 ValGlyPheValLeuHisSerAlaLeuLeuThProTyTyPheSerTyTySerHis 136
 Db 362 GTTGACTTATCTTCACTCTGCTCTGTGTGGCCGTACTTCTTGGAATATATAGTAT 421
 QY 137 ArgAsnHisHisAlaAsnThAsnSerLeuAspAsnAspGluValTyTyIleProLysArg 156
 Db 422 GTGGCCACCACTCAACACTGGCTCCTCGAGGCTATAGGCTTTGTGCCAAGCCA 481
 QY 157 LysSerLysValLysIleTySerLysLeuLeuAsnAsnProProGlyArgValPheThr 176
 Db 482 AATCTCACTGCTCGAGTGTATTCAGATGTAATGAACATCAACAGGAGGCTCCTCA 541
 QY 177 LeuValPheValLeuThLeuGlyPheProLeuTyTyLeuThAsnIleSerGlyLys 196
 Db 542 CTTCATCAATCACTCACTCTGCTGGTGGCCGTGTAATGAGCTTCAATGATATGGCA 601
 QY 197 LysTyTyGlyArgPheAlaAsnHisPheAspProMetSerProIlePheAsnAspArgGlu 216
 Db 602 CCATACGACCAATTTGATGATGATATGATACCTTACAGGCCCAATCTACACACCGTAG 661
 QY 217 ArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyTyAlaIleLysLeu 236
 Db 662 AGGCTACGAGACTTCTGATGATGCTGAGATTCGAGATTGTTGATCTCTATACCGT 721
 QY 237 LeuValAlaIleValGlyValAlaIleTyTyValIleAsnMetTyTyAlaIleProValLeuGly 256
 Db 722 ATGGCTTATGGAAGGCTGATGCTGATGTCATGTCATGCGGTATCCCTCTGTC 781
 QY 257 ValSerValPhePheValLeuIleThTyTyLeuHisHisThHisIleSerLeuProHis 276
 Db 782 GTGACGGCTTCTTGTCTTATCACTACTTGCAGCACATCCATCTATGCGACAC 841
 QY 277 TyAspSerThrgIuTyPAsnTrpIleLysGlyAlaLeuSerThrIleAspArgAspPhe 296
 Db 842 TACGATTCAACCGATGGATGGCTTGGGAGAGTTTGGCAACCTGAGACAGAGACTAT 901
 QY 297 GlyPheLeuAsnArg 301
 Db 902 GGGGTTCTTAACAG 916

RESULT 9
 CG442730/c 900 bp DNA linear GSS 17-SEP-2003
 LOCUS CG442730 900 bp DNA linear GSS 17-SEP-2003
 DEFINITION OGVS09TV ZM.0.7.1.5_KB zea maye genomic clone ZM08Ma0486A17,
 genomic survey sequence.
 ACCESSION CG442730
 VERSION CG442730.1 GI:34822716
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 900)

AUTHORS

WhiteJaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nuberger,A., Robbins,D. and Lakey,N.

JOURNAL

Consortium for Maize Genomics

COMMENT

Unpublished (2002)
Other_GSSs: OGVH509TH
Contact: Cathy WhiteJaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whiteJaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..900
/organism="Zea mays"
/mol_type="genomic DNA"
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methylation filtered genomic DNA library"

ORIGIN

Alignment Scores:

Pred. No.: 3.52e-112 Length: 900
Score: 1010.00 Matches: 170
Percent Similarity: 78.72% Conservative: 63
Best Local Similarity: 57.43% Mismatches: 59
Query Match: 49.34% Indels: 4
DB: 29 Gaps: 2

US-10-069-772-2 (1-377) x CG442730 (1-900)

QY 82 ProValTyrTrpPheCysGlnAlaSerIleLeuThrglyLeuTrpValIleGlyHisGlu 101
Db 900 CCGCTCTAGATCGACAAAGCGTGGTGCACCGGCTGTGATCGGCACGAG 841
QY 102 CysGlyHisAlaPheSerAspTyrGlnLeuIleAspPheValGlyPheValLeu 121
Db 840 TGTGGCCCAACGCGCTTCGAGAGACCGCTCTCGACGACATGTGGCTGTGTGCTG 781
QY 122 HisSerAlaLeuLeuThrProTyrPheSerTyrSerHisArgAsnHisAla 141
Db 780 CACTGTGCTGATGTGCTCCGACTTCTGTGAAAGTACAGCCAGCGGCACCATCTCC 721
QY 142 AsnThrAsnSerLeuAspAsnAspGluValTyrIleProLysArgLysSerLysValLys 161
Db 720 AACATTTGCTCTCCCTGAGCGGAGAGAGTGTGTGGCCCAAGAGAGAGAGAGAGAG 661
QY 162 IleTyrSerLys--LeuLeuAsnAsnProProGlyArgValPheThrLeuValPheArg 180
Db 660 TGGTACACGCGGTACGTGTGCAACAGCCCGGCGGCGCTGTCTCAATGCTGTGAG 601
QY 181 LeuThrLeuGlyPheProLeuTyrLeuLeuThrAsnIleSerGlyLysTyrClyArg 200
Db 600 CTAAACCTCGGAGTGGCACTGACTGGCCACCAAGTGTGGAGTGGCCCGGACCGGCG 541
QY 201 PheAlaAsnHisPheAspPheMetSerProIlePheAsnAspArgGluArgValGlnVal 220
Db 540 TTCCGCTTCCCACTAGACCCCTTACCGCCGATCTACAGACCGGAGCGGCCCGCATCTC 481
QY 221 LeuLeuSerAspPheGlyLeuLeuAlaValPheTyrAlaIleLysLeuLeuValAla 240
Db 480 TTCTGCTCGAGACGCGGCTGTGGCCCGGCTGTGGCTGTGCAAGCTGGCGGCGAGC 421
QY 241 LysGlyAlaAlaTyrValIleAsnMetTyrAlaIlePheProValLeuGlyValSerAlaPhe 260
Db 420 TTCGGGTTCTGTGGTGTGGCGGTCTACGCGGTGGCTGTGATTTGATTCGCGGTG 361
QY 261 PheValLeuIleThrTyrLeuHisIleThrHisLeuSerLeuProIleTyrAspSerThr 280

Db

360 CTGGGAACTGTCACCTTCTCTCAGACACACCGCGGCTTCCCGGCTAGACATCCAGC 301

QY

281 GluTrpAsnTrpIleLysGlyValLeuSerThrIleAspAspPheGlyPheLeuAsn 300

Db

300 GAGTGGAGCTGCGCGCGCGCGCTAGCCACATGACCGGATCTAGCGGCGCTTCAAC 241

QY

301 ArgValPheHisAspValThrHisIleThrHisValLeuHisIleLeuSerTyrIlePro 320

Db

240 CGCGTGTCCCAACATACACGACACACAGCTGCGGACCATCTTCTTCCACCGTGC 181

QY

321 HisTyrHisAlaLysGlyValAlaArgAspAlaIleLysPheProValLeuGlyGluTyrTyrLys 340

Db

180 CACTACACAGCGCGTGCAGGCTTACCAAGCGGATCAAGCCATCTCTCGGAGACTATCAG 121

QY

341 IleAspArgThrProIlePheLysAlaMetTyrTrpGlyValLysGluCysAlaIleTyrIle 360

Db

120 TTGACCCCGCCCGCCATCGCCAGCGGATGTGGCGCGAAGCTAGGAGTGTATTCATC 61

QY

361 GluProAspGluAspSerGluHisLysGlyValPheTyrTyrHisLys 376

Db

60 GAGCCCGAAGACGCG-----AGGGCATCTTATGTATCAACAG 22

RESULT 10

CF098768/C

LOCUS

OHN8F08.y3.ab1 OH N sunflower H. argophyllus (drought stress) 613 bp mRNA linear EST 22-JUL-2003

DEFINITION

Helianthus argophyllus cDNA clone OHN8F08, mRNA sequence.

ACCESSION

CF098768

VERSION

CF098768.1 GI:33137835

KEYWORDS

EST.

SOURCE

Helianthus argophyllus

ORGANISM

Helianthus argophyllus

REFERENCE

1 (bases 1 to 613)

AUTHORS

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,

Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J.,

Ellison,P., Kolkmann,J., Slabaugh,M.S., Livingston,K., Zhou,Y.,

Lai,Z., Church,S., Jackson,L. and Bradford,K.

Lecture and Sunflower ESTs from the Compositae Genome Project

http://compositae.ucdavis.edu/

Unpublished (2002)

Contact: Alexander Kozik [R.W.Michelmore]

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Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]

belongs to contig OH_Ca_Content96400, see http://cgpdb.ucdavis.edu/

for details.

Plate: OHN8 row: F column: 08.

FEATURES

source

Location/Qualifiers
1..613
/organism="Helianthus argophyllus"
/mol_type="mRNA"
/db_xref="taxon:73275"
/clone="OHN8F08"
/lab_host="E.coli"
/clone_lib="OH N sunflower H. argophyllus (drought stress)"
/note="Vector: pBSM-T; The library was constructed from three different sources (seedling, root and leaf) of RNA from a single genotype. cDNAs were pooled and cloned into a high-copy vector pBSM-T. Details of library construction can be obtained at http://cgpdb.ucdavis.edu/"

ORIGIN

Alignment Scores:

Pred. No.: 2.1e-108 Length: 613
Score: 977.00 Matches: 176

Db	Accession	Length	Source	Organism	Accession	Length	Source	Organism
Db	721 GACTCCACGAGTGGGAGTGGCTGGCGGCGGCTAGCCACCATGAGACCGGACATACGAC	780						
Qy	298 PheleAenAaGvAlPhenHiaspValThrsThrThiHsIvalLeuHsiHsleuIleSer	317						
Db	781 GCCCTCAACCGCGGTTCACAAACATCAACGACACACAGCGTGTGCAACATCTCTGTCC	840						
Qy	318 TyrIleProHsiThyHsiHsAlaIalysGlu	326						
Db	841 ACCGCGCCGCACTACCAACGCGGTGAG	867						
RESULT 12								
LOCUS	CD760583	876 bp	mRNA	linear	EST 01-JUL-2003			
DEFINITION	linFA02 Lin Linum usitatissimum cDNA, mRNA sequence.							
ACCESSION	CD760583							
VERSION	CD760583.1	GI:32372153						
KEYWORDS	EST.							
SOURCE	Linum usitatissimum (flax)							
ORGANISM	Linum usitatissimum							
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Linaceae; Linum.							
AUTHORS	1 (bases 1 to 876)							
TITLE	Cloutier S. and Fofana, B.							
JOURNAL	One Step RT-PCR on total RNA isolated from 12 after anthesis flax bolls							
COMMENT	Unpublished (2003) Contact: Dr. Sylvie Cloutier Cereal Research Centre, Agriculture and Agri-food Canada 195 Dafoe Rd, Winnipeg, MB, Canada R2T 2M9 Tel: (204) 983-2340 Fax: (204) 983-4604 Email: scloutier@agr.gc.ca The 'lin' sequences are derived from cloning of fragments obtained by One Step RT-PCR on total RNA isolated from 12 days after anthesis flax bolls Seq primer: M13 forward							
FEATURES	Location/Qualifiers							
Source	1..876							
	/organism="Linum usitatissimum"							
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	/cultivar="AC McDuff"							
	/db_xref="taxon:4006"							
	/issue_type="Bolls"							
	/dev_stage="12 days after flowering"							
	/lab_host="EMDH10B-TONA"							
	/clone_id="lin"							
	/note="Vector: pBluescript KS+ (Stratagene); Site_1: NotI Site_2: MluI; mRNA obtained from bolls 12 days after flowering"							
ORIGIN								
Alignment Scores:								
Pred. No.:	4,396-106	Length:	876					
Score:	960.00	Matches:	171					
Percent Similarity:	77.06%	Conservative:	44					
Best Local Similarity:	61.29%	Mismatches:	62					
Query Match:	46.90%	Indels:	2					
DB:	14	Gaps:	2					
US-10-069-772-2 (1-377) x CD760583 (1-876)								
Qy	35 lIeProThrHsiCyPheHsiAaGseValIleAaGse---SerTyrTyrValValHis	53						
Db	2 ATCCACGCGCACTGTTTCAAAAGCTCAATCCCGATGCTTGCTGTAGGTGGGATAC	61						
Qy	54 AspleuIleValAlaIaTyrValPheTyrTyrIleuAlaAenThrTyrIleProleuIlePro	73						
Db	62 GACCTCAACCATGACGCAATCTTCACTACATCGCACACTTACTTCACCTCTCCCT	121						
Qy	74 ThrProleuAlaTyrIleuAlaTyrProValTyrTrpPheCyGlnAlaSerIleleuThr	93						
Db	122 AGCCCTTCAACTACCTGCGCGGATCTACTAGCGCTCGACAGGCGTCAATCTCTACT	181						

Oy		94	GlyeurtPvAlIlegLYhiGICye6dYhiShiaIaPhesSerAsTyGLInleulle	113
Db		182	GGAGTATGGGTtTGCTCGCACCAGATGCCGTACCATGCCTTCAGGAATTACCAAGCGCTC	241
Oy		114	AapApIIeValGIypheValIleuHisSerXaIaleuleuthrProTYrPheSerTrplys	133
Db		242	GACCAcATGGTTGGCTTGCTCCTCCATTCGTCGCTCCTTGTTCTTACTTCCTTCGTAAG	301
Oy		134	TyrSerHISatgaAmHISHIAIdasnthrxanSerLeuAparnaBsgIuValTYrIle	153
Db		302	CACAGCCACCCGCCCACCATTCACAACGGGAATCGCTVgATCGTAGAGAGGTGTTTTC	361
Oy		154	ProLYsaRglYSerLySeryValIleIetySerLySleuASnaSPProProdLYar	173
Db		362	CCCAAGCAGAAGGCCGGAATCGGGGTGACTTCAGATCCTTAACACCACCTGGCCGT	421
Oy		174	ValphethrIleuValIpheArgLeuThrlengIYPheProLeuTYrLeuLeuthraSnile	193
Db		422	GTGATTCACATTTGGCCGTCACATTAAGCTCGGTGGCTCTGTACTTGATTCGAACGTC	481
Oy		194	SerGLyIsbLYrTYrGLYArghPheAlaamHISheAppPrometSerProIlephesn	213
Db		482	TCCGGAGAACCATATGAACCGGTGGCAATTCATTTGACCTTCACGGTCGATTTACAT	541
Oy		214	AsprgrGuARgVALGINValIleuSenSerAspPhegiLYLeuLyaIaValIphetylala	233
Db		542	GATGCCAGCAGCCTAATAGAGATATACCTTACGACCGAGGAATATTCACCGTGTGCTAACTC	601
Oy		234	IleLYsleuLeuValAlaIalalyGSLyAlaIaITryValIleaSmetTYrAlaIlePro	253
Db		602	CTATACAGACTCGTCCTCCACGAAAAGACCTGTTGGCGTCGTCATATACGAGCTCCA	661
Oy		254	VallengIyValSerValPhePheValIleuIlePhrTYrIleuHISHISTHISleuser	273
Db		662	CTATVTGATGAGATGAGATTCCTAGCTCTCACTTCATCACTTTCGCAACACACCATCTCTCT	721
Oy		274	LeuProHISrYAAsPserThrGLITripAsnTrp---IleLYSGIYAlaLeuSerThrIle	292
Db		722	TTTTGGCACTCAAAAGTCTCCGATGGGAGATGTGATGGCAGAGGCGCTCTCGACCGTG	781
Oy		293	AspaRAspPhegiLYPheLeuASnaYValPheHISAspValITHrISTHISval	311
Db		782	GATGAGACATPCGGGGTTACTCAACACGGTTCACAAACATCACCGATACATATGTC	838
RESULT_13				
CK210592		1084 bp	mRNA	linear EST 08-DEC-2003
LOCUS		FGAS022415	tritlicum aestivum FGAS: Library 5 GATE 7	tritlicum
DEFINITION		aestivum CDNA, mRNA sequence.		
ACCESSION		CK210592		
VERSION		CK210592.1	GI:39572982	
KEYWORDS				
SOURCE				
ORGANISM				
			tritlicum aestivum (bread wheat)	
			tritlicum aestivum	
			Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
			Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	
			Poideae; Triticeae; Triticum.	
			1 (bases 1 to 1084)	
REFERENCE				
AUTHORS			Allard,R., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gautier,D.,	
			Genewein,B., Graif,R., Gulick,P., Hrycan,L.D., Iatroche,A.,	
			Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,	
			Penniket,C., Roach,J.L. and Sarhan,P.	
			Functional Genomes of Abiotic Stress In Wheat and Canola Crops	
			Unpublished (2003)	
TITLE			Contact: Wm J Crosby	
JOURNAL			Bioinformatics	
COMMENT			University of Saskatchewan, Department of Computer Science	
			1C101 Engineering Building, 57 Campus Drive, Saskatoon,	
			Saskatchewan, S7N 5A9, Canada	
			Tel: 306 966 1769	
			Fax: 306 966 2033	
			Email:fgas_est@cs.usask.ca	

This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [23,806].

Plate: L58023 row: F column: 21.

FEATURES

source

1..1084
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: library 5 GATE 7"
/note="Vector: pCMV.SPORT6; Crown and developmental stages of spike formation in wheat cultivar Norstar. 4 mRNA populations were combined before constructing the library. The first mRNA population is from 1cm crown sections after 30 days of cold acclimation. The second is from 1cm crown sections after 11 days of deacclimation (before deacclimation plants were fully vernalized for 49 days). The third is from different developmental stages of spike formation (5 to 50mm) that still have not emerged from the leaf (dissection required). The last is from different developmental stages of spike and seed formation after having emerged from the leaf (visible). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NciI."

ORIGIN

Alignment Scores:

Pred. No.: 8.1e-106 Length: 1084
Score: 959.00 Matches: 174
Percent Similarity: 77.08% Conservative: 48
Best Local Similarity: 60.42% Mismatches: 62
Query Match: 46.85% Indels: 6
DB: 14 Gaps: 2

US-10-069-772-2 (1-377) x CK210592 (1-1084)

QY 88 GlnAlaSerIleLeuThgYLeuTrpValIleGlyHISgluCYeGlyHISAlaPhe 107
DB 37 CAGGGCTGCTGATGACGGGGCTCGGGTCATCGGACGAGTGGGGCATGACCTTC 96
QY 108 SerApYrYrGlnLeuIleAspAspIleValGlyPheValLeuHISerAlaLeuThr 127
DB 97 TCCGACTCTGCTGCTGATGACCGCGGCTCGGTCTCCACTCGGTGGCTCTCTC 156
QY 128 ProTYrPheSerTrpLYrSerIISarGAsnHISAlaAspThrAsnSerLeuAsp 147
DB 157 CCTACTCTCTGGAGATGACGCCACGTCGCCACACTTACACCGGGTGGCTGAG 216
QY 148 AsnAspGluValTYrIleProLYrAspLYrSerLYrValLYrTYrSerLYr--Leu 166
DB 217 CGCGATGAGGTTCCTGCCCAAGCAAGAGGGCGCTGGCTGTACACCCCTTACATC 276
QY 167 LeuAsnAspProGlyrYrGlyAlaPheThrLeuValPheAspGLeuThrLeuGlyPhePro 186
DB 277 TACAAACAACCCCGTGGCGCTGTCGTGCACTCGTCGACCTCACCCCTCGGGTGGCG 336
QY 187 LeuTYrLeuLeuThrAsnIleSerGlyLYrLYrTYrGlyrYrAspPheAlaAsnHISpHeAsp 206
DB 337 CTGACTGGGGCTTACAGCCCTCAGGCGCGCGTACCCGGGTGCTGCCCTGCACCTTCAC 396
QY 207 PrometSerProIlePheAsnAspArgGluArgValGlnValLeuLeuSerAspPheGly 226
DB 337 CCTTACGGCCGATTTACACGACCGGAGGAGCCAGATTTCATCTCAGACCTCGGA 456
QY 227 LeuLeuAlaValPheTYrAlaIleLYrLeuLeuValAlaAlaLYrGlyAlaAlaTrpVal 246
DB 457 GTGCTGGCGGTGTCACTGCTGTGAGACCGTGTGCTGGGTCTGGGGTGG 516
QY 247 IleAsnMetTYrAlaIleProValLeuGlyValSerValPhePheValLeuIleThrTYr 266

DB 517 GTGCGGCTTACGGCGCTGCCCTGTACTGTGAACGTTGGCTGTCCTGATCCTAC 576
QY 267 LeuHISerIleThrHISLeuSerLeuProHISrYrAspSerThrGluTrpAsnTrpIleLYs 286
DB 577 CTGACGACACCCACCGCGCTGCGGCTGCTACACTGACGAGTGGAGTGGCTGGCG 636
QY 287 GlyAlaLeuSerTrpIleAspArgAspPheLYrPheLeuAsnArgValPheHISAspVal 306
DB 637 GGGGGCTGGCCACCATGACCGGACATCGCATCTCCAACCGCGGTTCACAAATC 696
QY 307 ThrHISerIleValLeuHISerIleLeuIleSerTYrIleProHISrYrHISAlaLYsGlu 326
DB 637 ACGACACGACGCTGGCCACCATCTATCTCCACGACCGGCTACACGATGAG 756
QY 327 AlaArgAspAlaIleLYrProValLeuGlyGluTYrTYrLYrLYrIleAspArgThrProIle 346
DB 757 GCCACCAAGGAGATCAACCCATCTCGGCGAGTACTACAGTTGACGCCACCCCGCTC 816
QY 347 PheLYrAlaMetTYrArgGluAlaLYsGluCYrIleTYrIleGluProAspGluAspSer 366
DB 817 GCCAAGGACATGCGCGGAGGCCAG-GAGTGCATCTACGTGAGCCGAG----- 866
QY 367 GluHISerGlyValPheTrpTYr 374
DB 867 GACCG-CAGGGGCTTCTGTGATC 889

RESULT 14

CK270183

LOCUS

DEFINITION

EST716261 potato abiotic stress cDNA library Solanum tuberosum cDNA

clone POACR59 5' end, mRNA sequence.

ACCESSION

CK270183

VERSION

CK270183.1 GI:39827161

KEYWORDS

EST.

SOURCE

Solanum tuberosum

ORGANISM

Solanum tuberosum (potato)

REFERENCE

1 (bases 1 to 963)

Authors

Buell, C.R., Hart, A., Zismann, V., Kazamycheva, S.A. and Baker, B.

Generation of ESTs from abiotic stressed potato tissue

Unpublished (2003)

Other ESTs: EST716262

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1..963
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POACR59"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TorA"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering applications. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions

and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Alignment Scores:

Pred. No.:	2.08e-105	Length:	963
Score:	955.00	Matches:	164
Percent Similarity:	80.15%	Conservative:	46
Best Local Similarity:	62.60%	Mismatches:	52
Query Match:	46.65%	Indels:	0
DB:	14	Gaps:	0

US-10-069-772-2 (1-377) x CK270183 (1-963)

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Oy 113 lLeaApApIleValGlyPheValLeuHisSerAlaLeuThrProTyPheSerTrp 132
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 6 GTTGATGACACCGGTGACTTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 65

Oy 133 lyeTySerHisArgAsnHisAlaAsnThrAsnSerLeuAspAsnArgValTyr 152
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 66 AATATATGATCGTCGCCACACTCCACACTGCTCCCTCGAGCGGTAGGCTCTT 125

Oy 153 lLeProLyArgLySerLyValLyIleTySerLyLeuLeuAsnProProGly 172
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 126 GTGCCCAAGCCAAATCTCAGCTCGATTCGATTCGAATCTTGAACATCCACAGC 185

Oy 173 ArgValPheThrLeuValPheArgLeuThrLeuGlyPheProLeuTyrLeuThrAsn 192
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 186 AGGGTCTCTCACTTACATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245

Oy 193 lLeSerGlyLySerGlyArgPheAlaAsnHisPheAspProMetSerProIlePhe 212
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 246 GTATGTGGACACCATACGACCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 305

Oy 213 AsnAspArgGluArgValGlnValLeuLeuSerAspPheGlyLeuLeuAlaValPheTyr 232
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 306 AACAACCGTGAAGGCTACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365

Oy 233 AlaIleLySerLeuValAlaAlaLyGlyAlaAlaTyrValIleAsnMetTyrAlaIle 252
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 366 CTGCTATACCGTATGCTTACGATTAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 425

Oy 253 ProValLeuGlyValSerValPhePheValLeuLeuThrTyrLeuHisHisThrIleLeu 272
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 426 CCCCTCTCTGCTGTAACGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485

Oy 273 SerLeuProHisTyrAspSerThrGluTyrAsnTyrIleLyGlyAlaLeuSerThrIle 292
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 486 TCATTGCCACACTACGATTCACCGAGGAGTGGCTTACGGAGCTTGGCAACCTGT 545

Oy 293 AspArgAspPheGlyPheLeuAsnArgValPheHisAspValThrHisThrHisIleLeu 312
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 546 GACAGAGCTATGAGGGTCTTAACAAGGCTTCCCAACATCAACGACATCACTCACTG 605

Oy 313 HisHisLeuIleSerTyrIleProHisTyrHisAlaLyGlyAlaAsnArgAlaIleLyS 332
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 606 CACCATCTGTTCTCAACCATGCACTACACGAGATGAGGCAACCAAGCAAGTCAAG 665

Oy 333 ProValLeuGlyGluTyrTyrIleLeuAspArgThrProIlePheLyAlaMetTyrArg 352
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 666 CCACTACTCGAGACTACTACCAATTCATGGAACCCGATTTTCAAGGCAATGTGAGG 725

Oy 353 GluAlaLyGluGlyValTyrIleGluProAspGluAspSerGluHisLyGlyValAlaPhe 372
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 726 GAAGCTAAAGAGTCTCTACGTCGAGAAAGACGAAATCATCTCAAGGCAAGGTCTTTC 785
  
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Oy 373 TrpTyr 374
 Db 786 TGTATC 791

RESULT 15

BU238570

LOCUS

DEFINITION

Accession

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

Source

1.1080
 /organism="Descurainia sophia"
 /mol_type="mRNA"
 /db_xref="taxon:89411"
 /clone="Db01.13f05"
 /tissue_type="leaf, stem"
 /dev_stage="1-month seedlings - 1 cm tall - 8 leaf"
 /clone_id="Db01.AAFC_ECORC_cold_stressed_Flixweed_seedlin
 gs"
 /note="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: Eco RI;
 Site 2: Xho I; Plants were grown for 1 month at 20C/16
 hrs light/day (average 8 leaves, 1 cm tall, weight
 0.02g/plant). Then they were exposed to 20C, 12 hrs
 light/day, for 1 week. Library prepared by C. Piche using
 Stratagene kit."

ORIGIN

Alignment Scores:

Pred. No.:	1.02e-104	Length:	1080
Score:	950.00	Matches:	164
Percent Similarity:	78.81%	Conservative:	48
Best Local Similarity:	60.97%	Mismatches:	57
Query Match:	46.41%	Indels:	0
DB:	13	Gaps:	0

US-10-069-772-2 (1-377) x BU238570 (1-1080)

```

Oy 107 PheSerAspTyrGlnLeuIleAspAspIleValGlyPheValLeuHisSerAlaLeuThr 126
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 152 TTTCAGCACTACCGGTGCTGATGACACAGTGGCTTATCTTCTCTCTCTCTCTCTCT 211

Oy 127 ThrProTyrPheSerTrpLySerHisArgAsnHisAlaAsnThrAsnSerLeu 146
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 212 GTCCCTACTCTCTTGGAAATACATGATCGCGGTCAACATTCACACAGGATTCCTC 271

Oy 147 AspAsnAspGluValTyrIleProLyArgLySerLyValLyIleTySerLyLeu 166
    ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
Db 272 GAAGAGATGAAGCTTGTCCCAAGCAAGATTCGATCAAGTGTAGGCAAAATAC 331

Oy 167 LeuAsnAsnProProGlyArgValPheThrLeuValPheArgLeuThrLeuGlyPhePro 186
  
```

